EvolDir

August 1, 2017

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.

—— / ——

Conferences

Aarhus EvolutionOfFear Dec4-5

Dear researchers and students,

We wish to draw your attention to our open call for abstracts to the international multidisciplinary conference FEAR: Brain, Behaviour, Society on 4-5 December 2017 held at the Aarhus Institute of Advanced Studies < http://aias.au.dk/au-opportunities-at-aias/ > (AIAS). This two-day conference will bring together leading international researchers from a variety of fields to present newest knowledge on the topic of 'FEAR'. The conference is organized in 5 multidisciplinary sessions, each incorporating contributions from several fields.

Sessions: "Evolution and ecology of fear." "Fear in learning and memory." "Fear in clinical practice". "Strategies of fear". "Innate and learned fear. Read the call and much more at the conference website:

http://aias.au.dk/events/aias-conference-fear-brain-behaviour-society/ DEADLINE FOR SUBMITTING ABSTRACTS is 14 August 2017.

We appreciate if you would share this email in your relevant networks and with departments who might be interested in participating.

We hope to hearing from you and seeing you at AIAS for an inspiring conference.

Best wishes,

Magnus KjÃrgaard, AIAS Fellow and Lena Bering

Lena Bering Communications officer, MA Mobile: +45 2182 9843 E-mail: lber@aias.au.dk Web: www.aias.au.dk Twitter: @AIAS_dk < https://twitter.com/AIAS_dk >

AIAS, Aarhus Institute of Advanced Studies Aarhus University Høegh-Guldbergs Gade 6B, building 1632 8000 Aarhus C Denmark

Jessica Livia Barker <jbarker@aias.au.dk>

DurhamU DiversityConservation Sep14-15 2

Update on discussion meeting: Conservation of Adaptive Potential and Functional Diversity

14-15 September 2017, Durham University, UK

Registration open through to the date of the meeting, or until capacity reached. https://www.dur.ac.uk/conference.booking/details/?id=761 Abstract registration for talks closed, but now extended for Posters to 1 September, 2017 Please send poster abstracts to: cap.meeting@durham.ac.uk

Invited speaker presentations:

Chris Jiggins (Cambridge, UK): The origins of diversity in Heliconius wing patterns: Re-use of ancient variants and its implications for conservation.

Paul Hohenlohe (Idaho, USA): Evaluating the potential for a genetic marker panel of susceptibility to Tasmanian devil facial tumor disease.

Victor Soria-Carrasco (Sheffield, UK): Genome-wide heterozygosity and fitness in a field experiment with stick-insects.

Simone Sommer (Ulm, Germany): Does low diversity influence MHC immune gene expression level in endangered wild cheetahs?

Oscar Gaggiotti (St. Andrews, UK): Understanding associations between species and genetic diversity requires the use of consistent measures of biodiversity across levels of organisation.

Barbara Mable (Glasgow, UK): Changing environments and genetic variation: does inbreeding compromise short-term adaptive potential?

Rasmus Nielsen (Berkeley, USA): Genetic rescue from inbreeding depression and its evolutionary limits.

Chris Funk (Colorado, USA): Incorporating information on adaptation into conservation policy: integrating genomics into Endangered Species Act decisions.

Bob Wayne (Los Angeles, USA): Measuring adaptive and deleterious variation in threatened populations and its importance for conservation management.

Rob Fleischer (Smithsonian, USA): Genomic and transcriptomic assessments of host response to invasive pathogens.

Mike Bruford (Cardiff, UK): Population Transcriptomics, demographic history and high altitude adaptation in a predatory bird.

Violeta Fuentes (EMBL-EBI, UK): The International Mouse Phenotyping Consortium (IMPC): a functional catalogue of the mammalian genome that informs conservation.

There will also be a series of shorter talks chosen from among the submitted abstracts and a poster session.

Meeting sponsored by Springer-Nature and the Genetics Society.

"HOELZEL, RUS A.R." <a.r.hoelzel@durham.ac.uk>

Entebbe Uganda SpeciationInAncientLakes Jul29-Aug3

Dear colleagues, this is the first announcement for the International Symposium "Speciation in Ancient Lakes 8" (SIAL 8) that will take place from 29 July 3 August, 2018 in Entebbe, Uganda. This will be the first time for SIAL to be held in Africa and we are looking forward to celebrate the 25th anniversary of SIAL at the shores of famous Lake Victoria.

Host and Local Organizers: Mbarara University of Science and Technology, Uganda (MUST) and Justus Liebig University Giessen, Germany (JLU).

The conference venue will be at Laico Lake Victoria: laicohotels.com/laico-lake-victoria.

Organizers: Christian Albrecht (Germany), Björn Stelbrink (Germany) & Casim Umba Tolo (Uganda).

Scientific committee: Andy Cohen (USA), Douglas Haffner (Canada), Koen Martens (Belgium), Frank Riedel (Germany), James Russel (USA), Walter Salzburger (Switzerland), Oleg Timoshkin (Russia), Risto Väinolä (Finland), Bert Van Bocxlaer (France), Erik Verheyen (Belgium), Thomas von Rintelen (Germany), Frank Wesselingh (The Netherlands) & Thomas Wilke (Germany). Anticipated topics: Forgotten, neglected and not so ancient lakes; Ancient lake conservation where are we?; Next generation approaches to ancient lake topics; Comparative ancient lake studies; African issues; New horizons in ancient lake research; Towards true speciation studies in ancient lakes; A look into the past: Paleolakes and deep drilling projects; Parasites and health issues & PRIDE evolution and biodiversity of Ponto-Caspian lake systems.

More detailed information on registration, fees etc. will be provided at the end of the year.

We would highly appreciate if you could participate and forward this announcement to anybody interested in any ancient lake-related issues.

Website: sial-online.org/conferences/sial8

Contact: Christian.Albrecht@allzool.bio.uni-giessen.de

Björn Stelbrink <Bjoern.Stelbrink@allzool.bio.uni-giessen.de>

Marseilles 21stEvolBiol Sep26-29 program

Dear All the definitive Program of the 21st evolutionary biology meeting at Marseilles is available on aeeb.fr It is still possible to submit abstract for poster presentation. best regards Pierre

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

Marseilles 21stEvolutionaryBiol Sep26-29 Program

Dear All the program of the

21st evolutionary biology meeting at Marseilles September 26-29 will be available July 5 : at aeeb.fr

Few spots are available for poster presentation

best regards

Pierre

pierre.pontarotti@univ-amu.fr

Philadelphia Sept16-17 MolecularEvolution

Deadline is approaching for Early Bird registration for a two-day symposium at Temple University in Philadelphia (September 16-17, 2017)

On the first day (Saturday, September 16th, 2017), we will have the "Molecular Evolution informs Medicine" symposium, where we will highlight the impact of molecular evolutionary studies on the understanding, diagnosis, and treatment of disease. There will be sessions on Mendelian (rare) diseases, Complex diseases, Cancers, and Infectious diseases. Invited and contributed presentations will be showcased. You can still apply for presenting posters and talks.

On the second day (Sunday, September 17th, 2017), we will have the "Molecular Evolutionary Genetics" event, where we will celebrate academic contributions of Dr. Masatoshi Nei. There will be many talks from Nei students and long-time associates on evolutionary genomics and molecular phylogenetics.

More than 30 speakers are already confirmed (see program)

Program information is listed at http://igem.temple.edu/mem/program To register, click on http://igem.temple.edu/mem/registration To present a contributed talk or poster, visit http://igem.temple.edu/mem/abstracts For all inquiries, please contact mailto:igemevents@temple.edu

Sudhir Kumar Temple University

"s.kumar@temple.edu" <s.kumar@temple.edu>

Seattle PaleoMacroevolution Oct22-25

Dear All,

We are convening a topical session entitled "Biodiversity dynamics in the face of environmental change: Integrating paleontological and neontological approaches to macroevolution" at the 2017 Geological Society of America conference. The conference will be held 22-25 October in Seattle, Washington. Our session (T51) will focus on how environmental changes have shaped Earth's biodiversity through geologic time and how these macroevolutionary relationships might be used to understand the responses of extant species to current and projected environmental conditions. Invited speakers include Samantha Price (University of California, Davis), Andy Purvis (Natural History Museum London), and Alejandro Ordonez (Queen's University).

If you have a current project that fits the scope of our session we hope that you will consider submitting an abstract for consideration. Abstract submission will be open around April 1st, 2017 and close on August 1. We are keenly interested in putting together a slate of talks that span a diversity of disciplinary approaches and including presenters from neontological backgrounds who are interested in incorporating paleontological perspectives into their research. For more information about the conference: https://www.geosociety.org/GSA/Events/Annual_Meeting/GSA/Events/gsa2017.aspx . If you have any questions please do not hesitate to contact us and if you know others who might be interested please consider forwarding this announcement to them.

Best wishes,

Shan Huang (Senckenberg Biodiversity and Climate Research Centre, shan.huang@senckenberg.de) Paul Harnik (Franklin & Marshall College,paul.harnik@fandm.edu) Lee Hsiang Liow (Natural History Museum & Centre for Ecological and Evolutionary Synthesis, University of Oslo,l.h.liow@ibv.uio.no)

Paul Harnik Department of Earth and Environment Franklin and Marshall College PO Box 3003 Lancaster, PA 17604-3003 Phone: 717-358-5946 Email: paul.harnik@fandm.edu

paul.harnik@fandm.edu

TempleU EvolutionaryBiol Dec16-17

We are pleased to announce the following molecular evolution meeting hosted at Temple University (Philadelphia, PA, USA) this fall. With support from BMC Evolutionary Biology, the meeting "Theory and Models Meet Data in Evolutionary Biology and Genomics" is a free meeting that will take place on Dec. 16-17, 2017. The first day of the meeting will have a set of invited seminars, followed by a poster session on the morning of the second day.

Registration is necessary (through the website, even if you are not presenting a poster). Registration will enable you to upload a poster title/abstract and enable us to gauge the number of participants.

Confirmed speakers to date include Arndt von Haeseler (Vienna), Corina Tarnita (Princeton), Kateryna Makova (Penn State), Jody Hey (Temple), and Blair Hedges (Temple). I hope to see you there. For more information, see the website (which will be updated as additional information becomes available): igem.temple.edu/bmceb/. Please join us.

David Liberles Temple University

David A Liberles <tuf77157@temple.edu>

Trondheim HoleNestingBirds Oct30-Nov2

The Centre for Biodiversity Dynamics (CBD) at the Norwegian University of Science and Technology (NTNU) is pleased to announce that the Eighth International Hole-Nesting Birds Conference will be held from October 30 to November 2, 2017 in Trondheim, Norway. The conference aims to bring together leading academic scientists, researchers, research scholars and citizen scientists to exchange and share their experiences in research involving all aspects of hole-nesting birds.

The scientific program will consist of eight sessions for keynote speakers and contributed speakers to present their latest research results, ideas and challenges within the fields of population dynamics, behaviour, physiology, life-history strategies, speciation, genetics, dispersal and movement, and climate change.

In addition, there will be poster session, and a discussion session that will allow attendees to discuss research plans and challenges in parallel group sessions. A central focus will be to improve communication and interactions between different groups working on hole-nesting birds across Europe.

Deadline for registration and submission of abstracts for talks and posters is August 31, 2017. The CBD will offer some grants that provide financial support for some of those who may wish to attend the conference. Those with financial need for travel and/or accommodation may apply at the registration.

For more information, please visit the conference website: https://www.ntnu.edu/hnb-conference We are looking forward to seeing you all at the conference!

The Eighth International Hole-Nesting Birds Conference organizing committee: Bernt-Erik SÃther Marcel E. Visser Ben C. Sheldon Stefan J.G. Vriend

Stefan Vriend <stefan.vriend@ntnu.no>

UdoAlgarve UmaPonteEntreMares Jan24-26

(for English version, scroll down)

Caros colegas, ÃÂ com prazer que vos convidamos a participar no Primeiro Congresso de Biologia Marinha dos PaÃses de Expressao Portuguesa - Uma Ponte entre Mares, a realizar na Universidade do Algarve, Faro, Portugal, de 24 a 26 Janeiro de 2018. Os PaÃses de Expressao Portuguesa sao caracterizado por elevada biodiversidade marinha e sistemas oceanograficos complexos, englobando uma vasta area geografica. Nesta primeira edicao, as tematicas a abordar inserem-se em tres eixos principais: * Recursos Marinhos * Biodiversidade * Conservacao e Biologia Evolutiva

Os objectivos deste congresso passam pela disseminacao do que se faz na area da ciencia marinha nos PaÃses de Expressao Portuguesa, bem como a construcao de uma rede internacional de investigadores e o estabelecimento duma plataforma internacional para divulgar resultados e promover colaborac0es. Solicitamos a mais ampla divulgacao possÃvel deste evento, salientando que: * Data limite para submissao de resumos - 15 de setembro 2017 * Notificacao de aceitacao de resumos - 30 de setembro 2017 * Inscricao a preco reduzido ate 30 de outubro 2017

Todas as informac0es encontram-se online na pagina web em https://goo.gl/ZfueSN e os pedidos de esclarecimento podem ser enviados via email para cbiomar2018@gmail.com. Com os melhores cumprimentos, Rita Castilho e Romina Henriques Comissao Organizadora

-----

Dear Colleagues,

It is with great pleasure that we invite you to participate in the First Marine Biology Congress of Portuguese Speaking Countries - A Bridge between Seas, to be held at University of Algarve, Faro, Portugal, from 24 to 26 of January 2018 (in Portuguese).

Portuguese Speaking Countries are characterized by high marine biodiversity and complex oceanographic systems, encompassing a large geographic area.

In this first edition, the themes will be centred around three main areas:

*Marine Resources

*Biodiversity

*Conservation and Evolutionary Biology

The main aims of this Congress are to disseminate current projects in marine sciences from Portuguese Speaking Countries, as well as to build an international network of researchers and to establish an international platform to divulge results and foster collaborations.

We would like to ask for this event to be divulge widely through your channels.

Important dates to retain:

*Deadline for submission of abstracts: 15^th September 2017

*Deadline for accepting abstracts: 30^th September 2017

*Reduced registration fee until 30^th October 2017

More details can be found at https://goo.gl/ZfueSN and all queries can be directed to cbiomar2018@gmail.com

Kind regards,

Rita Castilho

and

Romina Henriques,

Organizing Commitee

Romina Henriques <rohenriques@gmail.com>

UPittsburgh Evolution Sep9 AbstractDeadlineJul14

Join us at the first annual Three Rivers Evolution Event (TREE) conference!

The Three Rivers Evolutionary Event (TREE) aims to bring together researchers from Western Pennsylvania and the surrounding areas to share and discuss research in evolutionary biology.

When and Where:

Saturday, September 9th, 2017 at the University of Pittsburgh.

Registration and Call for Abstracts:

Researchers of all stages and institutional affiliations are welcome to present. Abstract submission ends July 14th; however, registration will continue until the conference is full. To register and/or submit an abstract for a talk or poster, please see our website: https://sites.google.com/view/tree2017/-conference-information/registration *There is no fee for registration*.

Theme:

We welcome researchers interested in all aspects of evolutionary biology. The research of attending members is expected to span viruses, microbes, plants, invertebrates and vertebrates, and include anthropology, epidemiology, developmental biology, ecology, zoology, theoretical, applied, urban ecology, paleontology, and many other specialized research areas. Research may be observational or experimental, taking place under natural or controlled conditions.

Accommodations:

We have reserved a block of rooms at the Wyndham Pittsburgh University Center for both Friday September 8 and Saturday September 9. The Wyndham is located next to both Alumni and Langley Hall, where the conference will take place. Either reserve online or call 412-682-6200 Monday thru Friday between 8AM and 6PM EST and mention that you are with the Three Rivers Evolution Event in order to receive the discounted rate of $145/night.

Find all of our conference information here: https://-sites.google.com/view/tree2017 The TREE organizing committee

Dr. Wynn Meyer

Dr. Caroline Turner

Dr. Martin Turcotte

Melissa Plakke

Sebastian Echeverri

Contact us at biotree2017@gmail.com

biotree2017@gmail.com

UPittsburgh Evolution Sep9 TravelAwards

*We are now offering a limited number of small ($200) travel awards to facilitate attendance by those with limited travel resources. *

We have therefore extended the abstract submission deadline for the Three Rivers Evolution Event (TREE) to August 1st. Please register, submit abstracts, and apply for awards here: https://sites.google.com/view/-tree2017 Already registered? You may revise your information until the deadline of August 1st, using the link provided on your initial registration, or use the registration link to apply for awards only by selecting 'yes' on the questions about having previously registered and submitted an abstract.

What is TREE?

The Three Rivers Evolution Event (TREE) aims to bring together researchers from Western Pennsylvania and the surrounding areas to share and discuss research in all aspects of evolutionary biology. The research of attending members is expected to span viruses, microbes, plants, invertebrates and vertebrates, and include ecology, anthropology, epidemiology, developmental biology, zoology, theoretical, applied, urban ecology, paleontology, and many other specialized research areas. Researchers of all stages, institutional affiliations, and related fields (including ecologists, anthropologists, paleontologists, and similar fields) are welcome to present.

When and Where:

Saturday, September 9th, 2017 at the University of Pittsburgh.

On behalf of the TREE organizing committee Sebastian Echeverri, Graduate Student, Department of Biological Sciences, University of Pittsburgh Wynn Meyer, Postdoctoral Associate, Department of Computational and Systems Biology, University of Pittsburgh Melissa Plakke, Graduate Student, Department of Biological Sciences, University of Pittsburgh Martin Turcotte, Assistant Professor, Department of Biological Sciences, University of Pittsburgh Caroline Turner, Postdoctoral Associate, Department of Microbiology and Molecular Genetics, University of Pittsburgh

Contact us at biotree2017@gmail.com

biotree2017@gmail.com

Waimea Hawaii AdaptiveRadiation Jul22-25 2018

SAVE THE DATE FOR AGA2018!

We are now planning the next AGA President's Symposium, to be held at the Hawaii Preparatory Academy in beautiful Waimea, Hawai'i.

AGA symposia focus on a single topic and last for 2-3 days. They are small, friendly gatherings, and provide wonderful opportunities for researchers and students to engage with one another and share their science. The 2018 meeting will examine processes at the early stages of adaptive radiation, focusing on phenomena such as admixture, priority effects, and repeated evolution. Invited speakers will discuss their research in such areas as

§The role of allopatry vs sympatry in fostering initial divergence

§Interplay between isolation and mixing in divergence and adaptation

§The role of plasticity in facilitating adaptation

§The role and extent of hybridization and admixture, and at what stage they occur in the evolutionary process

§Repeated evolution of similar forms

§Conditions that facilitate adaptive radiation, and their relative rates and extents. Details will be available soon on the AGA website: http://www.theaga.org Best wishes,

Rosemary Gillespie AGA President 2018 theaga@theaga.org

Anjanette Baker <theaga@theaga.org>

WoodsHoleMA MobileDNA Aug31-Sept2

Registration and abstract submission is underway for the 2017 meeting on Mobile Genetic Elements: https://mbl-web.ungerboeck.com/wri/wri_p1_display.aspx?oc=3D10&cc=3DMOBILEDNA

Abstract submission deadlines: August 1 for talk and fellowship consideration; August 12 for poster presentations.

The 2017 Meeting "Mobile Genetic Elements" in Woods Hole, MA, USA will take place from Thursday, August 31 to Saturday, September 2 at the Marine Biological Laboratory (MBL). The meeting will bring together experimental and computational scientists seeking to narrow the existing gap between the fast-paced discovery of transposable elements (TEs) in silico, stimulated by exponential growth of comparative evolutionary genomic and metagenomics studies, and a limited number of experimental models amenable to in vitro and in vivo studies of structural, mechanistic, and regulatory properties of TEs and their impact on their prokaryotic and eukaryotic hosts. Special emphasis will be placed on the evolutionary aspects of TE-host interactions.

The meeting continues the series of bi-annual regional meetings held since 2007 in Woods Hole and in Cold Spring Harbor, and now covers a broader swath of the continent, following the affiliation between the MBL and the University of Chicago. Participants from any interested US and international labs are welcome. Half of the talks will be selected from submitted abstracts. We especially encourage abstract submissions from young scientists at the graduate, postdoctoral, and early-stage investigator levels. Limited financial support towards registration costs will be made available to selected presenters, as well as to members of under-represented minority groups. To qualify for reduced registration, please provide a brief justification to either of the organizers by e-mail upon abstract submission.

We look forward to welcoming you on Cape Cod!

Meeting organizers: Bill Reznikoff breznikoff@mbl.edu Phoebe Rice price@uchicago.edu Irina Arkhipova iarkhipova@mbl.edu

"iarkhipova@mbl.edu" <iarkhipova@mbl.edu>

ZooSociety London AvianEvolution Sep14-15

Do you study how birds are adapting to a rapidly changing world? We would like to invite you to join us at Bird Sense 2017 where we will discuss the flexibility and evolutionary potential of birds to respond to shifts in their environments. We will explore how research on avian sensory ecology is revealing how birds perceive the varying landscapes in which they live, and how we might tackle challenges faced in welfare, conservation and anthropogenic change.

Birds inhabit every continent of the world and virtually all available ecological niches, from cities to the frozen tundra, from tropical rainforests to deserts, and from mountain ranges to the ocean. They eat fruits and insects; snails and worms; cereal grains and plants; mammals and fish; beeswax; sap, and nectar. But in our human-modified world birds face many challenges their ancestors did not: the glass fronts of tall buildings, wind turbines and power lines, artificial daylight that turns night to day; and noisy air traffic that moves faster than any of their natural predators. But birds also cause conflicts for humans: they can be major pests of crops and cause nuisance in urban settings. Some birds are thriving; others are struggling.

Together, can we formulate questions, instruments and analyses to capture how birds make sense of their changing word?

Registration is open at: https://www.zsl.org/science/-whats-on/bird-behaviour-in-a-changing-world-with-a-special-focus-on-bird-senses Poster abstracts being accepted until August 31st.

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

GradStudentPositions

AberystwythU CockleGenetics

The genetic basis of recurrent mass mortality in Welsh cockle fisheries Aberystwyth University, IBERS

Project ID: AU30004 Annual Stipend: 14,340 Application Deadline: 10th August 2017

Recurrent mass mortalities of cockles have had a serious impact upon the shellfish industry in Wales. The successful candidate will use molecular methods, field work and laboratory-based experiments to investigate genetic changes associated with recurrent mass mortalities in Welsh cockle populations. Knowledge Economy Skills Scholarships (KESS 2) is a pan-Wales higher level skills initiative led by Bangor University on behalf of the HE sector in Wales. It is part funded by the Welsh Government's European Social Fund (ESF) convergence programme for West Wales and the Valleys.

The successful candidate will need to be resident in the convergence area on registration, and must have the right to work in the region on qualification. The successful applicant should have a minimum of a 1st or good 2:1 in a relevant degree, and be available to take up the studentship by 1st October 2017. The project is part-funded by the European Social Fund (ESF) through the European Union's Convergence programme administered by the Welsh Government. KESS II PhD scholarships are collaborative awards with external partners. (Applicants need to only apply, they do not need to search for partners).

To apply, please submit the following to the Postgraduate Admissions Office (address below) by 10th August 2017 1. A completed Research Programme Application Form, two references. Application and reference forms may be downloaded from http://www.aber.ac.uk/en/postgrad/howtoapply/ 2. A completed KESS II Participant proposal form (put the reference number AU30004 in the top right hand box of the application form) and an up-to-date CV. KESS II application forms are available to download at the link below. http://www.aber.ac.uk/en/rbi/staff-students/knowledge-economy- skillsscholarships/currentscholarshipvacanciesandapplicationforms/ 3. A PhD proposal of up to 1,000 words where you expand on your experience and interests and describe why you are a good candidate for this research studentship. Please refer to the Project

Value of Award: A stipend of 14,340 (rising in accordance with inflation for the remaining two years). Each scholarship has an additional budget for travel, equipment/consumables and training to support your research. KESS II PhD Scholarship holders do not pay fees.

Length: Full-time for 3 years. (Theses must be submitted 6 months after the funded three year study period.)

Training: The achievement of a Postgraduate Skills Development Award (PSDA) is compulsory for each KESS II scholar (The PSDA is based on a 60 credit award, which is an additional award to the PhD).

Eligibility: To be eligible to apply for a KESS II award, you must be resident, upon starting the scholarship, in the Convergence Area of Wales and you must be able to take paid employment in the Convergence area on completion of the scholarship.

The Convergence Area means the following counties of Wales: Isle of Anglesey Gwynedd Conwy Denbighshire Ceredigion Carmarthenshire Pembrokeshire Swansea Neath Port Talbot Bridgend Rhondda Cynon Taff Caerphilly Torfaen For further student eligibility criteria related to the individual projects, please view the details of the individual project above.

Informal enquiries should be made to Dr Joe Ironside at jei@aber.ac.uk or 01970 621518

Address for applications: Postgraduate Admissions Office Recruitment & Admissions Student Welcome Centre Aberystwyth University Aberystwyth SY23 3FB

Quote Reference AU30004

Closing date for applications 10th August 2017

Un o'r 4 prifysgol uchaf yn y DU a'r orau yng Nghymru am fodlonrwydd myfyrwyr. (Arolwg Cenedlaethol y Myfyrwyr 2016) www.aber.ac.uk Top 4 UK university and best in Wales for student satisfaction (National Student Survey 2016) www.aber.ac.uk jei@aber.ac.uk

AuburnU InsectEvolution

Graduate position: Auburn.U.Insect.Evolution The Hardy Lab at Auburn University (http://hardylab.skullisland.info/) is recruiting one PhD student and one MS student to start in the spring semester of 2018. Each position will be supported fully through research assistantships, including a competitive stipend and tuition waiver.

The PhD student will work on an NSF-funded project to study the species diversification of aphids in North America. This will entail phylogeny estimation from genomic data, niche modeling from geospatial data, and comparative statistical analyses. Background in any of these areas would be great, but the only thing that is required is an interest in the evolution and biodiversity of insects.

The MS student will study the evolutionary genetics of host-use adaptation in scale insects. This will entail a greenhouse-based selection experiment coupled with transcriptome analyses. No prior knowledge of these methods is required - just an interest in how plant-eating insects evolve (or in how gene expression changes with niche breadth). The experiments have been designed. What's needed is an enterprising student to do them.

If you are interested (or are interested enough to want more information) please send an email to Nate Hardy (n8@auburn.edu) with your CV and few words about yourself. Applicants must meet requirements of admission to the Auburn Graduate School (http://-www.grad.auburn.edu/). There is a rolling admission system. These vacancies will stay open until filled.

Nate HardyDepartment of Entomology and Plant PathologyAuburn University301 Funchess HallAuburn, AL 36849phone: 334 844-1171skype: llln8lll

n8@auburn.edu

llln8lll@yahoo.com

AustralianNatlU CoralEvoDevo

PhD opportunities in sponge and coral EcoEvoDevo

Multiple PhD opportunities in EcoEvoDevo of sponges and corals are available at the Research School of Biology, Australian National University. The projects are related to regeneration, biomineralization, evolution of developmental gene regulatory networks and microbiomes, see http://biology.anu.edu.au/-research/labs/adamska-lab-genomic-and-evolutionary-basis-animal-development for details. All projects provide exciting and varied research experience by combining cell and molecular biology approaches with bioinformatics and field work in temperate and tropical marine environments. The students will be based in the Adamska lab at the ANU, and will be involved in local, national and international collaborations. The successful candidates will commence the doctoral program in late 2017 or early 2018.

The positions come with substantial research and travel budgets, and the candidates are encouraged to apply for scholarships to fund personal living expenses. The ANU is administering domestic and international PhD scholarships ($26,682 per annum for a period of 3 years with a possibility of a 6-month extension). Scholarship application deadlines are 31st of August (international applicants) and 31st of October (domestic applicants). Queries regarding scholarship matters can be directed to rsb.studentadmin@anu.edu.au. Shortlisted candidates will receive support in preparing the scholarship applications, with a possibility of internal funding for "near miss" applicants.

Interested candidates should contact Maja Adamska maja.adamska@anu.edu.au by July 31st 2017, providing current CV, 500-1000 words description of research interest including preference for one or more of the listed projects, and contact details for two academic references.

Maja Adamska <maja.adamska@anu.edu.au>

BangorU Fish eDNA

FISHeEST - Using fish environmental DNA to assess the biodiversity and ecological status of estuarine ecosystems. PhD Annual Stipend: pounds 14, 340

Project Description: Biodiversity is an essential component of aquatic ecosystems, contributing to ecosystem function/services and used to monitor ecosystem health, both from a regulatory perspective and for nature conservation. In Europe, legislative drivers exist that require member states to monitor all water body types, including socio-economically important estuaries. The Water Framework Directive and similar future legislation use a range of biological quality indicators, including fish as key indicator groups to measure ecological status. Nevertheless, fish communities are highly challenging to assess, whether the focus is regulatory biomonitoring, invasive non-native, or rare species. A variety of netting and other monitoring methods exist, but all suffer from drawbacks including intensive personnel requirements, taxonomic or ecological bias, logistical challenges and in some cases, mortality of fish.

Macrobial environmental DNA (eDNA) is DNA isolated directly from an environmental sample (e.g. sediment, or water) and in recent years, a growing number of studies have shown that the analysis of fish eDNA provides assessment of fish communities that are as good as, or better than traditional approaches. Moreover, eDNA techniques offer a number of advantages over conventional techniques including reduced sampling cost, lower sampling bias, improved detection of a wide range of taxa and the increased availability of relatively cheap DNA analysis techniques. While substantial progress has been made in freshwater ecosystems, the proposed project here will take the development and deployment of this tool a stage further into more challenging, but ecologically critical estuarine habitats.

The aim of this fully funded studentship is the development and testing of an operational eDNA method for monitoring fish communities in estuaries in relation to biomonitoring, non-native invasive and rare species.

Examples of specific objectives would include: 1. Identification and development of a suitable laboratory methods 2. Working with NRW sampling staff, test field sampling techniques to (i) deliver a cost-effective balance between the number of samples collected and acceptable estimates of key metrics and / or detection thresholds; (ii) provide adequate sampling of biotopes and estuarine zones to deliver appropriate representation of taxonomic groups; (iii) identify the most appropriate seasons and / or conditions for data collection; 3. Compare eDNA data with results from conventionally collected surveys in order to identify strengths and weaknesses of the various techniques. 4. Evaluate the effectiveness of the tool for monitoring Habitats Directive and other species of biodiversity importance in estuaries.

Training will be provided in aquatic eDNA molecular ecology (DNA extraction, PCR and meta-barcoding), field sampling and monitoring, bioinformatics, population genetics, statistical modelling and scientific communication. Field work will take place around the Welsh coastline, potentially extending into the rest of the UK. The successful candidate will become a highly skilled, interdisciplinary graduate working at the interface between molecular ecology, environmental science and legislation, hosted by the vibrant Molecular Ecology and Fisheries Genetics Laboratory (http://mefgl.bangor.ac.uk/ with Profs. Simon Creer, Gary Carvalho and Dr. Mathew Seymour) and Natural Resources Wales (Dr. Tristan Hatton-Ellis), with co-supervision via Prof. Stefano Mariani (Salford) and Dr. Lori Handley (Hull).

Applicants should hold a minimum of a UK Honours Degree at 2:1 level or equivalent in subjects such as Biology, Ecology, Environmental or Natural Sciences, with a strong motivation to study eDNA biodiversity from a genetic and organismal perspective. Eligibility is restricted to UK and EU nationals only and candidates with Masters qualifications and First Class Degrees are particularly welcome to apply. If you are interested in applying, we would recommend contacting Prof. Simon Creer as early as possible (http://mefgl.bangor.ac.uk/staff/-si.php; s.creer@bangor.ac.uk; Twitter @spideycreer) and he will be on hand to assist with any questions related to the project and life in the group.

Applications will be achieved via a Motivation Letter, CV (including reference contact details), sent to s.creer@bangor.ac.uk (cc to Dr Penny Dowdney: p.j.dowdney@bangor.ac.uk) including 'FISHeEST Application' in the subject header.

Closing date for applications: 20th August 2017 with interviews predicted to take place in the first week of September and the studentship to start 1st October.

Where is Bangor? Bangor is located in North West Wales, UK, situated 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

---

Bergen MiteSystematics

A very good PhD grant available for a promising student in systematics of mites. Although the outreach part has a Nordic perspective, the taxonomic part is global, primarily Holarctic. The taxonomic and phylogenetic work integrates morphology and molecular data.

https://www.jobbnorge.no/en/available-jobs/job/-140272/phd-fellow-in-bio systematics-acarology-at-the-university-museum-of-bergen

Best regards,

Bjarte Jordal, PhD

Head of Department

Associate Professor in Systematic Entomology

The Natural History Museum

University Museum of Bergen

P.B. 7800, NO-5020 Bergen

Webpage: Bjarte Jordal

Research Group: "Phylogenetic Systematics and Evolution"

Associate Editor, BMC Evolutionary Biology

Subject Editor, Insect Systematics and Diversity

Bjarte Henry Jordal <Bjarte.Jordal@uib.no>

Berlin EvolutionOfVirulence

The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) is the largest freshwater ecology research institute in Germany. It is a member of the Forschungsverbund Berlin e.V. and the Leibniz-Association (www.wgl.de). The FVB manages 8 large research institutes in Berlin that have close links to all three universities in the German capital. IGB offers excellent laboratory and field facilities for interdisciplinary research, large-scale experimental facilities, and long-term research programs and data sets. IGB invites applications for a PhD position in Evolutionary Biology: "The Evolution of Virulence under Conditions of Frequent Multiple Infections" The position is available from 1st January 2018 (or November/December 2017) and limited to 3 years.

Project Description

Interactions between multiple parasite species (infecting the same host) can affect the evolutionary trajectory of virulence, with important ecological and epidemiological consequences. The goal of the proposed work is to elucidate implications of multiple infections on the evolution of (parasite) virulence. The successful candidate will use a combination of experimental evolution and field approaches to generate new and refined predictions regarding the virulence of parasites that spread into new habitats, where they encounter co-infecting parasites. He/she will use a model system consisting of the crustacean Daphnia and their microparasites. The proposed research is a collaboration between German and Israeli scientific teams: Prof. Justyna Wolinska from IGB and Freie Universität Berlin (http://www.igb-berlin.de/en/profile/justyna-wolinska) and Dr. Frida Ben-Ami from Tel Aviv University (http://fridaslab.weebly.com/), financed by the German Science Foundation (DFG). The position is mainly based in Berlin; however, a two-month research stay at the Tel Aviv University is planned. Funding for attending national/international conferences is available.

Duties and responsibilities

* laboratory experiments * field work (investigating geographical patterns of co-infections) * advance statistical analyses of experimental (life history and genomic) and field (environmental and genetic) data

Requirements

* MSc degree in biology, bioinformatics or related field * strong background in evolutionary biology, population genetics or ecology * hands-on experience with experimental work * experience in molecular or genomic research would be an advantage

* excellent analytical skills and very good knowledge in statistics * a basic knowledge in bioinformatics or programming would be advantageous * excellent communication and writing skills in English * good work ethic * creative thinking

Salary is paid according to the TVöD (65% position). In keeping with the IGB's policy regarding gender equality, female applicants are particularly encouraged. Severely disabled applicants with equal qualification and aptitude are given preferential consideration.

Enquiries or questions should be directed to Prof. Justyna Wolinska (wolinska@igb-berlin.de).

Please upload complete application documents as a single pdf-file including CV, a letter of motivation, copies of relevant degrees and contact details of three referees no later than 22nd August 2017 via the IGB's (http://www.igb-berlin.de/en/jobs) online job-application facility (button "Apply online").

Justyna Wolinska

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

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

Phone: +49 (0)30 64181 686; Fax: +49 (0)30 64181 682; email: wolinska@igb-berlin.de http://www.igb-berlin.de/en/profile/justyna-wolinska-0 http://www.igb-berlin.de/en/disease-evolutionary-ecology Justyna Wolinska <wolinska@igb-berlin.de>

GhentU EvolutionGastropods

PhD position_Ghent University_snail parasites.

Topic: Unravelling the role of Bulinus gastropods as intermediate hosts in Schistosoma disease transmission with state-of-the-art molecular techniques

Duration: 3 years with a possible extension

Start: October 2017

Vacancy description:

We are pleased to announce a PhD fellowship for a highly motivated, enthusiastic and independent person with a keen interest in evolutionary parasitology and the ecological context of snail-parasite-human disease transmission in aquatic habitats in Africa. The project is conceptualized in molecular ecology with a focus on the intermediate snail host rather than in a biomedical context. Experience with molecular biology and bioinformatics, and enthusiasm to participate in fieldwork at transmission sites in Africa are plus-points.

Project background:

Snail-borne diseases affect more than 300 million people worldwide but also lead to economic losses and mortality in livestock. Especially developing countries are affected but due to globalization and climate change the distribution of snail-borne diseases is changing. Because the distribution of the intermediate snail host species determines where snail-borne diseases occur, updated information on snail distribution and their role in parasite transmission is highly needed. Acquiring these insights is however hampered by taxonomic confusion in the group of host snails and lack of associated ecological and parasitological data.

The aim of this PhD project is to develop an efficient, sensitive and robust monitoring tool based on next-generation DNA-sequencing technology that will simultaneously detect the snail and associated parasite DNA. Applied to new and existing museum collections this will allow to 1) accurately define the complete helminth fauna of each snail species and their role in disease transmission; 2) combine genetics with morphology to improve snail identification in the field; and 3) use snail and parasite genetic data for comparative phylogeography.

Setting and requirements:

The project is funded by the Federal Science Policy of Belgium and will be developed in an inter-institutional collaboration between the Royal Museum for Central Africa (Tervuren, Belgium; Dr. Tine Huyse), Ghent University (Ghent, Belgium; Limnology Unit, Prof. D. Verschuren, Dr. Bert Van Bocxlaer), and the Justus-Liebig University (Giessen, Germany; Prof. Christian Albrecht). Ghent University is the diploma-granting institution for this PhD project. Training in the doctoral school will take place at Ghent University, whereas project-related tasks will be primarily developed at the Royal Museum for Central Africa (Tervuren); language is English and Dutch. Applicants should hold a master degree in biology, bio-engineering or biotechnology to be allowed into the PhD program at Ghent University. Master students who are graduating during the summer of 2017 are also welcome to apply.

More information on studying at Ghent University and living in Ghent can be found on the Ghent University webpage: (https://www.ugent.be/en/ghentuniv; https://www.ugent.be/en/staff).

Interested?

To apply for this position, please send the following information to tine.huyse@africamuseum.be: 1) a complete CV, including grades of the last completed year; 2) a short description of past research accomplishments and motivation to take on this project; and 3) the names and e-mail addresses of at least 2 references. To receive full consideration, please send your application by the 10^thof August. (Late applications will be considered until the vacancy is filled.) Interviews will take place in the week of the 4^th of September 2017.

More information: Informal inquiries can be sent to tine.huyse@africamuseum.be (http://www.africamuseum.be/museum/home/contact/staff/HUYSE_Tine) or Bert.VanBocxlaer@UGent.be (http://www.ugent.be/we/biology/en/research/limnology/bertvb.htm)

Tine Huyse Royal Museum for Central Africa Department of Biology Leuvensesteenweg 13 3080 Tervuren- BELGIUM TEL: 0032 (0)2 769 53 72 EMAIL: tine.huyse@africamuseum.be http://www.africamuseum.be/museum/renovation/sponsoring/index_html Tine Huyse <tine.huyse@kuleuven.be>

HumboldtU Berlin EvolutionaryGenomics

The Garfield Lab for Evolutionary Biology at the IRI for Life Sciences/Humboldt University of Berlin has an opening for a PhD student in the field of evolutionary genomics/developmental biology.

Our group focuses on understanding the evolution of developmental gene expression from a population genetics perspective. We are currently recruiting for a project aimed at understanding how gene regulatory networks evolve between closely related species of sea urchin using a combination of 'omics' methods, including single-cell sequencing, and computational analyses of DNA sequence evolution. The position offers training primarily in experimental biology, though students interested in computational and analytical methods are also encouraged to apply.

PhD candidates will have a Masters degree in Molecular Biology, Evolution, Genetics, or a related field and an interest in understanding evolutionary processes as well as the molecular mechanisms underlying development. Previous experience with modern genomics methods (e.g. high-throughput sequencing) is encouraged but not required. Strong communication and organisational skills are a must. Recruitment is through the IRI Graduate School, which offers numerous training opportunities as well as close interactions with our partner institutions (Charité and the Max Delbrück Center for Molecular Medicine) and collaborators at the nearby Museum of Natural History.

We offer a competitive salary according to German E13 TVöD/Bund (65%). Contracts are 3 years in duration with the possibility of extension. While the working language of the laboratory is English, some knowledge of German (or a willingness to learn) is encouraged. The position requires a flexible commitment of ˜3 hours of teaching per week during the academic semester.

Applications, including a motivation letter, CV, and contact details for two academic references should be sent as a single PDF to info@garfieldlab.org. Applications will be considered until the position is filled with the successful candidate starting in late August (exact starting date is flexible).

For more information, please visit our website at www.garfieldlab.org . David Garfield, PhD

Research Group Leader IRI Life Sciences Humboldt-Universität zu Berlin Philippstr. 13 (Haus 18, Rm. 224) 10115 Berlin, Germany

Office: +49 (0)30 2093-92382 Fax: +49 (0)30 2093-47908 info: www.garfieldlab.org email: david.garfield@hu-berlin.de

David Garfield <david.garfield@hu-berlin.de>

INRA France TickEndosymbioticBacteria

Graduate position: WHERE. INRA_FRANCE WHAT. MidichloriaTickInteractions

Ph.D. position: Role of Midichloria mitochondrii, endosymbiotic bacterium of the tick Ixodes ricinus, in the development of its host Supervisors Dr Olivier PLANTARD (France, Nantes, UMR INRA-Oniris BIOEPAR) Dr Davide SASSERA (Italy, Pavia, Dipartimento di Biologia e Biotecnologie, Universita degli Studi di Pavia)

Scientific background In temperate areas of the northern hemisphere, ticks are the most important group of disease vectors. In Europe, Ixodes ricinus, the most common tick species, transmits numerous pathogens including those responsible for Lyme diseases and Tick-Borne Encephalitis. Vector control against ticks is essentially based on the use of acarides, but its applicability is reduced for I. ricinus, due to its widespread ecological distribution and its broad host range, as this species is capable to feed on numerous vertebrates from both wildlife and domestic fauna. This tick species harbours an intracellular bacterium, Midichloria mitochondrii, vertically transmitted and present with 100% prevalence of females in natural populations. M. mitochondrii is unique due to its capability to invade host mitochondria, but its role in the host physiology is still unknown.

Project description The present Ph.D. project is focused on understanding the role of M. mitochondrii in the biology of I. ricinus, towards the development of a vector control method based on antisymbiotic control.

The first part of the thesis will aim to evaluate the effects of Midichloria on I. ricinus fitness by the comparison of several tick life-history traits between a wild strain (harbouring Midichloria) versus an aposymbiotic strain (obtained after antibiotic treatment). A dual transcriptomic approach will also be conducted to identify differentially expressed genes from both the bacteria and the ticks. A vaccination approach, targeting specific Midichloria proteins will be conducted on rabbits and their effect on tick engorgement will be assessed. Skills in evolutionary biology, parasitology, microbiology, molecular biology and bioinformatics are desiderable and will be positively evaluated for this Ph.D. project. Fluency in English is required for the proposed position, as it is the shared language between the two labs involved in this project. Fluency in French and/or in Italian will be helpful but not mandatory.

Funding notes This Ph.D. grant is funded for 3 years by the call of project Vinci of the Universite Franco-Italienne (https://www.universite-franco-italienne.org/) and will take place both in France (Nantes; UMR INRA-Oniris BioEpAR for 24 months ; https://www6.angers-nantes.inra.fr/bioepar/-L-unite2/Groupes-fonctionnel s/TiBoDi) and in Italy (University of Pavia; 12 months ; http://-sasseralab.unipv.it/). The annual gross amount is 21 096 euro.

Applicants should send a CV, a cover letter summarising past experience and interest in the project, and two reference letters to olivier.plantard@inra.fr and davide.sassera@unipv.it. The dead line is the 8th of september 2017. Applicants will be contacted to schedule an interview that will take place in september. The project starting date is flexible, from 1st October to the end of 2017.

References: Ninio, C., O. Plantard et al. (2015). “Antibiotic treatment of the hard tick Ixodes ricinus: Influence on Midichloria mitochondrii load following blood meal. ” Ticks and Tick-Borne Diseases, 6 (5), 653-657.

Sassera, D., N. Lo et al. (2006). “’Candidatus Midichloria mitochondrii’, an endosymbiont of the tick Ixodes ricinus with a unique intramitochondrial lifestyle.” International Journal of Systematic and Evolutionary Microbiology 56(11): 2535-40.

Sassera, D., N. Lo, et al. (2011). “Phylogenomic evidence for the presence of a flagellum and cbb3 oxidase in the free-living mitochondrial ancestor.” Molecular Biology and Evolution 28(12): 3285-3296.

Sassera, D., S. Epis, et al. (2013). “Microbial symbiosis and the control of vector borne pathogens in tsetse flies, human lice, and triatomine bugs.” Pathogens and Global Health 107(6): 285-292.

Olivier Plantard <olivier.plantard@oniris-nantes.fr>

KULeuven Belgium ComputationalPhylogenetics

The Laboratory of Clinical and Epidemiological Virology (Rega Institute - KU Leuven, Belgium; https://rega.kuleuven.be/cev/ecv/) is looking for a motivated PhD student to perform research in a multidisciplinary team. This constitutes an exciting opportunity to work on computational and statistical methods in molecular evolution with applications in infectious diseases.

Research group

The Evolutionary and Computational Virology Laboratory at the Division of Clinical and Epidemiological Virology (Rega Institute, KU Leuven) focuses on the evolutionary processes that shape viral genetic diversity. This encompasses large-scale epidemic processes, such as population growth and spatial dispersal (a popular topic in phylogeographic and phylodynamics research), as well as small-scale transmission histories and within-host evolutionary processes, including adaptation and recombination. It is our objective to gain better insights into these evolutionary and population genetic processes and to clarify how they relate to epidemic and disease dynamics. To this aim we plan to focus on statistical and computational developments to analyze the increasing amount of data brought about by massive sequencing studies, mainly in a framework of Bayesian phylogenetic inference, for which our research group holds a strong track record. We also aim to explore the applicability of novel models and statistical inference tools, developed as part of our research, in different fields of research.

Project

This project focuses on new developments in a popular Bayesian phylogenetic inference framework (BEAST: https://github.com/beast-dev/beast-mcmc) and its applications to important evolutionary problems, with a particular focus on infectious diseases.

The project involves the development of an integrated web system and database that allows users to register, upload and retrieve sequence data to and from the database. Each user will be able to determine the sharing policy for the data he/she has provided. Such a system should be easily distributed so that other research groups can deploy it on their own server(s) and put it to use without technical interventions. Further, this system will interface with the BEAST software package to analyze the sequence data in an efficient manner. The candidate is expected to design and implement such a system and determine an appropriate strategy to properly distribute the developed system as an easily installed/deployed software package.

Additionally, multiple parallelization ideas will be implemented in the BEAST software package. BEAST is mostly written in Java, with its high-performance computational library, known as BEAGLE, being implemented in C/C++. The goal is to develop and implement efficient parallelization strategies from both a computational and a statistical perspective. The computational aspect entails the implementation of popular routines typically used in computer architecture, whereas the statistical aspect entails the development and adaptation of novel transition kernels in a Bayesian phylogenetic inference framework.

Profile

The candidate for this PhD position should have a strong quantitative background, and preferably holds a master’s degree in computer science / informatics (or equivalent through experience), with an interest in statistics/mathematics and (bio)informatics. The candidate hence needs to be experienced in an object-oriented programming language such as Java or C/C++. The candidate should be sufficiently proficient in English, motivated to work in a team and publish his/her findings, and willing to travel.

Offer

The candidate will be able to perform research in a dynamic and multidisciplinary team (computer scientists, data analysts and evolutionary biologists), housed in the brand new facilities of the Rega institute at the University hospital campus, and guided by prolific supervisors. KU Leuven is one of the top universities in Europe and leads the Reuters ranking of Europe's most innovative universities for the second year in a row.

The targeted starting date will be October 1st 2017 and the candidate should obtain his/her master's degree by that time. All applicants are expected to submit a motivation letter, overview of their study results and two references (with their contact details).

Additional information, as well as the application procedure, can be found here: https://icts.kuleuven.be/apps/jobsite/vacatures/54182826 Please use the university's job portal when applying for this position. For more information, contact Guy Baele (guy.baele@kuleuven.be) or Philippe Lemey (philippe.lemey@kuleuven.be).

The closing date for completed applications is the 31st of July 2017. Interviews will be held shortly thereafter.

– Guy Baele, PhD.

— / —

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

---

LMU Munich SpongeGenomics SpeciesIdentification

PhD position in genomics of species identification in sponges (Phylum Porifera)

We invite applications for a 36-month PhD position in the project SpongeTaxonOMICs funded by the German Research Foundation (Deutsche Forschungsgemeinschaft, DFG) within the framework of the Priority Program SPP 1991 Taxon-OMICS. The project is located at the Department of Earth- and Environmental Sciences (Chair of Paleontology and Geobiology) and the GeoBio-CenterLMU of the Ludwig-Maximilians-Universität (LMU) München.

Sponges (Porifera) are difficult to identify and DNA barcoding does not reliably work for all lineages. In this project, we will develop a novel species identification assay based on target enrichment and Illumina sequencing. The project involves shallow sequencing of several Tethya genomes and comparisons against our recently sequenced Tethya wilhelma genome to identify informative loci for species identification. The developed assay will be verified against a test set of Tethya species and by museomics, testing samples of family Tethyidae primarily from the Queensland Museum (Brisbane, Australia) but also from other resources. The developed assay will subsequently be expanded to broader taxonomic scope. The Sponge Barcoding Database (www.spongebarcoding.org) will be further developed and adapted to accommodate new data for species identification.

We are seeking a highly motivated applicant, ideally trained in evolutionary bioinformatics, with excellent and demonstrated bioinformatics expertise as well as a sound background in biology, who is willing to tackle the challenging task of working with the genomes of non-bilaterian animals. Laboratory skills are not necessary but will be considered a plus. The successful candidate will also contribute to the lab's ongoing genome sequencing efforts and contribute to expand the bioinformatic tools available in the lab. High-performance computing is available in the lab (LINUX cluster, Galaxy Server) as well as through the Leibniz Rechenzentrum (www.lrz.de).

The successful candidate will join an international and dynamic lab focussing on the geobiology and evolution of marine animals. More information about the lab can be found at www.geobiology.eu. There will also be ample opportunity to interact with PhD students and faculty of the new Horizon 2020 Marie SkÂ^{3}odowska-Curie Actions Innovative Training Network (ITN) "Comparative Genomics of Non-Model Invertebrates" (IGNITE; www.itn-ignite.eu), that starts on January 01, 2018.

Requirements: M.Sc. in Biology, Bioinformatics or a related field; demonstrated expertise and understanding of molecular evolution including phylogenetic methods, expertise in processing and analysing next generation sequencing data; excellent English language skills; programming skills (e.g., in commonly used bioinformatic languages such Perl, Python, R, etc.) and experience with LINUX. Evidence of this expertise must be provided. German language skills are not necessary, the working language of the group is English. The position is available for 36 months, and will be paid according to the German salary scheme TV-L E13 (65%).

Application: Send application including letter of motivation, CV, if available PDFs of your most significant publications, and contact details of 2 referees in a single PDF (only) by email to geobiologie@geo.lmu.de. Informal enquiries may be directed to Professor Gert Wörheide through the same email address. Application deadline is 15 September 2017.

The Department of Earth- and Environmental Sciences, Palaeontology & Geobiology of the Ludwig-Maximilians-Universität Munich offers an excellent multidisciplinary research environment, one of its particular strength being due to the close interaction between Geosciences and the Faculty of Biology in the framework of the GeoBioCenterLMU (http://www.geobio-center.uni-muenchen.de).

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 been repeatedly voted Germany's most livable city and is among the Top 5 most livable cities worldwide. The LMU Munich is an Equal Opportunity/Affirmative Action Employer and has an affirmative action policy for the disabled.

Please note: Education is free in Germany and PhD students do not have to pay student fees, except a nominal registration fee of about 110 euro per semester, which covers some costs for public transportation in Munich.

– Prof. Dr. Gert Wörheide Department of Earth and Environmental Sciences, Division of Paleontology & Geobiology & GeoBio-CenterLMU Ludwig-Maximilians-Universität München, and

— / —

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

MacquarieU 2 AvianEvolution

Apply by 21st July

We are pleased to announce two opportunities available for a start from mid to late 2017

1: Adapting to a foreign climate: the reproductive ecology of the house sparrow in Australia The house sparrow (Passer domesticus) was introduced into Australia in the 1860's and has since become well established across a broad range of climates in both countries. This project will take advantage of this 'experimental' introduction to focus on behavioural and physiological adaptations to different climates through a field-based comparative approach. This research will complement our existing work on related questions in endemic Australian species and will provide insight into the capacity of avian species to adapt to changing climates. This project will involve periods of field-work in Broken Hill, Armidale and Hobart in Australia, along with a range of behavioural, molecular and physiological assays. The project will involve collaboration with other groups in Australia and the US.

2: The challenge of growing in a hot climate (in the zebra finch) In recent years we have characterised the very hot conditions in which zebra finches are raised (with nests regularly exceeding 40 degrees (C)), as well as identifying adverse effects of these conditions on embryonic development, offspring growth, and adult sperm. This project will investigate the adaptations that this iconic and well-studied species has to deal with the extreme climate in which it lives. The project will take a variety of approaches including behavioural work, and assays of metabolism and physiology. The research will combine fieldwork and laboratory work. The project will be run in collaboration with Dr Christine Cooper (Curtin University, Western Australia), Prof. Pierre Deviche (Arizona State University, US), and Prof. Pat Monaghan (Glasgow, UK).

Both of these projects are supported by ARC Discovery Project funds.

Application The Department of Biological Sciences at Macquarie University is a vibrant environment which offers excellent support to postgraduate students. A Macquarie University Excellence in Research Scholarship has already been assigned to one of these projects, but there are other scholarship opportunities available to suitably competitive candidates. International candidates are welcome to apply for any of the projects listed above.

The MQRES full-time stipend rate is $26,682 pa tax exempt for 3 years (indexed annually). In addition to external grant support for projects, there is additional internal funding (up to $17,000) available to cover direct research expenses and conference travel.

Applicants should have a research-based MSc, or Honours in a related discipline, and additional relevant research experience. For these projects an ability to work in remote and harsh conditions as well as experience in capturing and handling animals is desirable. A driving licence is required for all projects.

Applications should include 1) your CV, 2) a brief statement of your reasons for applying (max. 500 words) and the project you are applying to work on, 3) contact details of two academic referees, 4) your nationality (for scholarship eligibility purposes). Applications should be submitted electronically as a single PDF file.

Applications for these positions (and any initial enquiries) should be emailed by 21st July 2017 to: simon.griffith@mq.edu.au Prof. Simon Griffith, Dept. of Biological Sciences, Macquarie University, Sydney, NSW 2109, Australia

simon.griffith@mq.edu.au

MasseyU PlantEvolGenetics

Position: A PhD scholarship is available to study in the broad field of Plant Evolutionary Genetics

We are seeking an enthusiastic individual for a PhD scholarship in the field of Plant Evolutionary Genetics. Research may be in the areas of population genetics, quantitative genetics, molecular evolution, genetic pathway evolution, polyploidy, speciation, or related. All projects will likely have a strong bioinformatics component. Ultimately, the project, training, and supervisor team will be tailored to suit the interests of the successful candidate. This position will be funded (including fees) by a Massey University Doctoral Scholarship (http://www.massey.ac.nz/massey/admission/scholarships-bursaries-awards /doctorate-scholarships/doctorate-scholarships_home.cfm). Successul applicants will have a BSc Honors, MSc or equivalent in Botany, Genetics, Molecular Biology or a similar field.

The position is available in the lab of Dr Vaughan Symonds (http://vvsymonds.massey.ac.nz) at Massey University in Palmerston North, New Zealand. The lab group has diverse interests that include population genetics, molecular evolution, quantitative genetics, and conservation. The supervisor team will be assembled to best support the successful candidate and project. To apply for the position, please send the following to v.v.symonds@massey.ac.nz with "PhD Scholarship" as the subject:

(1) letter of interest (2) CV (3) academic transcripts (4) the names and contact details for three references

The deadline for applications is July 31, 2017. Applications will be considered on a rolling basis until the position is filled. International applicants are welcomed. Starting date is flexible but should be no later than 15 December 2017. Please feel free to email any questions about the scholarship or project.

Vaughan Symonds, PhD Senior Lecturer in Plant Molecular Genetics Massey University Palmerston North, New Zealand 4442

"Symonds, Vaughan" <V.V.Symonds@massey.ac.nz>

MaxPlanck Jena 5 EvolutionaryBiol

"5 PhD positions in Molecular and Chemical Ecology and Evolution"

The International Max Planck Research School (IMPRS) "The Exploration of Ecological Interactions with Molecular and Chemical Techniques" in Jena, Germany, invites applications for 5 PhD positions beginning in January 2018. The overarching research topic is the use of molecular, chemical and neuroethological techniques to experimentally explore ecological interactions under natural conditions. The main focus is on the relationship between plants, microbes and herbivores, and their environment, as well as the evolutionary and behavioral consequences of these interactions. We offer 15 exciting projects focusing on different organisms and approaches. The complete list of projects offered including project descriptions is available on our website (http://imprs.ice.mpg.de/ext/index.php?id=420#header_logo).

We are looking for enthusiastic PhD students with strong interests in the above-described central topic. Applicants should have or be about to obtain a Masters or equivalent degree in one of the following fields: ecology, evolutionary biology, bioinformatics, analytical chemistry, entomology, neurobiology, molecular biology, biochemistry, plant physiology and genetics. Exceptional candidates with a Bachelor's degree may also be considered. All our projects are highly integrative and require willingness to closely collaborate with researchers of different backgrounds.

The Research School is a joint initiative of the Max Planck Institute for Chemical Ecology, Friedrich Schiller University, and the Leibniz Institute for Natural Product Research and Infection Biology Jena. We offer state-of-the art equipment, an excellent research environment, supervision by a thesis committee and a structured training program including scientific courses, training in transferable skills and internal conferences. Successful candidates will receive a Max Planck support contract. There are no tuition fees and the working language is English.

Application deadline is August 18, 2017. For detailed information on the IMPRS, projects offered and application requirements, please visit our website: http://imprs.ice.mpg.de/ . Please apply online from July 10, 2017, at: https://imprs-reg.ice.mpg.de/ .

Projects offered in 2017 Please find below a list of projects we offer for this year's recruitment. All projects are highly integrative and require the collaboration between different research groups. Applicants can identify up to three projects of interest. It is possible to change project preferences during the recruitment in Jena.

Project 1: Surfing the surface: Hydrophobins on fungal hyphae Supervisors: Prof. Dr. Erika Kothe, Institute for Microbiology, Friedrich Schiller University Jena; Prof. Dr. Jonathan Gershenzon, Department of Biochemistry, Max Planck Institute for Chemical Ecology; Dr. AleÃ' SvatoÃ', Research Group Mass Spectrometry, Max Planck Institute for Chemical Ecology

Project 2: Mycorrhizal roots and flowers - does a common signaling system lead to phenotype associations among AMF and pollination preferences in a native tobacco? Supervisors: Prof. Dr. Ian Baldwin, Department of Molecular Ecology, Max Planck Institute for Chemical Ecology; Prof. Dr. Erika Kothe, Institute for Microbiology, Friedrich Schiller University Jena

Project 3: Towards GC-MS: Adapting SIRIUS and CSI:FingerID for Electron Ionization fragmentation Supervisors: Prof. Dr. Sebastian Bocker, Chair of Bioinformatics, Friedrich Schiller University Jena; Prof. Dr. Georg Pohnert, Chair of Instrumental Analytics, Friedrich Schiller University Jena; Dr. AleÃ' SvatoÃ', Research Group Mass Spectrometry, Max Planck Institute for Chemical Ecology

Project 4: Multiple chemical compounds from Mortierella hyalina, a root-colonizing fungus, promote plant performance Supervisors: Prof. Dr. Ralf Oelmuller, Department of Plant Physiology, Friedrich Schiller University Jena; Dr. Axel Mithofer, Department of Bioorganic Chemistry, Max Planck Institute for Chemical Ecology

Project 5: Opposing the mustard-oil bomb with a glutathione bomb Supervisors: Dr. Franziska Beran, Research Group Detoxification and Sequestration in Insects, Max Planck Institute for Chemical Ecology; Prof. Dr. David Heckel, Department of Entomology, Max Planck Institute for Chemical Ecology

Project 6: The role of plant defense mechanisms for maintaining the diversity of host races in the pea aphid Supervisors: Dr. Grit Kunert, Research Group Plant-Aphid Interactions, Max Planck Institute for Chemical Ecology; Prof. Dr. Jonathan Gershenzon, Department of Biochemistry, Max Planck Institute for Chemical Ecology; Dr. Axel Mithofer, Department of Bioorganic Chemistry, Max Planck Institute for Chemical Ecology; Prof. Dr. Ralf

— / —

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

---

MPICE UExeter EvolutionColouration

Project no 12

How bright and how nasty: the economics of variable aposematic traits

Supervisors: Hannah Rowland, MPI for Chemical Ecology; Jon Blount, University of Exeter, UK

Deadline for application: August 18, 2017

More information: http://imprs.ice.mpg.de/ext/index.php?id=home Supervisors: Hannah Rowland, MPICE; Jon Blount, University of Exeter, Penryn Campus.

Background: Many species of animals, plants and microorganisms have evolved to use defensive chemicals to reduce the likelihood of being ingested by predators (Ruxton, Sherratt, & Speed, 2004). Aposematic species advertise these chemical defences with conspicuous or distinctive colours (Poulton, 1890). This paring of visual and chemical cues causes predators to learn about prey more quickly (Gittleman & Harvey, 1980), remember them for longer (Roper & Redston, 1987), and make fewer discrimination errors (MacDougall & Dawkins, 1998). Warning colours are selected for their reliability as an indicator of defence (Sherratt, 2002) - a qualitatively honest signal. What is much less clear, however, is whether variation in conspicuousness within or among species provides fine-grained information about levels of defence - a quantitatively honest signal (Summers, Speed, Blount, & Stuckert, 2015).

There is a growing body of theoretical and empirical evidence that warning colours can be related in some way to the defence that it advertises (Blount, Speed, Ruxton, & Stephens, 2009; Darst, Cummings, & Cannatella, 2006; Leimar, Enquist, & Sillentullberg, 1986; Summers & and Clough, 2001). This project will focus on testing the link between warning colours and chemical defences. You will investigate how prey optimize their aposematic defences by quantifying a set of fitness costs and benefits.

Project Description: You will test the predictions of Blount et al. (2009). They proposed a 'resource competition' model to explain variability in aposematic traits. The premise of this model is: if sequestration or production and maintenance of aposematic defences and conspicuous signals compete for access to a shared physiological resource (for example, antioxidant molecules), then in low resource states, prey are predicted to invest equally in conspicuousness and defence. This would result in a positive correlation between these traits, which would indicate honest signalling. There will be two avenues of research:

1. Are aposematic defences costly to generate?

Aposematic signals sometimes incorporate structural colours, for example in butterflies, but invariably they include pigments such as carotenoids, flavonoids, melanins, ommochromes, papiliochromes, pteridines and porphyrins. Such pigments have a long-chain conjugated polyene structure, which absorbs visible light and imparts colour, but also deactivates reactive oxygen species (ROS) that arise due to electron leakage during ATP production. If antioxidant defences become overwhelmed by ROS (i.e. oxidative stress), serious damage is sustained by DNA, lipids, proteins and carbohydrates. Plant secondary metabolites are commonly sequestered and utilised for chemical defence by insects; such allelochemicals are powerful pro-oxidants. It has been hypothesised that toxin-sequestering insects therefore require robust antioxidant defences if they are to avoid oxidative stress. Similarly, species that produce their own secondary defences may risk oxidative stress caused by metabolic expenditure for foraging, toxin (or weapon) production and storage, as well as direct pro-oxidant effects of toxins (Blount et al. 2009).

You will test the fundamental assumptions of the resource competition model (Blount et al. 2009): (1) that aposematic displays are costly in terms of fecundity, (2) that secondary defences can incur oxidative stress; and (3) that oxidative stress can reduce the capacity of individuals to produce aposematic displays.

2. Are aposematic defences costly to use?

Key work by Endler and Mappes (2004) examined the role of variation in predator responses to aposematic prey. It is one of the few recent theoretical treatments to consider variation in aposematism in detail. You will investigate how varied aposematic signal strengths protect an individual during attack. Some predators may release very well-defended prey effectively unharmed. In contrast, other predators may always cause substantial injury to such prey, even though the prey have high values for aposematic traits. You will test whether variation in death rates caused by variable injury rates from attack are linked to investment in defences.

Candidate profile:

- MSc or 1^st Class Degree in biology/zoology/biochemistry, with a strong background in evolutionary biology.

- Determination of oxidative stress requires a range of assays

— / —

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

Munich CrustaceanEvolution

Doctoral position - Palaeo-Evo-Devo of malacostracan crustaceans

We are seeking a highly motivated PhD student to take part in the investigation of the evolutionary history of malacostracan crustaceans, including extant and fossil representatives. The project is funded by the German Research Foundation (DFG).

The project is based on an interdisciplinary approach, in which developmental data of extant and fossil species are incorporated into an evolutionary framework, shortly referred to as palaeo-evo-devo. The major data base is provided by morphological investigations of extant and fossil specimens with modern imaging methods. Data are interpreted in a strict phylogenetic framework.

Focus groups of research are isopods and meiuran decapods. Both groups exhibit a large diversity of morphology and developmental patterns and have a rich fossil record. Specimens will be provided via scientific collections, fieldwork is not considered.

The prospective PhD student does not necessarily need to have experience with the imaging methods or systematic groups mentioned above, but is expected to gain expertise early in the course of the project. The project includes a distinct amount of traveling to collections in Germany and abroad. The results of the project are expected to be presented regularly at national and international conferences by the prospective PhD student as well as published in peer-reviewed journals.

The successful candidate will be based in the work group of Functional Morphology of Animals at the campus Martinsried south-west of Munich, in close proximity to Munich. Child care facilities as well as schools are nearby.

We offer: DFG-funded PhD position (75%) for 36 months; interdisciplinary research project and working environment; modern imaging equipment (macro- and microscopic)

We expect: MSc (or equivalent) in Biology or Palaeobiology; good English communication skills (oral and written); ability to work in teams; high motivation; keen interest in zoological evolutionary questions

The position is limited to 36 months with a presumed starting date of November 01, 2017.

Applications of women are strongly encouraged. Severely challenged persons will be given preference in case of otherwise equal qualifications.

Please send your application to jhaug@bio.lmu.de before September 01, 2017. The application should include CV, transcript of records, letter of motivation and the names and contact details of potential referees.

For further information contact:

Dr. Joachim T. Haug, LMU Munich, Biocenter - Department of Biology II, Großhaderner Str. 2, 82152 Planegg-Martinsried, Germany, Phone 1: +49-89-2180-74132 or 74171;

http://www.zoology.bio.lmu.de/people/joachim_haug/index.html Dr. Joachim T. Haug LMU Munich Biocenter - Department of Biology II and GeoBio-Center Großhaderner Str. 2 82152 Planegg-Martinsried Germany Phone 1: +49-89-2180-74171 Phone 2: +49-89-2180-74132 Email: jhaug@bio.lmu.de joachim.haug@palaeo-evo-devo.info

Website of Carolin and Joachim T. Haug: http://www.palaeo-evo-devo.info Joachim Haug <jhaug@biologie.uni-muenchen.de>

Rothamsted UK AphidLandscapeGenetics

10 days left to apply to this exciting PhD to study landscape genetics of pest aphids and applying it to improving pest management. *Deadline 10 July

*A full Waitrose - BBSRC CTP funded PhD position is open to work on population genetics and the evolution of resistance in aphids. The project is a collaboration between Rothamsted Research, University of Warwick, and G's, a leading lettuce producer.

"Using landscape genomics to improve management of insect pest species"

Insect pests have a widespread negative impact in agriculture, resulting in very large economic loses. Monitoring and surveillance of pest species is fundamental to control their populations and reduce the damage they inflict on crops. This is because an early detection improves the chances of controlling them before they spread out and increase their population size. However, studying the migration of small insects can be problematic due to the difficulty of tracking individuals. In addition, resistance to pest control methods, whether to insecticide or to host-plant resistant cultivars, is becoming an increasingly important issue. Inferring the population structure of pest species and the connectivity across populations and landscapes is key to understand migration patterns, which can be used to inform pest surveillance and control schemes. This fully-funded project provides an exciting opportunity to apply population genomics and evolutionary concepts to improve insect pest management and understand the evolution of resistance.

The project will use /Nasonovia ribisnigri/, the currant-lettuce aphid, as a model system to evaluate how landscape genomics can be used to improve aphid surveillance and control the spread of resistance alleles. The currant-lettuce aphid, /Nasonovia ribisnigri/, is a major pest of lettuce crops responsible for large economic losses. One of the most efficient way to reduce aphid infestations and damage is growing host-resistant lettuce cultivars that stop aphids from colonising the plant. However, the capacity of breaking the host-plant resistance mechanism (Rb) has recently evolved in some biotypes. In these circumstances, surveillance and monitoring of crops becomes of great importance to produce early warning information that would improve targeted control of /N. ribisnigri /before aphids enter the lettuce head. However, the paradox is that whilst winged aphids are quick to colonise the lettuce crop in spring they are unusually scarce in both water traps and suction traps.

Understanding the migration patterns of the species is, therefore, fundamental to design efficient methods of capture and control. For this, the project will use genomics to infer the population structure and the levels of gene flow between populations of /N. ribisnigri/ at different geographic scales and different landscapes. This knowledge will be used to develop surveillance methods that maximise the observation of individuals of the species at the early stages of their migration into the crops. Furthermore, these results combined with the development of genome-wide markers for the Rb phenotype will provide fundamental information about the evolution and spread of resistance across the UK.

*Application deadline is the 10 July and the starting date is October 2017. *

Informal enquiries to ramiro.morales-hojas@rothamsted.ac.uk are very welcome.

Application procedure and further information can be found at:

https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=84993&LID=1573 Eligibility: UK citizens and EU citizens who have resided in the UK for 3 or more years.

Ramiro Morales-Hojas

–

Dr. Ramiro Morales-Hojas Molecular Ecologist / Entomologist Rothamsted Insect Survey Biointeractions and Crop Protection Department Rothamsted Research

e-mail: ramiro.morales-hojas@rothamsted.ac.uk; r.moraleshojas@gmail.com web-site: https://-sites.google.com/site/ramiromoraleshojas/ web-site: http://www.rothamsted.ac.uk/insect-survey r.moraleshojas@gmail.com

SGN Frankfurt MammalianEvolution

Sehr geehrte Damen und Herren,

gerne möchten wir auf Ihrem Jobportal die folgende PhD-Stellenausschreibung veröffentlichen.

—

Job offer ref. #11-17018

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. SGN conducts natural history research with almost 800 employees and research institutions in six federal states. Within SGN, the Senckenberg Biodiversity and Climate Research Centre (BiK-F) explores the interactions between biodiversity, climate, and society.

Senckenberg BiK-F invites applications for a

PhD position in Evolutionary Genomics of Vertebrates (50 %)

There is an exciting opportunity for a talented and motivated applicant to join the working group of Prof. Dr. Axel Janke. The applicant is expected to be closely involved in evolutionary, population or phylo-genetics to study speciation in mammals (bears, giraffe, kangaroos or allies) at the genomic level.

Your profile: • Master degree in Biology, Genetics, Bioinformatics or a related field • Strong interest and proven skills in evolutionary, population or phylo-genetics • Experience in analyzing genomic data • Very good written and oral communication skills in English • Interest to be involved in an international and interdisciplinary group to expand the work to species distribution modeling, paternal inference and conservation genetics

Salary and benefits are according to a full time public service position in Germany (TV-H E 13, 50%). The contract should start on October 1st, 2017 and will initially be limited until September 30th, 2020. The Senckenberg Biodiversity and Climate Research Centre supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung. Please send your application, mentioning the reference of this job offer (ref. #11-17018) before July 30th, 2017 by e-mail (attachment in a single pdf document) and including a cover letter detailing research interests and experience, a detailed CV and a copy of your Master degree to:

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

For scientific enquiries please get in contact with Prof. Dr. Axel Janke, axel.janke@senckenberg.de

—

Vielen Dank für Ihre Mühen.

Mit freundlichen Grüßen /Best Regards

Jessica Helm Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß Â§22 BGB) Senckenberganlage 25 60325 Frankfurt am Main

Besucheradresse: Voltastraße 1, 60486 Frankfurt am Main (5. Obergeschoss)

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

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Gruppe Personal & Soziales - 1319 Elsen, Carina

Mitarbeiter/in Personalbeschaffung (Recruiting) - 1313 di Biase, Maria - 1313 Helm, Jessica - 1478 Gajcevic, Isabel

Fax: 0049 (0)69 / 7542-1467 Mail: recruiting@senckenberg.de

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)

Senckenberg forscht für Ihr Leben gern! www.200jahresenckenberg.de recruiting <recruiting@senckenberg.de> recruiting <recruiting@senckenberg.de>

StAndrews ComputationalEvolGenomics

PhD in Computational Biology

Applications are invited for a PhD position to work with Dr. Carolin Kosiol at the Centre of Biological Diversity of the University of St. Andrews, Scotland. Starting date will be the 27th September 2017 or shortly thereafter. The position will be funded for 3.5 years.

The PhD project is part of a larger project entitled "Genome-wide molecular dating" (https://www.wwtf.at/programmes/mathematics/MA16-061) The recent sequencing of genomes of closely related species and of many individuals from the same species enables the study of speciation and the inference of the history of populations. Standard phylogenetic methods reduce entire populations to single points in genotypic space by modelling evolution as a process in which a single gene mutates along the branches of a phylogeny. In this project, we envisage developing new theory and software to tackle the problem of species tree estimation and molecular dating genome-wide. Visits to Vienna, Budapest and Aarhus for collaborations with Gergely Szöllösi and Asger Hobolth are possible.

The successful candidate should have a strong interest in applying quantitative methods and modelling to Biology. They will have a degree in Bioinformatics, Computer Science, Statistics, Mathematics, Physics or a related field. Prior experience with either population genetics or comparative genomics is a benefit. Preferably the candidate will have experience in programming language such as C, C++, Java and a scripting language such as Python or Perl.

To receive full consideration, applicants should submit a single PDF file by e-mail with the following items before August 15 to ck202@st- andrews.ac.uk : * A cover letter with a brief summary of previous research experience and motivation for the position. * Curriculum Vitae.

The University of St Andrews is committed to promoting equality, which is further demonstrated through its working on the Gender and Race Equality Charters and being awarded the Athena SWAN award for women in science, HR Excellence in Research Award and the LGBT Charter. More details on diversity online: http://www.st-andrews.ac.uk/hr/edi/diversityawards/ Carolin Kosiol Lecturer in Bioinformatics University of St Andrews St Andrews Fife KY16 9TH United Kingdom Email: ck202@st-andrews.ac.uk Tel: +44-(0)1334-463598

"ck202@st-andrews.ac.uk" <ck202@st-andrews.ac.uk>

UAuckland2 MicrobialFungalEvolution

Two PhD positions are available in the Goddard Lab at the University of Auckland, New Zealand. Both projects will use a combination of next-generation DNA sequencing to evaluate aspects of microbial community ecology and population biology and understand how this relates to fungal populations associated with vines and winemaking. These projects will build on a body of work in this area at the University of Auckland (http://www.goddardlab.auckland.ac.nz), be strongly aligned with the Vineyard Ecosystem's program (https://www.nzwine.com/en/innovation/-innovation-new-zealand-wine/vineyard-ecosystems/), and collaborate strongly with Plant and Food Research (http://www.plantandfood.co.nz) and New Zealand Winegrowers (https://www.nzwine.com/en).

Project 1 - Microbes beyond the soil

There is significant market and industry desire to produce wine in ways that maximises the quality and distinctness but does so using environmentally responsible methods that minimise impact and increase the longevity of vineyards. The MBIE Vineyard Ecosystems (VE) programme makes a paradigm shift and takes a holistic approach and focusses on a core set of sites and evaluates the impact of two main management styles on vineyard health, quality and longevity.

However, the VE programme does not consider the effects of these different management approaches on the microbial biodiversity on ripe fruit and the resulting juice. This is important as these microbial communities play a role in defining the complex mix of compounds that affect wine aroma and flavour. This project will focus on Sauvignon blanc due to its economic weight and that we understand these systems best in terms of microbial ecology and wine chemistry. While Saccharomyces yeasts are the main species that drive fermentation, the range of other species that dominate on ripe fruit, in juice and early ferment also affect key flavour compounds. This project proposes to evaluate the species present on ripe grapes and see if and how these might change leading up to harvest, into the winery and early ferment. Importantly the project will evaluate how vineyard management might affect these communities and their effect on a key set of esters and thiols.

Project 2 - Integrating habitats in the vineyard ecosystem

The wine industry and the public in general are interested in ways to produce wine that maximises ecological sensitivity and sustainability yet produces high quality products. Our scientific understanding of how different agricultural approaches affect ecosystems as a whole is growing, but large gaps in our knowledge persist. The MBIE Vineyard Ecosystem program addresses some of these gaps, and is evaluating the effect of 'conventional' and 'future' management approaches on vineyard ecosystems across six years. Microbes and invertebrates are an important aspect of vineyard ecosystems as these define disease pressure (there are fungal, bacterial and insect pests and diseases), fruit quality, and, once in the winery, fermentation dynamics and wine quality (especially if spontaneous ferments are used). The MBIE program only has resources to evaluate biodiversity in soil as a proxy for the vineyard ecosystem; however, our very recent work shows that at a single time point in Sauv ignon blanc: 1) microbial diversity differs among habitats in vineyards (soil, vine-bark, and ripe fruit); 2) that management approaches affect the diversity in each of these habitats differentially; and 3) that biodiversity in juice and thiols in final spontaneously fermented wines do not differ by management approach. Whether this pattern holds across multiple years, different regions and different varieties is thus worthy of investigation. We propose to do this here. Such a project will produce solid academic outputs and valuable information for growers and winemakers regarding the effects of management on vineyards ecosystems and the quality of the wine deriving from these, and thus is precisely aligned with the MBIE Vineyard Ecosystem program.

Formal application should comprise a CV and covering letter to Dr Sarah Knight by 1st August at wineresearchnetwork@auckland.ac.nz.

Please state which project you prefer, but we will also consider combined applications to both projects. Informal enquires may be addressed to both Dr Sarah Knight and Prof Matthew Goddard (m.goddard@auckland.ac.nz).

"s.knight@auckland.ac.nz" <s.knight@auckland.ac.nz>

UAuckland PlantAnimalInteractions

PhD Scholarship available: Sensory ecology of a resilient ancient deceiver, the Splachnaceae dung mosses (The University of Auckland, New Zealand)

How do plant-animal interactions survive and adapt in a changing world? The extraordinary Splachnaceae mosses grow on animal carcasses and dung, and use bright colours and rotten odours to lure flies into acting as spore dispersers. Splachnaceae are generally hosted by the remains of native mammals, e.g. in Australia, they grow on dung from wombats, wallabies and Tasmanian Devils. Splachnaceae specimens have also been found with preserved mammal remains, e.g. giant Irish deer and Canadian caribou.

In New Zealand/Aotearoa, the biota is bird dominated with no native land mammals ?C the Splachnaceae mosses are now hosted by introduced mammals, e.g. goats. Could Aotearoa Splachnaceae's original hosts be extinct moa or other herbivorous birds like takahç or putakitaki? Or seal or seabird colonies? Which insects are fooled into dispersing Aotearoa Splachnaceae? Our pilot data suggests dung beetles may be an extra courier here.

This project aims to use behavioural ecology, chemical ecology, spectral modelling, paleoecology and ancient DNA to discover how mosses mimic the scents and odours of dung to deceive spore-dispersing insects, switch between bird, mammal, native and introduced hosts, as we explore how networks can respond to introduced species and megafaunal extinctions. There is scope to develop the project to suit your interests and aspirations as you develop your career.

The successful applicant will benefit from working with established and productive researchers at the world class University of Auckland (New Zealand's leading university) and Landcare Research/Manaaki Whenua. The dynamic Ecology Ngâtahi group, hosted by the Joint Graduate School for Biosecurity and Biodiversity, has many international and NZ PhD, MSc and Hon students, with diverse research taxa and approaches, including terrestrial, marine, behaviour, conservation, entomology, ornithology, invasive species etc.

If you are looking for a totally unique project that you can lead and make your own, a newly established study system with fantastic pilot data, a welcoming and collegial postgrad environment, and great supervisors to launch you on your academic career, this could be your perfect PhD!

Supervisory team: main supervisor is Dr Anne Gaskett (behavioural and sensory ecologist, specialising in plant-insect interactions, School of Biological Sciences, University of Auckland, New Zealand). Cosupervisor is Dr Jamie Wood (paleoecologist and ancient DNA lab manager, Landcare Research/Manaaki Whenua, Lincoln, New Zealand).

Location: The project is based in Auckland, New Zealand, with fieldwork in New Zealand and optionally Australia.

Funding: PhD scholarship providing $NZD27,000 stipend per annum for 3 to 3.5 years (includes fees). Research costs will be offset by your annual $2700? student-managed research fund, and we will provide opportunities (and support!) to apply for further travel/conference funding.

Resources: Own desk in a pleasant, collegial work environment at the University of Auckland; use of shared lab facilities (incl. microscopy, GC-MS); field first aid training provided; access to the wonderful outdoors of New Zealand and Australia; live in the beautiful, multicultural harbour city of Auckland; and professional, motivated and supportive supervisors who love research and a good work-life balance.

Essential requirements: First class Masters or Honours in ecology, evolution or animal behaviour; proven English written and spoken communication skills; experience in managing data and statistical analyses; enthusiasm and motivation; creative problem solving; ability to work independently and as part of a team; experience in leading, organising and conducting field-based research; a driver's licence (absolutely essential for field work); enjoyment of tackling both big evolutionary questions and small natural history questions; satisfaction in making and sharing discoveries.

Ideal but not essential requirements: peer-reviewed publications; experience in insect and moss identification, experience in gas chromatography-mass spectrometry and/or spectral modelling, a love of moss - or at least an interest in developing a love of moss! Experience with basic DNA techniques (DNA extraction, PCR, sequence analysis) useful but not essential.

Applications: please email a letter addressing the essential and ideal requirements listed above, a 2-page CV including details of 2 referees who can be contacted, and a sample of your writing (ideally the introduction to your Hons or MSc thesis) to Dr Anne Gaskett (a.gaskett@auckland.ac.nz).

Applications close —

Start date: negotiable, but before Dec 2017

Duration: 3 ?C 3.5 years

All applicants meeting the criteria are encouraged to apply. The University of Auckland is committed to meeting its obligations under Te

— / —

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

---

UBasel EvoDevoNeuroEvolution

Graduate position:

UBasel.EvoDevoRegulatoryEvolution

A fully funded PhD position is available in the Laboratory of Regulatory Evolution (Tschopp group) at the Zoological Institute, University of Basel, Switzerland.

Our research interests focus on two main questions: How is phenotypic diversity generated during vertebrate embryogenesis? And how can developmental processes be modified to drive morphological evolution? The present project will investigate the potential for developmental plasticity in the limb neuromuscular system in response to changes in dactyly, i.e. altering digit numbers. Specific questions we will address include: How are muscle patterning and motorneuron axonal pathfinding coping with changes in digit numbers in vertebrate hands and feet? How is motorneuron pool complexity in the spinal cord affected by additional digit targets in the periphery? We will use a range of methods, including experimental embryology in chicken, genetic mouse models, axonal backfilling, NextGeneration-Sequencing and functional experiments using gene knock-down and overexpression.

The project builds on solid foundations of confirmed preliminary data. For more information please visit http://evolution.unibas.ch/tschopp/research/index.htm The successful candidate will have a Master (or equivalent) in developmental biology and/or molecular biology, and ideally will have skills in experimental embryology, neurobiology and NextGeneration-Sequencing. A basic understanding of Unix and the R language for statistical computing would be beneficial.

Please send your application with a brief statement of motivation, CV and contact(s) for references (where applicable) to patrick.tschopp@unibas.ch Evaluation will begin mid-August 2017 and suitable candidates will be contacted shortly after - earliest starting date is Sept. 1st 2017.

"patrick.tschopp@unibas.ch"
<patrick.tschopp@unibas.ch>

UBielefeld TheoreticalEcologyEvolution

2 PhD positions in Theoretical Ecology and Evolution to work with Meike Wittmann in the new research group for Theoretical Biology at Bielefeld University, Germany (please apply by August 24)

The new research group for Theoretical Biology works on modeling ecological and evolutionary processes as well as interactions between them. The group is interested, for example, in mechanisms for the maintenance of species diversity and genetic diversity. Another research area is the biology of small populations, in particular how ecological and evolutionary processes jointly determine the fate of such small populations, that is whether they go extinct or recover in the long term.

There are two open positions for PhD students interested in pursuing research in one of these areas. The specific PhD projects will be defined together with the successful candidates. Examples for research questions are: Under what conditions can loss of genetic variation lead to the extinction of small populations (genetic Allee effects)? How can we use genome-wide sequence data from multiple species in an ecological community to learn about species interactions?

- Research tasks (75%): * Development of eco-evolutionary models * Mathematical analysis of models * Implementation in a programming language, e.g. in R, C++, Python * Simulation studies * Collaboration with empirical research groups at the Faculty for Biology * Writing scientific publications

- Teaching in Ecology (2 LVS) (20%)

- Organizational tasks in the research group (5%)

Applicant's Profile The successful candidate is expected to have: - University degree (by start of position) in a relevant scientific discipline, e.g. biology, mathematics, physics, or bioinformatics - Interest in both biological and mathematical questions - Ability to work both independently and as part of a team - Excellent oral and written communication skills - Good English skills

The successful candidate should preferably have: - Programming skills, e.g. in R, Python, or C++ - Experience with mathematical modeling - Experience in leading exercise sessions/tutorials

Remuneration Salary will be paid according to Remuneration level 13 of the Wage Agreement for Public Service in the Federal States (TV-L). As stipulated in Â§2 (1) sentence 1 of the WissZeitVG (fixed-term employment), the contracts end after a period of three years. In accordance with the provisions of the WissZeitVG and the Agreement on Satisfactory Conditions of Employment, the length of contract may differ in individual cases. The employment is designed to encourage further academic qualification. The positions are advertised as 65 % part-time jobs. In individual cases, this percentage may be reduced on request, as long as this does not conflict with official needs. Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a variety of health, counselling, and prevention programmes. Bielefeld University places great importance on a work-family balance for all its employees.

Application Procedure For full consideration, your application (cover letter detailing your motivation and relevant experiences, CV, copies of certificates, and contact details for at least one reference) should be received preferably via email (a single PDF document) sent to meike.wittmann@uni-bielefeld.de by the 24th of August 2017. Please mark your application with the identification code wiss17201. Please do not use application portfolios and send only photocopies of original documents because all application materials will be destroyed at the end of the selection procedure. Further information about Bielefeld University can be found on our homepage at www.uni-bielefeld.de . Postal Address Universität Bielefeld Fakultät für Biologie, Theoretical Biology Juniorprofessorin Dr. Meike Wittmann Postfach 10 01 31 33501 Bielefeld

Contact Juniorprofessorin Dr. Meike Wittmann 0174 6240723 meike.wittmann@uni-bielefeld.de

Bielefeld University has received a number of awards for its achievements in the provision of equal opportunity and has been recognized as a family friendly university. The University welcomes applications from women. This is particularly true with regard both to academic and technical posts as well as positions in Information Technology and Trades and Craft. Applications are handled according to the provisions of the state equal opportunity statutes. Applications from suitably qualified handicapped and severely handicapped persons are explicitly encouraged.

Links to official advertisement: English version:

— / —

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

---

UCopenhagen HostPathogenChemicalCoEvolution

The Department of Plant and Environmental Sciences, Faculty of Science at University of Copenhagen is offering a PhD scholarship in Host-pathogen co-evolution to work in the Section for Organismal Biology. The 3-year position is expected to commence 1 December 2017. —

Description of the scientific environment — The Department of Plant and Environmental Sciences (PLEN) constitutes a highly competitive, stimulating, and international research environment. The PhD project will be carried out within the research theme Host-pathogen coevolution in the research group of Insect-Pathology and Biological Control affiliated to the Section of Organismal Biology (SOBI). SOBI provides a highly dynamic environment with a long history of studying host-pathogen interactions in a number of systems, ranging from insect, mammal and plant hosts to pathogenic fungi, bacteria, and macroparasites. We pursue internationally competitive excellence in a multinational research environment where English is the working language. The PLEN research laboratories are located at the Frederiksberg Campus of the University, close to the centre of Copenhagen, one of the most liveable cities of the World. —

Project description — Transmission to new susceptible host is crucial for a pathogen, and the biological world is rife with examples of pathogens that manipulate host behavior to enhance host transmission. This mind-control can go beyond the infected host and for example exploit the mate-seeking behavior of healthy males that becomes significantly more attracted to infectious females than uninfected females. The project will use a newly established laboratory host-pathogen system of the fungal pathogen Entomophthora muscae and Dipteran insect hosts for exploring the pathogen induced alterations in host chemistry, including chemical analysis and electro-antennal responses to -volatile compounds and dual-transcriptomics of host and pathogen. The research is fundamental with considerable applied potential in attract-and-kill biological control strategies. —

Supervision — The principal supervisor is Associate Professor Annette Bruun Jensen. The daily supervisor is Assistant Professor Henrik H. De Fine Licht (hhdefinelicht@plen.ku.dk, phone +45 35320097). —

Job description The position is available for a 3-year period and your key tasks as a PhD student at SCIENCE are: — -Manage and carry through your research project — -Attend PhD courses — -Write scientific articles and your PhD thesis — -Teach and disseminate your research — -Work for the department — -To stay at an external research institution for a few months, preferably abroad —

Formal requirements — Applicants should hold an MSc degree in Biology or equivalent, with good results and good English skills. As criteria for the assessment of your qualifications, emphasis will also be laid on previous publications (if any) and relevant work experience. — — The starting salary is currently at a minimum DKK 312.879 including annual supplement (+ pension up to DKK 43.219). Negotiation for salary supplement is possible. —

Enquiries or questions should be directed to Assistant Professor Henrik H. De Fine Licht (hhdefinelicht@plen.ku.dk).

Please upload complete application documents including Cover Letter, 1-2 page research plan based on the project description, CV, Diploma and transcripts of records (BSc and MSc), Acceptance Letter for the relevant MSc Programme at SCIENCE, if any, Other information for consideration, e.g. list of publications (if any), Full contact details (Name, address, telephone & email) of 1-3 professional referees no later than 15nd August 2017 via the UCPH's (http://employment.ku.dk/phd/) online job-application facility (http://employment.ku.dk/-phd/?show=145518).

Henrik Hjarvard de Fine Licht, Assistant Professor, PhD Section for Organismal Biology, Department of Plant and Environmental Sciences University of Copenhagen, Thorvaldsensvej 40, 1871 Frederiksberg C. Denmark Tel: +45 3532 0097 Email: hhdefinelicht@plen.ku.dk Homepage: http://plen.ku.dk/english/employees/?id=-194704&vis=medarbejder Personal homepage: https:/-/sites.google.com/site/henrikdefinelicht/ Henrik Hjarvard de Fine Licht <hhdefinelicht@plen.ku.dk>

UFribourg ComputationalPaleogenomics

PhD position in Computational Paleogenomics Statistical and Computational Evolutionary Biology Group, Prof. Wegmann University of Fribourg, Switzerland

Who we are: We are a young, international and enthusiastic group at the University of Fribourg, Switzerland, aiming at characterizing the evolutionary and ecological processes shaping the realm of biological diversity we see today. To achieve this, we design and evaluate new statistical and computational approaches to infer complex evolutionary histories and subsequently, apply them to the wealth of data currently being generated, primarily from the latest sequencing approaches. A recent focus of the lab was on the development of tools to analyze next-generation sequencing data that properly account for genotyping uncertainty resulting from low-depth and post-mortem damage prevalent in ancient DNA.

Your tasks: Currently, we seek a highly motivated PhD student to join our research group and to address questions regarding large scale population movements in human history and pre-history using ancient DNA. For this the successful candidate will develop new and extend existing population genetic methods, and in particular model-based inference tools, for ancient DNA data, and then apply these tools to newly generated data sets. This work will be mostly of a statistical and computational nature, involving explicit modelling, simulations and data analysis, yet there is also an option to contribute to data generation with our collaborators in a dedicated paleogenetic laboratory at the University of Mainz, Germany.

What we offer: We offer a stimulating research environment, well embedded in the strong evolutionary- and population genetics community in western Switzerland. We are part of the Swiss Institute of Bioinformatics (SIB) and boost excellent research facilities, including state-of-the-art high-performance computational infrastructures. Fribourg is a lively university town with pleasant surroundings (such as the Alps) and an excellent quality of life. It is located only 20 minutes from the capital of Switzerland, Bern, and just a little over an hour from Geneva and Zürich. While some knowledge of German or French is beneficial for living in Switzerland, it is not essential. The working language in our lab and institute is English.

What you bring: Applicants for this position should have a Master degree (or equivalent) in biology, population genetics/genomics, bioinformatics, computational biology, computer science, statistics or a related field. Good knowledge of written and spoken English is expected. While experience in programming is not required (but an asset), we expect candidates to be highly motivated to acquire skills in programming and statistical inference, for which we are happy to provide state-of-the-art training.

The position is fully funded with a competitive salary for three years, with the possibility to extend by one additional year. The successful candidate should ideally start in October 2017, or soon thereafter.

To receive full consideration, applicants should submit a single PDF file by e-mail with the following items before August 15 to daniel.wegmann@unifr.ch:

* A cover letter with a brief summary of previous research experience and motivation for the position. * Curriculum Vitae. * Copies of degree certificates and list of coursework, including grades. * Names, addresses and e-mails of two professional references.

Further information: http://www.unifr.ch/-biology/research/wegmann/ https://-www.isb-sib.ch/groups/fribourg/sceb-wegmann.html “daniel.wegmann@unifr.ch”

<daniel.wegmann@unifr.ch>

UGottingen PlantSystematics

The Department of Systematics, Biodiversity and Evolution of Plants, Albrecht-von-Haller-Institute for Plant Sciences, Faculty of Biology and Psychology at the Georg-August-Universitat Gottingen is looking to fill the position of

PhD position in Plant Systematics

This position should be filled by 1^st October 2017 (plus/minus one month). The regular working hours will be 65% (currently 25,87 hours per week), with a limited contract of 3 years. Salary: Pay grade 13 TV-L.

The position is within the DFG project "The biodiversity of apomictic polyploid plants: the case of Ranunculus auricomus" (pending granting) and is aiming at species delimitation and an evolutionary classification of this Eurasian plant group, by using genomic tools, morphometry, and flow cytometry.

The successful candidate will hold a highly qualified Master or equivalent degree in Biology, with a focus on research in Biological Systematics. We expect experience in molecular systematics or population genetics, and next-generation sequencing techniques. Research will require a good understanding of plant evolution, analytical skills, a high motivation to learn new techniques, and excellent scientific English, preferably documented by publications. For material collection, field experience in botany and an EU valid driving licence B is advantageous. The researcher will work in a highly motivated team of PhD students and postdocs within the Department. The post will give the successful applicant the opportunity to pursue a doctoral degree within the doctoral programs of the Faculty. Our PhD program offers a comprehensive mentoring program, specific methodical courses, research visits in partner labs, opportunities for conference presentations, gaining teaching experience, and further support for career development.

The University of Gottingen is an equal opportunities employer and places particular emphasis on fostering career opportunities for women. Qualified women are therefore strongly encouraged to apply in fields in which they are underrepresented. The university has committed itself to being a family-friendly institution and supports their employees in balancing work and family life. The mission of the University is to employ a greater number of severely disabled persons. Applications from severely disabled persons with equivalent qualifications will be given preference.

Please send your application with the usual documents in electronic form by 20th August 2017

to Georg-August-Universitat Gottingen,

Department Systematics, Biodiversity and Evolution of Plants (with herbarium),

Untere Karspule 2, 37073 Gottingen,

e-mail: elvira.hoerandl@biologie.uni-goettingen.de.

If you have any questions, please contact Prof. Elvira Horandl, e-mail: elvira.hoerandl@biologie.uni-goettingen.de.

Elvira Hoerandl <ehoeran@uni-goettingen.de>

UGroningen EvolutionaryEcol

We are seeking a highly motivated individual to carry out PhD research in the field of evolutionary ecology. The successful candidate will split his/her time between the University of Stirling (UofS, Biological & Environmental Sciences) supervised by Dr Lynsey Bunnefeld and the University of Groningen (UofG, Institute for Evolutionary Life Sciences) supervised by Prof. Rampal S. Etienne. Dr. Alex Pigot from University College London will also be central to project development and supervision. For more information, please see https://www.findaphd.com/-search/ProjectDetails.aspx?PJID=87897&LID=1455 "r.s.etienne@rug.nl" <r.s.etienne@rug.nl>

UIceland SpeciationEvolReprodBar

PhD position in biology, Institute of Life and Environmental Sciences, University of Iceland

A full PhD position in biology is open for applications, at the Institute of Life and Environmental Sciences for the project: Evolution of reproductive barriers in sympatric Arctic charr morphs.

How is phenotypic integrity maintained in the face of gene flow? What is the effect of hybridization on development and fitness? What are the molecular mechanisms behind hybrid incompatibilities? These and related questions will be addressed by a team of researchers, and a capable PhD student responding to this advertisement.

The project The Arctic charr (Salvelinus alpinus) of Lake Thingvallavatn is ideally suited to address these questions. The Lake was formed at the end of the last glacial epoch just 11-10 thousand years ago and despite its young age it now harbors four morphs of Arctic charr, whose distinct variation in life history characteristics, behavior and trophic morphology suggest rapid adaptive diversification, possibly followed by or causing build-up of reproductive barriers. The focus of this project will be on the two smaller Thingvallavatn morphs, planktivorous- (PL) and small benthic-charr (SB), which have diverged along the limnetic - benthic ecological axis, and inhabit different parts of the lake. Breeding populations of both morphs are large and their spawning overlaps spatially and temporally seemingly presenting ample opportunities for cross-mating. Yet, population genetic studies show that they constitute distinct populations, which suggests effective reproductive barrier(s). We intend to cast light on the nature of these barriers. The central hypothesis underlying our investigation is that reproductive isolation between SB and PL Arctic charr is partly due to strong negative selection against hybrid offspring and/or differences in the exact timing of spawning (i.e. time of the day), precise spawning location and/or mating behavior. The Ph.D. projectâ euro s aims are to: i) Assess hybrid survival and fitness during embryonic and early larval development ii) Study gene expression during development of hybrid and pure morph crosses iii) Study the spawning behavior of the two morphs and their interaction in the wild and in the lab. The applicant must have completed an M.Sc. degree in Biology or related fields from a University approved by the University of Iceland's Graduate School. Those with an advanced degree including at least a 60 ECTS credits thesis project will be given precedence. Diving experience is a plus.

We are seeking a student with dedication, drive and good theoretical background in evolution, developmental and molecular biology and an interest in animal behavior. The work involves planning and executing sampling in the field, acquisition and analysis of high-throughput sequencing data and numerical analyses, designing laboratory experiments. The position will be at the University of Iceland and the work will take place there. Experts at the University of Aberdeen, Scotland and the Holar University College, Iceland, will also participate in the project. Application deadline is 1st of August 2017. The PhD study should be completed within four years of full time study. The PhD student may be involved in teaching, for two semesters maximum. The selected candidate will have to formally apply for PhD studies at the University of Iceland in due time. Applications should be submitted here: https://-ugla.hi.is/radningar/index.php?sid=2448&starf=192 accompanied by i) a letter of intent (maximum two pages) explaining interest in working on this project, the reason to pursue a PhD, hopes to gain and learn during the PhD studies and what makes them suitable for this project ii) CV, iii) transcripts of university diplomas, courses taken at bachelor and masters level, iv) degree project thesis and vi) names and contact information of two persons that could provide letters of references. The student will join the Arctic charr group at the Institute of Life and Environmental Sciences, under the supervision of Sigurdur S. Snorrason, Arnar Palsson and Zophonias O. Jonsson. The Arctic charr group consists of several PhD students and senior personnel, and has collaborators in Iceland, Denmark, Scotland and Canada. The combined expertise covers population ecology and genetics, molecular biology and bioinformatics. At the institute we have well equipped molecular biology labs, and instruments and computer pipelines for high throughput sequencing, are accessible there or at collaborating centers. For further information contact: Kalina H. Kapralova (kalina@hi.is) or Sigurdur S. Snorrason (sigsnor@hi.is) Further information on Arctic charr group at the University of Iceland:

— / —

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

---

UIllinois SymbiosisEvolution

The Heath lab at the University of Illinois at Urbana-Champaign is looking for motivated graduate students interested in evolutionary genetics of plant-microbe symbioses. The Heath lab uses a variety of approaches (fieldwork, sequencing, quantitative genetics) in a number of legume-rhizobium systems to answer fundamental questions about how mutualisms evolve in nature, and the molecular basis of symbiosis evolution. Find out more about what we do at our website (http:/-/www.life.illinois.edu/heath/Heath_Lab/HOME.html). Students can apply through either the Program in Ecology, Evolution and Conservation (http://-sib.illinois.edu/peec/) or the Department of Plant

Biology grad program (http://www.life.illinois.edu/-plantbio/graduateAdmissions.htm).

Champaign-Urbana is a great college town midway between three major cities (Chicago, St. Louis, Indianapolis), with great food and drink, abundant culture, and affordable cost of living.

University of Illinois and the Heath lab are committed to a diverse workplace, and prospective students of all races, genders, and sexual orientations are encouraged to apply.

Email Katy Heath (kheath@life.illinois.edu) for more information.

Katy Heath <kheath@life.illinois.edu>

UMelbourne BeetleEvolution

PhD Project Available (Commencing 2018) School of BioSciences, The University of Melbourne, VIC, Australia, 3010

I am seeking a PhD student to join an interdisciplinary project involving thermal adaptations, colour, near-infrared reflectance properties, and nano-structures in beetles. The project is funded by the Hermon Slade Foundation and the University of Melbourne. I am particularly keen to recruit students with a background or interest in the interface between biology and optical physics.

Project description

Animals have evolved remarkable and unique ways of controlling light (e.g. fluorescence, iridescence). Until now, biologists have focused almost exclusively on how ultraviolet (UV) and human-visible wavelengths are manipulated to produce the diversity of colours and optical effects we see in nature. However, the way near-infrared wavelengths of sunlight are controlled to affect body temperature is critical to survival; yet the adaptive significance of near-infrared variation remains almost entirely unexplored in animals.

This project will characterise near-infrared variation in leaf beetles (Chrysomelidae) and reveal its adaptive significance using experimental approaches. The project will also reveal how the nano-scale architectures of beetle cuticles control UV-visible and near-infrared light, enabling them to balance camouflage, communication and thermal requirements. Discovery of nano-structures to manipulate near-infrared light has exciting potential biomimetic applications.

Requirements

Successful applicants will be assisted in applying for an Australian Postgraduate Award (for Australians) or an International Postgraduate Research Scholarship (for Internationals) through the University of Melbourne. To be competitive, a First-class Honours or Masters Degree (or international equivalent) or publication in international journals are essential. Please send applications by 1st October or earlier.

To apply, please send A) A brief letter outlining your research interests; B) a CV, C) your academic transcript/grades, D) contact details of two referees (including a previous research supervisor).

For further information, and to submit applications, please contact:

Devi Stuart-Fox

d.stuart-fox@unimelb.edu.au

https://devistuartfox.com/ Â'

Katrina Rankin <katrina.rankin@unimelb.edu.au> Katrina Rankin <katrina.rankin@unimelb.edu.au>

UNeuchatel HostParasiteInteractions

A *PhD position in the evolutionary ecology of host-parasite interactions* is available for up to 4 years in Prof. Jacob Koella's lab at the University of Neuchâtel.

I am looking for an enthusiastic, motivated, and independent biology graduate whose MSc degree has a strong component in evolution, ecology or parasitology. My lab currently works on (i) the effect of infection by malaria on the behavioural and physiological responses of mosquitoes to insecticides, and (ii) the role of oxidative stress in linking the life-history of mosquitoes and their immune response against malaria and microsporidians. We consider these topics (and host-parasite associations in general) with a strong evolutionary perspective, but work on them with a combination of genetics, physiology, immunology, behavioural ecology and mathematical modelling. The details of your project will be adapted to suit your interests, and you will be expected (and given the time) to have considerable input in developing the project. My lab is strongly collaborative, so you can expect to be involved to some degree in other projects going on in the lab.

The position requires some teaching of biology labs for undergraduate (in French) and graduate (in English) students, and you will have the opportunity to supervise student projects.

The position is available as of November 1, 2017. The starting salary is about 41000 Fr..

Neuchâtel is an attractive city in the French part of Switzerland with a high quality of life. It is located on the shore of Lake Neuchâtel with the Jura mountains to the North and a view of the Bernese alps to the South. For outdoors enthusiasts, this is an excellent area for outdoor activities such as hiking, climbing or skiing.

If you are interested in the position, please send me (jkoella@gmail.com) a 1-2 page cover letter indicating research interests and background, your CV, and two letters of reference before August 20, 2017.

Jacob Koella

Jacob Koella

Institut de Biologie Université de Neuchâtel rue Emile-Argand 11 2000 Neuchâtel Switzerland

Jacob Koella <jkoella@gmail.com>

UNewSouthWales SexualCompetition

PhD Student Position - UNSW Sydney: Economic inequality as a driver of sexual competition and gendered traits

This is an exceptional opportunity for students interested in how evolved traits interact with economic circumstances to shape behaviour in contemporary societies. Students may be trained in evolutionary biology, psychology, anthropology, economics or other disciplines.

This position is supported by the generous Scientia PhD Scholarship Scheme at UNSW Sydney, Australia. In addition to a stipend of $40K p.a. There is a $10k p.a. Travel allowance, and other opportunities for career development.

The supervisory team is: Professor Rob Brooks - evolutionary biology A/Prof Pauline Grosjean - economics Dr Khandis Blake - evolutionary social psychology

DESCRIPTION: We propose to test the exciting new idea that economic inequality among households also shapes mating competition, giving rise to many of the stark sex differences in dress, spending patterns, and mental and physical health that pervade societies. While wealthy Western countries have progressed steadily toward gender-equitable opportunities over the last century, differences between women and men in aggression, interests and the incidence of diseases like anxiety and depression have, paradoxically, increased. It is clear that ossified old ways of understanding gendered traits as either biologically essential or socially constructed have little to offer in terms of further understanding. Our approach transcends old territorial boundaries, and promises a newer, better and more general way to understand gendered behaviours, including those implicated in harm to mental health, safety, and happiness. The work will involve both experimental psychological research and analysis of economic data.

The project will be designed in collaboration between student and supervisors. There may be opportunities for field work in Australia or the Pacific.

This is a highly competitive scheme, with excellent support, open to students from any country. Interested students must express interest by 21 July (20 July in the Western hemisphere due to time differences). To earn more and to express interest visit:

http://www.2025.unsw.edu.au/apply/scientia-phd-scholarships/economic-inequality-driver-sexual-competition-and-gendered-traits Up to 2 students will be asked to submit full applications in August.

There is also a lot more about the scheme at http://www.2025.unsw.edu.au/apply/ < http://www.2025.unsw.edu.au/apply/scientia-phd-scholarships/economic-inequality-driver-sexual-competition-and-gendered-traits >

Robert Brooks <rob.brooks@unsw.edu.au>

UValencia LocalAdaptation

GRADUATE POSITION: UniValencia.ICBiBE.EcolEvol

This is a call for candidates for a 3-y graduate student contract to investigate on "LOCAL ADAPTATION, POPULATION DIFFERENTIATION AND REPRODUCTIVE ISOLATION". The contract is granted by the "Santiago Grisolia" program (search on Internet; in Spanish), with start date scheduled for October 1, 2017. The candidate must have a university degree by a non-Spanish institution in biology, ecology, evolution or similar.

The project will focus on within-species pre-mating and post-mating partial reproductive isolation between natural populations of rotifers that has diverged genetically, with stress in divergence due to local adaptation to environmental uncertainty.

The successful candidate will work in the Evolutionary Ecology Lab at the Cavanilles Institute of Biodiversity and Evolutionary Biology of the University of Valencia (EcoEvoLab-ICBiBE-UV), supervised by Manuel Serra (Manuel.Serra@uv.es). EcoEvoLab-ICBiBE-UV cooperates with several laboratories in USA and UK.

Candidates must meet the requirements of the official call, which will appear shortly in the bulletin of the Valencia Community Government. A narrow application time-window (10 days, from the official opening to the deadline) is expected. Anticipating this, the interested students should submit as soon as possible his/her expression of interest to Manuel Serra, including a brief introducing letter, a CV and the name of two faculty or researchers able to report on the candidate record and capability. This submission does not substitute the formal application, which should be submitted according to the formalities of the official call.

Eligibility requirements are: (1) Residence/nationality. (a) To be a national of the EU, or(b) to be a national of a country with an agreement with the EU –ratified by Spain– allowing the free movement of workers, or (c) to be a work permit holder granted by the Spanish government. (2) To have a university degree by a non-Spanish institution. (3) To be in possession of at least 300 ECTS credits, a Master's degree or equivalent. (4) To have finished the studies after January 31, 2014.(5) Not to be in possession of the title of Doctor. (6) To be competent in English or Spanish.

Selection criteria will consider: Interest and experience in ecology. Interest and experience in evolutionary biology. Skills in general laboratory technics, data analysis and molecular methods. English level. Capacity for teamwork

Manuel Serra

Professor of Ecology

Cavanilles Institute for Biodiversity and Evolutionary Biology

University of Valencia (Spain)

http://icbibedb.uv.es/personal/web/serram
https://www.uv.es/serram Manuel Serra <Manuel.Serra@uv.es>

Jobs

BowdoinC Maine ConservationBiology

Position Announcement

Bowdoin College invites applications for a tenure-track position jointly appointed in Biology and Environmental Studies to begin July 2018. We are searching for an environmental biologist working on problems of relevance to an Environmental Studies program, with possible emphases in community, ecosystem, and/or population ecology; potential fields could include, among others: conservation biology, fisheries, ecotoxicology, or limnology. Bowdoin is located in coastal Maine with convenient access to a diverse range of natural habitats including meadows, forests of differing species composition, the Gulf of Maine, the White Mountains and the major rivers that drain them, Merrymeeting Bay (a large freshwater tidal system), urban centers, and agriculture. The College maintains three unique field sites in support of teaching and research: the Coastal Studies Center, a 114 acre preserve on Harpswell Sound, which includes a flowing seawater laboratory and small boat fleet; the Bowdoin Scientific Station on Kent Island in the Bay of Fundy; and 260 undeveloped acres of sandplain grassland, oak-pine forest and pitch pine heath barren adjacent to campus.

Bowdoin welcomes applications from candidates committed to the instruction and support of a diverse student population and those who will enrich and contribute to the College's ethnic and cultural diversity. We value a community in which students of all backgrounds are warmly welcomed and encouraged to succeed. Candidates who have experience working with a particular group of students in the context of Biology and Environmental Studies are encouraged to address this in their cover letter.

The successful candidate will be appointed at the assistant professor level and will offer courses relevant to Biology and Environmental Studies that address contemporary environmental issues. The teaching load is three courses per year and may include the following: contributions to Introduction to Environmental Studies or Perspectives in Environmental Science, which are part of the core course sequence in the Environmental Studies major; advanced courses in the candidate's area of specialty; interdisciplinary capstone courses for Environmental Studies; courses designed for non-majors that meet the College's Inquiry in the Natural Sciences graduation requirement; and occasional contributions to the introductory curriculum in Biology. It is expected that advanced courses and those designed for non-majors might cross list in Biology and Environmental Studies.

The successful candidate must possess a strong commitment to undergraduate education and demonstrate the potential to develop an active and productive research program that involves undergraduate students. Ph.D. required; postdoctoral experience preferred. Bowdoin College offers strong support for faculty research and teaching. There is internal funding in support of research, a junior sabbatical leave, and an accelerated post-tenure sabbatical schedule. We recognize that recruiting and retaining faculty may involve considerations of spouses and domestic partners. To that end, where possible, the College attempts to accommodate and respond creatively to the needs of spouses and partners of members of the faculty.

Bowdoin College accepts only electronic submissions. Please visit https://careers.bowdoin.edu to submit a cover letter, a curriculum vitae, a statement of research plans, a statement describing teaching philosophy/experience, and the names and contact information for three references who have agreed to provide letters of recommendation upon request.

Review of applications will begin September 15.

Founded on the Maine coast in 1794, Bowdoin is one of the oldest and most selective coeducational, residential liberal arts colleges in the country. Located in Brunswick, Maine, a 30-minute drive north of Portland, the College is in an area rich with natural beauty and year-round outdoor activities. Bowdoin's reputation rests on the excellence of its faculty and students, its intimate size, its strong sense of community, and its commitment to diversity (31.5% students of color, 5% international students and approximately 15% first-generation college students).

Bowdoin College complies with applicable provisions of federal and state laws that prohibit unlawful discrimination in employment, admission, or access to its educational or extracurricular programs, activities, or facilities based on race, color, ethnicity, ancestry and national origin, religion, sex, sexual orientation, gender identity and/or expression, age, marital status, place of birth, genetic predisposition, veteran status, or against qualified individuals with physical or mental disabilities on the basis of disability, or any other legally protected statuses. For further information about the College please visit our website: http://www.bowdoin.edu .

— / —

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

CarletonU BehaviouralEvolution

The Department of Biology at Carleton University invites applications from qualified candidates for a tenure-track faculty position at the level of Assistant Professor in the area of Behavioural Ecology, beginning July 1, 2018.

Applicants will have a Ph.D. and preferably postdoctoral experience in the relevant discipline, with a strong commitment to excellence in both teaching and research. The successful candidate will be expected to strengthen our research and teaching programs in Behavioural Ecology. He/she will establish an externally-funded, independent and vibrant research program, and contribute to graduate and undergraduate teaching and training in research.

The Department of Biology has research strengths in most areas of Biology as well as in Biochemistry. The Department offers a variety of undergraduate honours programs in Biology, and contributes to several joint programs in the Faculty of Science. The Department also offers graduate programs in Biology at the M.Sc. and Ph.D. levels. Our facilities include greenhouses with a comprehensive plant collection of several thousand specimens, environmental chambers, teaching and research gardens, molecular biology and biochemistry research facilities, and aquatic facilities. Carleton University is located in Ottawa, the capital of Canada and a major center for research and development. The Department of Biology enjoys close research interactions with several government departments and organizations in the National Capital Region. Please consult the following web sites for more information about Carleton University and the Department of Biology: www.carleton.ca www.carleton.ca/biology Qualifications: The successful candidate will have a Ph.D. in Biology, or a related field, and postdoctoral or relevant experience in Behavioural Ecology.

Application instructions: Application materials should be sent electronically as one PDF file to Biology@carleton.ca to the attention of: Chair, Search Committee for Assistant Professor in Behavioural Ecology, Department of Biology, Room 209, H.H.J. Nesbitt Biology Building, 1125 Colonel By Drive, Ottawa, Ontario K1S 5B6 Canada.

The electronic PDF file should include the following: a cover letter, the names and contact information for three referees, a curriculum vitae, a statement of current and future research interests, and a statement of your teaching philosophy with a list of Biology and Biochemistry courses you would be interested in teaching or developing. Course descriptions can be found at: http://calendar.carleton.ca/undergrad/courses/BIOL/ http://calendar.carleton.ca/undergrad/courses/BIOC/ http://calendar.carleton.ca/grad/courses/BIOL/ Please indicate in your application if you are a Canadian citizen or permanent resident of Canada.

About Carleton University: Join our intellectual and collaborative community of scholars. Carleton University is a dynamic and innovative research and teaching institution with a national and international reputation as a leader in collaborative teaching and learning, research and governance. To learn more about our University and the City of Ottawa, please visit www.carleton.ca/provost . Carleton University is strongly committed to fostering diversity within its community as a source of excellence, cultural enrichment, and social strength. We welcome those who would contribute to the further diversification of our University including, but not limited to: women; visible minorities; First Nations, Inuit and Métis peoples; persons with disabilities; and persons of any sexual orientation or gender identity and expressions.

Applicants selected for an interview are asked to contact the Chair of the Search Committee as soon as possible to discuss any accommodation requirements. Arrangements will be made in a timely manner.

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

——

Susan M. Bertram, PhD Professor Department of Biology Carleton University Ottawa, Ontario, Canada

Email: Sue_Bertram@carleton.ca Phone: 613-520-2600 x1585 Website: http://suebertram.ca/ Blog: http://labchirps.wordpress.com/ Twitter: @sue_bertram Office: CTTC 4631

SueBertram@cunet.carleton.ca

CarletonU PlantPopulationGenetics

The Department of Biology at Carleton University invites applications from qualified candidates for a tenure-track faculty position at the level of Assistant Professor in the area of Plant Molecular Population Genetics/Genomics, beginning July 1, 2018.

Applicants will have a Ph.D. and preferably postdoctoral experience in the relevant discipline, with a strong commitment to excellence in both teaching and research. The successful candidate will be expected to strengthen our research and teaching programs in Plant Molecular Population Genetics/Genomics. He/she will establish an externally-funded, independent and vibrant research program, and contribute to graduate and undergraduate teaching and training in research.

The Department of Biology has research strengths in most areas of Biology as well as in Biochemistry. The Department offers a variety of undergraduate honours programs in Biology, and contributes to several joint programs in the Faculty of Science. The Department also offers graduate programs in Biology at the M.Sc. and Ph.D. levels. Our facilities include greenhouses with a comprehensive plant collection of several thousand specimens, environmental chambers, teaching and research gardens, computational infrastructure, and molecular biology and biochemistry research facilities. Carleton University is located in Ottawa, the capital of Canada and a major center for research and development. The Department of Biology enjoys close research interactions with several government departments and organizations in the National Capital Region. Please consult the following web sites for more information about Carleton University and the Department of Biology: www.carleton.ca and www.carleton.ca/biology

Qualifications:

The successful candidate will have a Ph.D. in Biology, or a related field, and postdoctoral or relevant experience in Plant Molecular Population Genetics/Genomics.

Application instructions:

Application materials should be sent electronically as one PDF file to Biology@carleton.ca to the attention of: Chair, Search Committee for Assistant Professor in Plant Molecular Population Genetics/Genomics, Department of Biology, Room 209, H.H.J. Nesbitt Biology Building, 1125 Colonel By Drive, Ottawa, Ontario K1S 5B6 Canada.

The electronic PDF file should include the following: a cover letter, the names and contact information for three referees, a curriculum vitae, a statement of current and future research interests, and a statement of your teaching philosophy with a list of Biology and Biochemistry courses you would be interested in teaching or developing. Course descriptions can be found at:

http://calendar.carleton.ca/undergrad/courses/BIOL/
http://calendar.carleton.ca/undergrad/courses/BIOC/
http://calendar.carleton.ca/grad/courses/BIOL/
Please indicate in your application if you are a Canadian citizen or permanent resident of Canada.

About Carleton University:

Join our intellectual and collaborative community of scholars. Carleton University is a dynamic and innovative research and teaching institution with a national and international reputation as a leader in collaborative teaching and learning, research and governance. To learn more about our University and the City of Ottawa, please visit www.carleton.ca/provost . Carleton University is strongly committed to fostering diversity within its community as a source of excellence, cultural enrichment, and social strength. We welcome those who would contribute to the further diversification of our University including, but not limited to: women; visible minorities; First Nations, Inuit and Métis peoples; persons with disabilities; and persons of any sexual orientation or gender identity and expressions.

Applicants selected for an interview are asked to contact the Chair of the Search Committee as soon as possible to discuss any accommodation requirements. Arrangements will be made in a timely manner.

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

Alex Wong <AlexWong@cunet.carleton.ca>

CornellU ArthropodBiosystematics

Martha N. and John C. Moser Professor of Arthropod Biosystematics and Biodiversity

The Department of Entomology at Cornell University seeks to fill a tenure-track position in terrestrial arthropod biosystematics and biodiversity at the Assistant or Associate level (as appropriate). The study of biodiversity is a rapidly changing field and we seek a candidate who has expertise in one or more emerging areas of systematics, including (1) bioinformatic approaches to the discovery of biological diversity and its taxonomic description, (2) high-throughput sequencing and genomic approaches to phylogenetic reconstruction, and (3) digitization of biological collections and the large-scale use of collections-based data. We are particularly interested in candidates who make use of cutting-edge methods to document and validate patterns of biodiversity, generate phylogenetic hypotheses, and test evolutionary hypotheses in a robust conceptual framework.

Pursuant to approval by the Cornell University provost, the incumbent will also be appointed as the Martha N. and John C. Moser Professor of Arthropod Biosystematics and Biodiversity. The initial term of appointment to this prestigious, endowed chair would be three years for an assistant professor or five years for an associate professor. Appointment to the Martha N. and John C. Moser Professorship of Arthropod Biosystematics and Biodiversity is renewable, upon endorsement by the college and the university.

Faculty Position: Assistant Professor of Arthropod Biosystematics and Biodiversity*

*It is anticipated that the appointment will be made at the Assistant Professor level, although an early Associate appointment may be considered in exceptional circumstances.

Tenure track, academic year position

50% Research, 25% Teaching, 25% Admin

Starting date: by July 1, 2018

Responsibilities:

* Research (50%) - The successful candidate will be expected to develop and sustain a strong, internationally recognized, and well- funded research program in the area of arthropod biodiversity and systematics. She/he will train graduate students in the Field of Entomology and actively mentor undergraduate students interested in biodiversity research. * Teaching (25%) – The successful candidate will teach a course in Model-Based Phylogenetics and Hypothesis Testing (Entom 4610) on biennial basis, and contribute to course offerings in the area of insect diversity, systematics, and evolution. * Admin (25%) – The successful candidate will serve as Curator of the Cornell University Insect Collection (http://cuic.entomology.cornell.edu/). The Curator will be expected to supervise the Collection Manager, develop grants to support and grow the CUIC, and determine the future direction of the CUIC. She/he will interact with other collections-based programs on campus (e.g., L.H. Bailey Hortorium, Plant Pathology Herbarium, and the Cornell University Museum of Vertebrates).

Qualifications: A Ph.D. in entomology, systematics, phylogenetics, or closely related area in biodiversity and systematics. A demonstrated record of excellence in systematics and biodiversity research as evidenced by publication in peer-reviewed journals is desired. Preferred qualifications include postdoctoral experience, commitment to (and abilities in) team research, ability to communicate effectively with students, colleagues and external stakeholders.

Salary: Competitive, commensurate with background and experience. An attractive fringe benefits package is available.

Application procedure: Applicants must upload into Academic Jobs online a letter of application, curriculum vitae, three selected reprints, and a statement of teaching and research goals and plans. Applicants should also arrange to have three confidential letters of recommendation submitted through Academic Jobs online at https://academicjobsonline.org/ajo/jobs/9291 Review of submitted applications will begin September 1, 2017

Inquiries may be directed to:

Dr. Cole Gilbert

Department of Entomology

Cornell University

Ithaca, NY 14853

Email: cg23@cornell.edu

The Department actively encourages applications from women and minority candidates.

Department Affiliation: The successful candidate will be a faculty member of the Cornell University College of Agriculture and Life Sciences, and will be based in the Department of Entomology in Ithaca, NY (https://entomology.cals.cornell.edu/). A mentoring program for new faculty provides guidance and assistance.

Bryan N. Danforth, Professor and Chair Department of Entomology 3124 Comstock Hall Cornell University Ithaca, NY 14853-2601 phone: 607-255-3563/FAX: 607-255-0939 email: bnd1@cornell.edu Lab website:

— / —

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

DukeU LabTech MolecBioGenomics

Job: DukeU.LabTech.MolecBio.Genomics

An Associate in Research position is available, starting in Fall 2017, in the Tung lab at Duke University. The Tung lab studies the relationship between behavior, the social environment, and genetics and genomics. We combine detailed phenotypic and demographic information with modern genomic data sets on gene regulation and epigenetics. Current projects focus on the gene regulatory mechanisms linking social adversity and health in rhesus macaques, trade-offs associated with helper-breeder transitions in meerkats and mole rats, the epigenetic signature of early life ecological and social adversity, and the genomic and phenotypic consequences of hybridization in wild baboons. Duties will include performance of basic molecular biology laboratory techniques, including DNA and RNA sample extraction and sample preparation for high-throughput sequencing, and responsibility for day-to-day logistics, including purchasing, shipping and receiving, and working with trainees in the lab.

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

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

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

For more information about the lab and our work, see: * http://www.tung-lab.org/* If interested, email resume, including contact information for two references, to Tawni Voyles, *tawni.voyles@duke.edu*

Duke University is an Equal Opportunity/Affirmative Action/ADA Employer committed to providing employment opportunity without regard to an individual's age, color, disability, genetic information, gender, gender identity, national origin, race, religion, sexual orientation, or veteran status.

voyles.tn@gmail.com

HarvardU GlobalChangeAdaptation

TENURE-TRACK PROFESSOR IN GLOBAL CHANGE ECOLOGY

Harvard University

Faculty of Arts and Sciences

Department of Organismic and Evolutionary Biology

Position Description: The Department of Organismic and Evolutionary Biology seeks to appoint a tenure-track professor in Global Change Ecology, with an emphasis on terrestrial ecosystems at physiological, population, community, or ecosystem levels from ecological or evolutionary ecology perspectives. We are especially interested in individuals who conduct rigorous observational and/or experimental work in the field and/or lab that advances our understanding of how climate change, land transformation, and species interactions, introductions or extinctions are affecting terrestrial ecosystems at local, regional and global scales. In addition, we would be interested in individuals who are advancing our understanding of how to conserve biodiversity in natural and human-dominated landscapes, the role of biodiversity in the maintenance of ecosystem services, and the dynamics of coupled human-natural systems. Successful candidates will be expected to develop an innovative research program and contribute to teaching at the undergraduate and graduate levels, particularly in the areas of ecology, conservation biology or global climate change. Applications from, or information about, female and minority candidates are especially encouraged. The department has strong linkages to a number of allied departments and institutions, including the Dept. of Earth and Planetary Science, Harvard Forest, Arnold

Arboretum, Harvard University Herbaria, Harvard Museum of Comparative Zoology, and Harvard Center for the Environment. The appointment is expected to begin on July 1, 2018.

Basic Qualifications: Doctorate in Ecology or related discipline required by the time the appointment begins.

Additional Qualifications: Demonstrated strong commitment to teaching is desired.

Special Instructions: Please submit the following materials through the ARIeS portal (http://-academicpositions.harvard.edu/postings/7705). Candidates are encouraged to apply by October, 1 2017; applications will be reviewed until the position is filled.

1. Cover letter

2. Curriculum Vitae

3. Teaching statement (describing teaching approach and philosophy)

4. Research statement

5. Names and contact information of 3-5 referees, who will be asked by a system-generated email to upload a letter of recommendation once the candidate's application has been submitted. Three letters of recommendation are required, and the application is considered complete only when at least three letters have been received.

6. Publications or copies of creative works, if applicable

Harvard is an equal opportunity employer 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 veteran status, or any other characteristic protected by law.

Contact Information: Prof. Paul Moorcroft, Search Committee, Department of Organismic and Evolutionary Biology, Faculty of Arts and Sciences, Harvard University, Cambridge, MA 02138.

Contact Email: Paul Moorcroft c/o Damari Rosado (damari_rosado@harvard.edu)

"Preheim, Christopher S." <cpreheim@oeb.harvard.edu>

LeipzigU EvolutionAdaptation

Leipzig University and iDiv, the German Center for Integrative Biodiversity Research, offer the following position:

Junior Research Group Leader 'Evolution & Adaptation' (f/m)

* full time employment * working location: Leipzig * initially limited until 30 September 2020 * salary: pay grade (Entgeltgruppe) 15 TV-L

Applications are accepted until 3 September 2017. Please use our application portal under apply.idiv.de.

For more informations see here: https://www.idiv.de/-fileadmin/content/Vacancies_PDF/Vacancies_2017/177_2017_Advert_Junior_Group_Leader_EA.pdf

"Winter, Marten" <marten.winter@idiv.de>

MaxPlanckInst Seewiesen 4 FieldAssist AvianEvol

The Department of Behavioural Ecology and Evolutionary Genetics at the Max Planck Institute for Ornithology in Seewiesen, Bayern, Germany (see http:/-/www.orn.mpg.de/2622/Department_Kempenaers), is seeking three to four field assistants to work from 1st November 2017 to 30th April 2018.

These assistants will work as part of a long-term study on the reproductive biology of a blue tit (Cyanistes caeruleus) population in a protected forest site in Southern Germany.

Work will include: . catching birds at feeders and nest-boxes using traps and/or mist nets . measuring and banding birds . maintenance of electronic nest-box and feeder hardware and equipment . setting up experimental equipment . data collection, entry, and management

Successful candidates must have experience in catching and handling birds, including extensive experience in mist netting. Applicants should also be highly motivated and well organised, with capabilities of working both in a group and independently. Field work hours can be long and tiring, thus applicants must be prepared to work in all types of weather conditions, at any time (including weekends and holidays), with typically only one day off per week.

The working language at the Institute is English, so good knowledge of the language is required. A full, clean driver's licence is essential, with driving experience of at least one year. Experience in driving vehicles with manual transmission is also a necessity. Applicants from outside the EU must ensure they are eligible to remain in Europe for the duration of their contract.

Successful candidates should be vaccinated against Tick Borne Encephalitis (TBE or FSME) before commencing the field work. In addition, applicants should be aware that Lyme disease spread by ticks is common in the area, and should inform themselves about the disease in advance.

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

In an effort to employ more people with disabilities, the Max-Planck-Society specifically encourages people with disabilities to apply for the position. To increase the employment of women in areas where they are underrepresented, the Max-Planck-Society also encourages women to apply for this position.

Review of applications and calls for interviews will begin in September 2017. If you are interested in applying for one of the field assistant positions as described above, please apply (including your CV) via email to kbeck@orn.mpg.de

Kristina Beck Department of Behavioural Ecology and Evolutionary Genetics Max-Planck-Institute for Ornithology Eberhard-Gwinner-Straße, House 7 82319 Seewiesen Germany

"Beck, Kristina" <kbeck@orn.mpg.de>

MaxPlank Ornithology TechAssist

The Max Planck Institute for Ornithology in Seewiesen (near Starnberg) is an internationally oriented research institute, which deals with experimental and theoretical basic research mainly in the field of evolutionary genetics, behavioral ecology and neurobiology. The Research Group of Evolutionary Physiology (Group Prof. Dr. Michaela Hau) is hiring a:

Technical assistant (reference number 04/16)

to work within a one-year/part-time (50%) contract or half-year/full-time

Main duties: To support the working group in carrying out scientific experiments within the research program "Bioenergetic-endocrine perspective of telomere dynamics" (DFG funded project, for more details please refer to Dr. Stefania Casagrande http://www.orn.mpg.de/-person/47215/2606). The study will be carried out in a wild passerine species and represents a combination of laboratory and field work.

Main Requirements: - Completed training as biological-technical assistant, or corresponding qualification due to professional experience. - Previous experience in scientific laboratory work (qPCR). - Able to carry out field research (catching, bleeding and behavioral observation) independently. - Willing and motivated to perform behavioral observations. - Interested in research and able to work both independently and in team. - English skills to properly communicate in an international environment. - Possession of the driving license B. - Ability and willingness to acquire new knowledge independently, as well as sharing it with the group.

What we offer: An interesting and varied activity awaits you in an internationally oriented, modern research institute. The remuneration is paid according to the collective agreement of the public service (TVöD) according to your qualification. In addition, the usual services of the public service are granted. The position is limited to one year part time (50%) or half-year in full-time due to the duration of the project.

The Max Planck Society has set itself the goal of employing more severely disabled people. Applications for severely handicapped persons are expressly desired.

If you are interested, please send your application documents (reference number 04/16), preferably by e-mail in one pdf document, to personal@orn.mpg.de before 07.07.2017.

Max Planck Institute for Ornithology Human Resources Department reference number 04/16 Eberhard-Gwinner-Str. D-82319 Seewiesen

Stefania Casagrande PhD Max Planck Institute for Ornithology Lab of Evolutionary Physiology Eberhard-Gwinner-Str. Haus 5 82319 Seewiesen - Germany Tel: +49 8157 932 248

"Casagrande, Stefania" <scasagrande@orn.mpg.de>

MortonArboretum ForestConservation

This position is targeting those with a background in plant sciences, ecology, evolutionary biology, informatics and/or molecular biology with both lab and field experience. Here is the full job announcement:

Position Available: Research Assistant I (Forest Ecology & Tree Conservation Biology)

Classification: Full-time, Non-exempt

Department: Science and Conservation

General Summary: Support the Forest Ecologist and Tree Conservation Biologist at The Morton Arboretum. These research programs combine elements of field ecology, genetics, and modeling, to advance the preservation and conservation of trees in their natural environments and in living collections (e.g. arboreta). The Research Assistant will participate in planning and executing laboratory and field work using a variety of instruments and methods, assist with lab management, organize and order supplies, maintain and inventory equipment, train and oversee volunteers. This individual will be be involved with the entire research process from data collection and analysis to manuscript preparation. The ideal candidate will be independently motivated and able to contribute to the intellectual development of projects though reading papers, designing studies, and independently analyzing data. There will be opportunity for the individual to collaborate on papers, present research at national meetings, and work with collaborators on international projects.

Qualifications: Applicants should have a strong background in plant sciences, ecology, evolutionary biology, informatics and/or molecular biology with both lab and field experience. A Bachelor's degree in Ecology, Natural Resources, Evolutionary Biology, Botany, Informatics, or related field is required and a Master's degree and/or at least one year experience in laboratory, field, or statistical research is strongly preferred. May require software experience specific to the area of research. Must possess a valid driver's license, which is subject to insurability and an annual Motor Vehicle Record (MVR) report. Proficiency with Microsoft Office Suite and Gmail and other Google applications beneficial.

Success Factors: Must be well organized, communicate clearly, solve problems, be able to work without close supervision (after training), quickly learn new skills, and have strong attention to detail and meticulous record keeping. The applicant must demonstrate curiosity, an ability to multi-task, an enthusiasm for ecology and genetics, and an interest in developing a broad range of skills in forest biodiversity science. Work will include a mixture of office, laboratory, and field work. Good written and oral communication skills. Clear thought, visual acuity, and manual dexterity needed.

Physical Demands and Work Environment: The physical demands and work environment characteristics described here are representative of those that must be met by an employee to successfully perform the essential functions of this job. Reasonable accommodations may be made to enable individuals with disabilities to perform these essential functions.

- Physical Demands: Requires some physical activity: walking over varied terrain, bending, limited lifting and carrying (up to 50 lbs. assisted). Use of chemicals may be necessary. Some out of state travel required.

- Work Environment: Office environment and Arboretum grounds. Work is performed indoors and outdoors, in a variety of weather conditions.

- Equipment: General office equipment, field and laboratory equipment, including specialized equipment relating to particular field of research, hand tools, Arboretum pick-up truck and/or utility vehicle.

For full consideration, please apply before August 14. The position will ideally start at the end of September. To apply, visit http://mortonarb.org/employment The Morton Arboretum is an equal opportunity employer committed to achieving a diverse workforce.

[MortonArbLogo-Green_transparent%2520bkgrd.jpg] Colleen Emrick | Human Resources Specialist The Morton Arboretum | 4100 Illinois Route 53 | Lisle, Illinois 60532 T 630-719-7997 | F 630-725-2040 | cemrick@mortonarb.org | mortonarb.org

Colleen Emrick <cemrick@mortonarb.org>

MountSinai NewYork DataScientist PopulationGenetics

ICAHN SCHOOL OF MEDICINE AT MOUNT SINAI Open Data Scientist Position in Dr. Ron Do Lab A computational data scientist position is available immediately in Dr. Ron Do's lab. The Do lab is in the

Charles Bronfman Institute for Personalized Medicine, Department of Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai, New York, New York.

The Charles Bronfman Institute for Personalized Medicine is an interdisciplinary institute to advance personalized health and health care. One of the institute's key resources is the BioMe electronic health record (EHR)-linked Biobank, an ancestrally diverse population of >34,000 individuals recruited from throughout New York City. BioMe has a longitudinal design and captures and full spectrum of common and rare biomedical phenotypes. BioMe is also rich in genetic data, including genome-wide array genotypes, and exome (N ˜34,000) and whole genome (N ˜15,000) sequencing data.

Dr. Do's lab focuses on determining the genetic and biological bases of complex disease. The group pursues these interests by utilizing approaches from statistical genetics, population genetics, human genetics and genetic epidemiology.

Current lab research areas include: (1) Causal inference of biomarkers with complex disease; (2) Identification of biological processes of complex disease using functional data; (3) Inferring the strength and mode of natural selection for complex disease; (4) Rare variant association studies using sequencing data; (5) Data mining in electronic health records.

The successful candidate will have the opportunity to work on large-scale cutting-edge sequencing, genotyping and high-throughput functional data. Some duties and responsibilities include: developing computational pipelines to analyze large-scale sequencing data, data mining in EHR-linked data, statistical modeling and methods development.

Lab members will benefit from collaborations with neighboring labs in the Charles Bronfman Institute for Personalized Medicine, the Center for Statistical Genetics, and the Icahn Institute for Genomics and Multiscale Biology.

The term for this position is for 3 years with possibility of an extension depending on successful progress and available funding. A competitive salary, benefits and travel opportunities will be offered commensurate with experience and qualifications.

Job Qualifications: 1. Candidates should have a Ph.D., M.D. or equivalent doctorate in Computer Science, Statistics, Bioinformatics, Statistical Genetics, Computational Biology or a related discipline.

2. Candidates should have proficiency in programming (e.g. Perl or Python) and statistical computing (e.g. R).

3. Candidates should have a track record of scientific productivity and/or leadership.

Please send inquiries via email to ron.do@mssm.edu. Informal inquiries are welcome.

Ron Do, Ph.D. | Assistant Professor in Genetics and Genomic Sciences | The Charles Bronfman Institute for Personalized Medicine | The Center for Statistical Genetics | The Icahn Institute for Genomics and Multiscale Biology | Icahn School of Medicine at Mount Sinai | Website: http://labs.icahn.mssm.edu/dolab/ "Do, Ron" <ron.do@mssm.edu>

MPIO Seewiesen EvolutionCognition

The Max Planck Institute for Ornithology (MPIO) in Seewiesen (located near Starnberg, about 50 km from Munich) is an internationally renowned research institution with more than 200 employees working in four departments and nine research groups. The research group of Comparative Cognition (Dr. Auguste von Bayern) runs a research station in collaboration with the Loro Parque Fundación (LPF) on Tenerife, Spain and invites applications for

1 Biological Technical Assistant

The biological technical Assistant position, in part time (minimum 75%) or full time, is available to work in the research group of Dr. Auguste von Bayern at the Comparative Cognition research station on Tenerife, Spain. We are interested in the evolution and mechanisms of complex cognition in birds using a comparative approach.

Main tasks:

The technical assistant will support the research team in carrying out cognitive studies both in the lab of the CCRG and in the breeding station of the LPF, and will also assist in the lab organization. The work will comprise several tasks and will vary. It will require planning, constructing and maintaining experimental equipment (woodwork, metalwork and working with Acrylics), setting up and maintaining technical equipment (cameras, touchscreens, sound recorders, lab computers and the internal server), data organization and programming software (e.g. for touchscreen studies) as well as websites. It will also include some basic animal care duties (our parrots require individual weight monitoring, feeding and enrichment), as well as training and monitoring new team members in lab maintenance and animal care duties. Potentially, it might also involve some practical/experimental work with the parrots, data analysis, preparation of public outreach videos/materials and preparation of tissue samples.

Requirements:

You have a completed training as a biological-technical assistant or have a corresponding qualification due to your professional experience. Applicants should have technical and practical skills and a background or at least a strong interest in Biology and/or Computing Sciences. They have (or will shortly have) a completed degree in a relevant subject and ideally they have previous experience with scientific work/work with animals e.g. in animal cognition, avian neuroanatomy or analysis of animal behavior and/or programming. A high level of responsibility/reliability, high self-motivation and ability to work independent and in a team is an absolute must. Additionally, flexibility, good time management and organization skills are required. We encourage people with a scientific interest to apply because involvement in the studies is possible. Proficient English is mandatory, additional Spanish skills are desirable.

The starting date will be summer/autumn 2017 but no later than 30th of September 2017. The position is available initially for two years but can be extended subject to satisfactory performance. For further information, please do not hesitate to contact Dr. Auguste von Bayern e-mail: avbayern@orn.mpg.de.

The remuneration is paid according to the collective agreement of the public service (TVöD) according to the qualification and the activity to be transferred, up to salary group 9A (TV EntgO Bund), either 75% part time or full time.

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

Please submit a cover letter (describing your interests, experience and goals), your CV, copies of degree certificates and a list of three references as one single PDF preferred via e-mail to: personal@orn.mpg.de

or via mail to:

Max Planck Institute for Ornithology

Human Resources Department

Eberhard-Gwinner-Str.

D-82319 Seewiesen

Deadline for applications: 1.08.2017

“anastacia.k@web.de” <anastacia.k@web.de>

NOAA Seattle MarineMolGenetics

Marine Molecular Geneticist I (Jumeau, AK)

Lynker Technologies, LLC has an immediate opening for a qualified marine molecular geneticist to fill a position on a contract with the NOAA Fisheries service.

This role involves supporting Lynker’s National Marine Fisheries Service (NMFS) operations at the Alaska Fisheries Science Center (AFSC) in Juneau, AK.

Lynker collaborates with the Auke Bay Laboratory (ABL) Marine Ecology And Stock Assessment (ABL/MESA) Ted Stevens Marine Research Institute (TSMRI) to genetically identify juvenile Sebastes melanostictus and Sebastes aleutianus, two closely related rockfish species that are difficult to positively identify using morphological measurements. We are also investigating stock structure of Prince William Sound herring, capelin and arctic cod in the Chukchi Sea, and pollock to understand stock structure in the northern reaches of Alaska, which provide a critical link to the local ecosystem, but have not recovered since the Exxon Valdez oil spill.

As a molecular geneticist participant in the ABL Genetics Program, you will assist in NOAA’s annual stock composition analyses of both Chinook and chum salmon bycatch samples collected by the Observer Program and Bering Sea BASIS research cruises. Your work will contribute to NOAA’s unified model for ocean salmon distributions, which is used by the North Pacific Fishery Management Council to develop policy recommendations for managing the groundfish fisheries and stocks in line with the Magnuson Stevens Act (MSA).

Your key responsibilities will include: * Follow established protocols to process fish and tissue samples and isolating DNA. Teach new lab members how to perform this task.

* Follow established protocols to assist genetic stock identification, species identification and population structure projects using molecular techniques such as DNA electrophoresis, genotyping, and polymerase chain reaction. Microsatellite genotyping will be performed with Ap-

plied Biosystems 3130xl and 3730xl Genetic Analyzers, and SNP genotyping will be performed with TaqMan chemistries assayed on a Life Technologies' QuantStudio real time PCR system. Teach new lab members how to perform these tasks.

* Maintain sample inventory, make general lab solutions, assist in lab cleanup, and assist in stocking of lab supplies.

* Identify and recommend modifications to laboratory techniques and follow established maintenance procedures for lab equipment.

* Assist in data entry and statistical analysis for genetic analyses.

To be considered, you must meet the following minimum qualifications: * A minimum of a Bachelor's degree in a biological science with college level coursework in genetics and three (3) years demonstrated field capability related to the task order. A Master's degree from an accredited college or university with a major in a related field of study may be substituted for two (2) years of the required experience.

* Three (3) years of progressively higher level graduate education leading to a Ph.D, or a Ph.D. from an accredited college or university with a major in a related field of study with an emphasis on molecular biology, population genetics, evolutionary biology, or forensic science may be substituted for the required experience.

* At least 6 months experience working in a genetics laboratory environment.

* Significant experience genotyping samples for microsatellite analysis.

Additional highly desired qualifications include: * Significant experience using a Life Technologies 3130xl or 3730xl Genetic Analyzer for DNA sequencing or genotyping.

* Significant experience programming a PerkinElmer Janus automated workstation and automated DNA extraction robots (Corbett or Qiagen QIAcube).

* Significant knowledge of Life Technologies Genemapper software for scoring microsatellite markers.

* Familiarity with genotyping salmon using DNA microsatellite and SNP marker sets

Please send your resume, list of references, and explanation of how you meet the requirements above to recruiting@lynkertech.com.

Liz Tarquin <ltarquin@lynkertech.com>

OaklandU ComputationalBiol FunctionalGenomics

Tenure-Track Faculty Position in Computational Biology/Functional Genomics

Department of Biological Sciences, Oakland University, Rochester, Michigan, USA

The Department of Biological Sciences at Oakland University invites applications for a tenure-track assistant professor position in Computational Biology/Functional Genomics.

The candidate should establish a competitive research program applying computational approaches to address cutting-edge biological questions. Areas of interest include data science/big data analytics, modeling of molecular and/or biological systems, "-omics" approaches, and other biologically-relevant computational methods.

The candidate must have a Ph.D. in computational/biological sciences or related area and at least two years of postdoctoral experience with a strong publication record. The successful candidate will be expected to develop a vigorous, extramurally funded research program, mentor graduate (MS and PhD) and undergraduate students, and teach undergraduate and graduate courses.

The successful candidate will be encouraged to establish collaborations within and outside the biology department and participate in the recently established interdisciplinary Center for Data Science and Big Data Analytics. Laboratory space and competitive start-up funds will be provided.

The Department of Biological Sciences (http://www2.oakland.edu/biology/) is a vibrant and growing department that places the highest priority on both research and academic excellence. Faculty members enjoy a highly supportive research environment and successfully compete for external grants. In addition to a talented undergraduate population, the department also has an active and growing graduate program with many opportunities to mentor students at the Master's and Ph.D. levels.

Oakland University is a nationally recognized doctoral research institution located on 1,443 acres of scenic land in the cities of Rochester Hills and Auburn Hills in Oakland County, Michigan. The University has 132 bachelor's degree programs and 138 graduate degree and certificate programs. Academics include programs in the College of Arts and Sciences, School of Business Administration, School of Education and Human Services, School of Engineering and Computer Science, School of Health Sciences, School of Medicine and School of Nursing.

Review of applicants will begin after September 8, 2017 and will continue until the position is filled.

Oakland University is an Equal Opportunity Employer and a NSF funded ADVANCE institution, committed to increasing diversity in the STEM fields. Women and minorities are encouraged to apply.

_

Fabia U. Battistuzzi, Ph.D. Assistant Professor Department of Biological Sciences Oakland University battistu@oakland.edu 248-370-3593

Fabia Ursula Battistuzzi <battistu@oakland.edu>

OklahomaStateU IntegrativeBiology

(Note: the ad below ad does not specify subfield but includes evolutionary biology)

The Department of Integrative Biology at Oklahoma State University invites applications for a tenure-track Assistant Professor position. We seek applicants who will complement and expand our departmental strengths (see http://integrativebiology.okstate.edu).

Responsibilities include establishing an extramurally funded research program, mentoring M.S. and Ph.D. students, and teaching at the undergraduate and graduate levels. Applicants must have postdoctoral experience and a strong scholarly record.

To apply, email a single pdf document containing: 1) a cover letter, 2) curriculum vitae, and 3) separate research and teaching statements to biologysearch@okstate.edu; also arrange to have three letters of reference sent in support. Application review will begin October 10, 2017 with employment beginning August 2018. For questions please email biologysearch@okstate.edu.

Oklahoma State University is an Affirmative Action/Equal Opportunity/E-verify employer committed to diversity and all qualified applicants will receive consideration for employment and will not be discriminated against based on age, race, color, religion, sex, sexual orientation, genetic information, gender identity, national origin, disability, protected veteran status, or other protected category. OSU is a VEVRAA Federal Contractor and desires priority referrals of protected veterans for its openings. OSU will not discharge or in any other manner discriminate against employees or applicants because they have inquired about, discussed, or disclosed their own pay or the pay of another employee or applicant. However, employees who have access to the compensation information of other employees or applicants as a part of their essential job functions cannot disclose the pay of other employees or applicants to individuals who do not otherwise have access to compensation information, unless the disclosure is (a) in response to a formal complaint or charge, (b) in furtherance of an investigation, proceeding, hearing, or action, including an investigation conducted by the employer, or (c) consistent with the contractor's legal duty to furnish information. 41 CFR 60-1.35(c)

"daniel.moen@okstate.edu" <daniel.moen@okstate.edu>

Otago NewZealand BioinformaticsReFellow

Bioinformatics Research Fellow

Department of Zoology, University of Otago, New Zealand

Job ID: 1701336

We are seeking a motivated person with advanced experience in bioinformatics to provide support for a range of research projects. This role will require extensive analytic and programming experience, as well as familiarity with current genomic technologies. It will also involve creation of new program code and use of existing bioinformatics software, as well as training and supervision of students using bioinformatics capabilities within the Zoology, Botany and other Division of Sciences Departments.

This full-time position is for a three year fixed term and is available from Friday, 1 September 2017.

Specific enquiries may be directed to Dr Sheri Johnson, Department of Zoology, sheri.johnson@otago.ac.nz

For further information about the position, the Department, and to apply, see:

https://otago.taleo.net/careersection/2/-jobdetail.ftl?job=3D1701336 Application deadline:

Sunday, 6 August 2017.

sheri.johnson@otago.ac.nz

PennsylvaniaStateU HumanEvolutionaryMedicine

Assistant or Associate Professor in the Evolutionary Anthropology of Human Health

The Department of Anthropology (http://anth.la.psu.edu) and the Huck Institutes of the Life Sciences (www.huck.psu.edu) at The Pennsylvania State University invite applications for a tenure-track, early to mid-career scholar whose research uses an evolutionary perspective to inform understandings of human health, starting in August 2018. Topical and methodological areas are open, but the research program of the successful candidate will be integrative and trans-disciplinary, drawing on various approaches from across the anthropological, evolutionary, and biomedical sciences. The candidate could deepen and/or broaden the Department of Anthropology's existing health-related research strengths in human diversity, human genomics, developmental biology, functional anatomy, quantitative imaging, cell culture and animal models for human biology and disease, biocultural-environment interaction, human-pathogen coevolution, and other areas. The new faculty member will also benefit from Penn State's exceptional cross-departmental research environment while they contribute to University-level efforts in developing interdisciplinary expertise on the evolutionary mechanisms of human health. The successful candidate will have opportunities to train graduate students in the top-ranked Department of Anthropology program and through various Huck Institutes of the Life Sciences-sponsored intercollege programs, and as part of a new (pending final approval) MD-PhD in Anthropology program in cooperation with the College of Medicine.

Review of applications will begin September 8, 2017 and continue until the position is filled. Direct questions regarding this faculty position to Dr. George Perry (ghp3@psu.edu).

Applications should be submitted online and include: 1) a one-page cover letter, 2) a curriculum vitae with educational background, employment history, and a list of publications; 3) a two-page future research program statement; 4) a one to two-page teaching statement; and 5) the names, affiliations, and email addresses of three professional references. Apply online at https://psu.jobs/job/72742 CAMPUS SECURITY CRIME STATISTICS: For more about safety at Penn State, and to review the Annual Security Report which contains information about crime statistics and other safety and security matters, please go to http://www.police.psu.edu/clery/, which will also provide you with detail on how to request a hard copy of the Annual Security Report.

Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to all qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national origin, disability or protected veteran status.

grgperry@gmail.com

Reunion France InsectEvolution

The hired researcher will have to sudy the evolution of insect behavior among other things.

*****

Cirad seeks a talented scientist for a permanent researcher position in Reunion island (France) on the chemical ecology of arthropods. Application will be online. Deadline for application September, 5th. More information here: http://www.cirad.fr/emplois-stages/postes-a-pourvoir/chercheurs/chercheur-euse-specialiste-en-ecologie-chimique-des-arthropodes-a-la-reunion This position will contribute to research activities aimed at generating knowledge to improve methods of management and control of pests in agrosystems.

Among these pests, several species of fruit flies (Tephritidae) are of major economic importance for fruit and vegetable sectors in tropical environments. In Reunion, eight species of fruit flies of economic interest are present, and effective attractants lack.

A better understanding of the behavior of insects, such as their response to various attractants, and how these attractants can also play a role in attracting natural enemies (such as parasitoids) is essential for understanding trophic interactions. For example, studies of resource-seeking behavior must take into account the variability of behavior and its evolution. These techniques use, in particular, techniques such as electrophysiology or olfactometry. To do this, the UMR within the Plant

Protection Pole (3P), labeled by the GIS IBiSA, has a technical platform dedicated to entomological work, including ethology (olfactometers, flight tunnel and a chain GC-EAD and GC-MS for electrophysiology)

Virginie RAVIGNE <virginie.ravigne@cirad.fr>

SalveReginaU 1yrTeaching EukaryoticCellEvolution

Visiting Assistant Professor, Eukaryotic Cell Biology Apply through https://salve.interviewexchange.com/jobofferdetails.jsp?JOBID=81410 Category: Academic / Faculty RSS feed of all Jobs Subscribe to Job Alerts Department: Biology and Biomedical Science Locations: Newport, RI Posted: Feb 13, '17 Type: Full-time

About Salve Regina University: Salve Regina University, ranked among the best institutions of higher education in the United States by U.S. News & World Report, is a comprehensive Catholic University located in scenic Newport, Rhode Island. Salve Regina offers challenging academic programs in a highly supportive environment and an innovative core curriculum that provides students with a solid foundation and broader perspective. The historic, 75-acre campus enrolls approximately 2,500 men and women and offers Associate, Baccalaureate, and Master's degrees, the Certificate of Advanced Graduate Study, and two doctoral programs.

Job Description: The Department of Biology and Biomedical Science is pleased to announce an opening for a Visiting Assistant Professor in the area of Eukaryotic Cell Biology to start September 1st, 2017. Salve Regina University is a mission driven institution with a focus on excellent undergraduate education. Applicants should possess a Ph.D. in biology or related field and have relevant teaching experience. The successful candidate will be expected to teach 21 contact hours a year. The length of the appointment is for 1 year. The successful applicant will have an opportunity to collaborate with departmental faculty as well as, mentor undergraduate students and gain experience in writing grants.

Requirements: The successful candidate must have an earned Ph.D. in a related area of biology by time of hire. Teaching and postdoctoral research experience is preferred but not mandatory. Candidate must be strongly committed to excellence in undergraduate teaching and academic advising. They should also have an ability to communicate effectively and to use technology effectively in teaching and learning, and to work collaboratively.

Additional Information: Salve Regina University offers generous benefits to eligible employees including: health and dental coverage, life insurance, long-term disability, 403B plan, tuition benefits and more.

Salve Regina University is an Equal Opportunity/Affirmative Action employer. The University actively seeks diversity among its employees.

John-David Swanson <jd.swanson@salve.edu>

SanDiegoStateU ComputationalEvolutionaryBiology

Assistant Professor: Computational Evolutionary Biology at San Diego State University: Sciences: Biology

Location: San Diego, CA

—

THE DEPARTMENT OF BIOLOGY AT SAN DIEGO STATE UNIVERSITY invites applications for a tenure-track faculty position in *COMPUTATIONAL EVOLUTIONARY BIOLOGY* at the Assistant Professor level. We are seeking a candidate whose research program centers around the use and development of modern computational methods to answer fundamental questions in evolutionary biology. Specific areas of research interest might include, but are not limited to: patterns/processes of species diversification, biogeography and macroecology, phenomics (large-scale phenotypic analysis), phylogenomics and population genomics, and comparative genomics or transcriptomics. We expect to hire a candidate who creatively bridges evolution and other fields of biology, with a demonstrated strength in organismal biology.

Candidates should have a Ph.D. in Evolutionary Biology or a related field, relevant post-doctoral experience, and a strong record of research accomplishments and funding. The successful candidate should also display a commitment to undergraduate and graduate teaching. Teaching responsibilities will include participation in undergraduate biology courses, and additional graduate courses in the candidate's areas of expertise. The successful candidate will participate in the MS and Ph.D. programs in Evolutionary Biology and may also participate in the department's MS and Ph.D. programs in Cell and Molecular Biology, and Ecology. Preference will be given to candidates that can and wish to train graduate students in more than one graduate program.

SDSU is a large, diverse, urban university and Hispanic-Serving Institution with a commitment to diversity, equity, and inclusive excellence. Our campus community is diverse in many ways, including race, religion, color, sex, age, disability, marital status, sexual orientation, gender identity and expression, national origin, pregnancy, medical condition, and covered veteran status. We strive to build and sustain a welcoming environment for all. SDSU is seeking applicants with demonstrated experience in and/or commitment to teaching and working effectively with individuals from diverse backgrounds and members of underrepresented groups. The College of Sciences is host to a large number of federally-funded minority training programs (described at http://www.sci.sdsu.edu/casa/).

Application Instructions

Apply via Interfolio.Review of applications will begin *September 15, 2017*, and will continue until the position is filled. Incomplete applications are not guaranteed full consideration.

Apply Now < https://dossier.interfolio.com/apply/-43326 >

Marshal Hedin <mhedin@mail.sdsu.edu>

Smithsonian 3 Technicians

The Department of Invertebrate Zoology at the Smithsonian National Museum of Natural History has 3 openings for Museum Technicians. The positions are multifunctional and utilize a variety of skill sets with collections management, IT development, taxon expertise, and data management. Although the add for them all is identical, the jobs will each be a bit different and be varied and interesting positions.

These are federal positions (which unfortunately means you must be a US citizens to apply) starting at GS-7 with promotion potential to GS-11. Having worked with invertebrate specimens is a requirement.

The postings will only be open for a short time - just 2 weeks! Please email me if you have questions or you can contact the chair of the search committee, Bill Moser (moserw@si.edu).

https://www.usajobs.gov/GetJob/ViewDetails/-474199300 (open to the public)

https://www.usajobs.gov/GetJob/ViewDetails/-474199000 (open only to federal employees)

Karen Osborn Research Zoologist/Curator of Polychaetes, Peracarids and Plankton Department of Invertebrate Zoology w 202.633.3668 osbornk@si.edu http://invertebrates.si.edu/osborn/ http://orcid.org/-0000-0002-4226-9257 SMITHSONIAN INSTITUTION NATIONAL MUSEUM OF NATURAL HISTORY Facebook < https://www.facebook.com/nmnh.fanpage/ > | Twitter < https://twitter.com/NMNH > | Instagram < https://www.instagram.com/smithsoniannmnh/ >

Mail: Department of Invertebrate Zoology, Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012, Washington, D.C. 20013-7012 USA

Courier Address: Smithsonian Institution, MR 0163, Natural History, West Loading Dock, 10th and Constitution Ave NW, Washington, D.C. 20560

"Osborn, Karen" <OsbornK@si.edu>

SriLanka EvolutionaryBiology

Vacancies at the National Institute of Fundamental Studies, Kandy Sri Lanka. Research Professor, Associate Research Professor, Research Fellow

Vacancies are available for candidates who can perform cutting-edge research in the research areas of Molecular Life Sciences and Environmental Sciences in the broadest senses.

Qualifications -

A Degree from a recognized institution with specialization in mathematics/physics/chemistry /life science/ social science/ philosophy with First class or Second class (Upper Division) Honours.

OR

A Degree from a recognized institution with specialization in mathematics/ physics/ chemistry/ life science/ social science/ philosophy with Second Class (Lower Division) Honours with at least one year postgraduate research experience.

OR

A Degree from a recognized institution with specialization in mathematics/ physics/ chemistry/ life science/ social science/ philosophy or a degree with at least Second Class Honours with minimum of two years postgraduate research experience. AND ii. A Ph. D degree from a recognized institution in mathematics/ physics/ chemistry/ life science/ social science/ philosophy.

OR

A Master's degree (M Phil.) and two years research experience after obtaining the M Phil degree and obtaining a minimum of 50 marks according to the marking scheme of the NIFS.

An additional 35% of the basic salary will be paid for contract basis positions.

Successful applicants will contribute 10% of their remuneration to EPF while the institute's contribution will be 15% to EPF and 3% ETF.

Those interested should forward their applications under registered cover to be received not later than 21 days of the date of this notice. Please indicate the position and the research area you wish to apply at the top left corner of the envelope. Each such application should include the Curriculum Vitae with testimonials from two non-related referees and a comprehensive 1-2 page research proposal which is expected to be carried out at NIFS.

Director

National Institute of Fundamental Studies

Hantana Road

Kandy

Sri Lanka

Tel: +94 081-2232002

Fax: +94 081-2232131

Date of the advertisement: 16.07.2017

Closing Date: 08.08.2017

Suresh Benjamin <suresh.benjamin@gmail.com>

Sydney PathogenGenomics

Research Fellow in Pathogen Genomics

Sydney Medical School - Westmead

Reference no. 1309/0617

- Join an organisation that encourages progressive thinking

- Be valued for your exceptional knowledge and experience in pathogen genomics

- Full time fixed term for two years; further offers possible dependent on funding and need

About the opportunity

The position will be based at the Sydney Medical School-Westmead and the Centre for Infectious Diseases and Microbiology-Public Health (CIDM-PH). CIDM-PH is an interdisciplinary translational research group within the Microbiology and Infectious Diseases Departments of the Westmead Clinical School, Western Sydney Local Health District, Australia and Pathology West - Institute of Clinical Pathology and Medical Research. This position is funded by the NHMRC Project Grant APP1102170 "Genomics dissection and prevention of bacterial transmission events" administered by the University of Sydney.

With this position we are seeking an enthusiastic, early career researcher to participate in the newly funded NHMRC project grant. This Research Fellow will interrogate genomic variables of bacteria involved in foodborne outbreaks and will develop genomic methods of tracking disease transmission pathways. He/she will also be expected to participate in genomic data generation and synthesis and analysis of genomic, clinical and epidemiological data, in collaboration with other investigators. The position is based at the Public Health Pathogen Genomics Unit, Centre for Infectious Diseases and Microbiology, Westmead Clinical School and the Institute of Clinical Pathology and Medical Research - Pathology West. The Research Fellow will also join the Westmead Node of the Marie Bashir Institute for Infectious Diseases and Biosecurity (MBI).

About you

The University values courage and creativity; openness and engagement; inclusion and diversity; and respect and integrity. We see the importance in recruiting talent aligned to these values in the pursuit of research excellence. We are looking for a dedicated researcher who has:

- A PhD in biomedical science, genomics or bioinformatics experience commensurate with appointment at Research Fellow level

- Research experience in molecular diagnostics and molecular epidemiology of infectious diseases

- Experience in bacterial genomics and bioinformatics

- High level oral and written communication skills

- evidence of an ability to work both independently and co-operatively with others, and to provide leadership

- previous experience in collaborative research programs (desirable).

About us

Since our inception 160 years ago, the University of Sydney has led to improve the world around us. We believe in education for all and that effective leadership makes lives better. These same values are reflected in our approach to diversity and inclusion, and underpin our long-term strategy for growth. We're Australia's first university and have an outstanding global reputation for academic and research excellence. Across our campuses, we employ over 6000 academic and non-academic staff who support over 60,000 students.

We are undergoing significant transformative change which brings opportunity for innovation, progressive thinking, breaking with convention, challenging the status quo, and improving the world around us.

For more information on the position and University, please view the candidate information pack available from the job's listing on the University of Sydney careers website.

All applications must be submitted via the University of Sydney careers website. Visit sydney.edu.au/recruitment and search by the reference number to apply.

Closing date: 11.30pm 4 August 2017

The University of Sydney is committed to diversity and social inclusion. Applications from people of culturally and linguistically diverse backgrounds; equity target groups including women, people with disabilities, people who identify as LGBTIQ; and people of Aboriginal and Torres Strait Islander descent, are encouraged.

If we think your skills are needed in other areas of the University, we will be sure to contact you about other opportunities.

The University of Sydney

The University reserves the right not to proceed with any appointment.

Brittney Mcanena <brittney.mcanena@sydney.edu.au>

TheBroadInstitute ComputationalBiol

Computational Biologist - Bacterial Genomics Group

Broad institute of MIT and Harvard, Boston, MA, US

Job description

The bacterial genomics group at the Broad Institute of MIT and Harvard is seeking a creative and highly motivated Computational Biologist. The ideal candidate should be broadly conversant with bioinformatics techniques for genomic data analysis, and will use this knowledge to help us understand 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, made significant contributions to their area of study, and enjoys working across diverse projects in a team environment.

Requirements

- A Ph.D. in Computer Science, Bioinformatics, Biostatistics, Mathematics, Physics, Biology, 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
- Familiarity with DNA next-generation sequencing data
- Comfort and experience with programming for biological data analysis
- Understanding of bacterial genetics preferred
- Experience with metagenomic data analysis preferred
- Demonstrated attention to detail
- Excellent ability to communicate scientific material
- Excellent organization and time management skills
- Excellent collaborative skills and unrelenting enthusiasm for genomic science
- EOE/Minorities/Females/Protected Veterans/Disabilities

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.

The Bacterial Genomics Group within the Genome Center for Infectious Diseases at the Broad Institute 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 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.

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.

EOE Minorities/Women/Protected Veterans/Disabled

Andrea Petrosino <andrea@broadinstitute.org>

TulaneU PlantEvolution

The Department of Ecology & Evolutionary Biology at Tulane University invites applications for two tenure-track positions at the Assistant Professor Level. Candidates are required to have a Ph.D. in a related field at the time of application and postdoctoral research experience is preferred. The desired areas of specialization are (1) Plant Molecular Ecologist and (2) Animal Physiological Ecologist. For details about these positions and to apply, please see (1) https://apply.interfolio.com/42576 and (2) https://apply.interfolio.com/42577 Plant Molecular Ecologist

The Department of Ecology & Evolutionary Biology at Tulane University invites applications for a tenure-track faculty position at the Assistant Professor level with a research focus on the application of molecular techniques (e.g., population genetics, molecular genomics) to address ecological and/or evolutionary questions in plants. Preference will be given to researchers whose work complements one or both of our departmental concentrations in tropical biology and river/coast ecosystems. We are also interested in candidates whose research can be applied to restoration and conservation issues.

The position is 60% research, 10% service and 30% teaching, with lab space and a competitive start up package to be provided. The faculty member will be responsible for teaching one course per semester and will rotate among 3 or 4 different courses. In addition to teaching, faculty members mentor Ph.D., M.S. and B.S. students in Tulane's School of Science and Engineering.

The vision of the Department of Ecology and Evolutionary Biology is to be recognized as a center for solution-based science in ecology and evolutionary biology with foci in tropical and river-coast ecosystems. We aim to conduct translational research: basic scientific advance is not only an end in itself but also a means to providing solutions to global environmental challenges. The department maintains interactions with nationally and internationally recognized programs. For example, Tulane is a member of the Organization for Tropical Studies and our students and faculty interact with study abroad courses worldwide. Locally, our department is involved in the Riversphere - A Center of Excellence in Renewable Energy Systems, and The ByWater Institute. Along with a shared molecular facility within our department, we collaborate with the School of Science and Engineering to use the Coordinated Instrumentation Facility.

The department participates actively in multiple community-engaged Tulane University activities, including the Center for Engaged Teaching and Learning, Girls in STEM at Tulane (GIST), Boys at Tulane in STEM (BATS), the Taylor Center for Social Innovation and Design Thinking, and Tulane's mandatory two-tiered service learning requirement for undergraduates (CPS). We are fully committed and proactive in seeking ways to achieve the goal of a diverse and inclusive academic community of faculty, staff and students and we seek individuals who will actively support this goal.

Tulane University is a member of the prestigious Association of American Universities, a select group of the 62 leading research universities in the United States and Canada with 'preeminent programs of graduate and professional education and scholarly research.' Tulane is located in the historic Gulf Coast city of New Orleans, which is known for its culture, food and music.

Qualifications

The successful candidate must have a Ph.D. degree in Biology, Ecology, Evolutionary Biology, or a related field. Postdoctoral research experience is strongly preferred.

APPLICATION INSTRUCTIONS

To apply please submit the following: (1) Cover letter, (2) Curriculum Vitae, (3) statement of research accomplishments and future directions, (4) teaching statement, (5) up to three publications and (6) name and contact information (address, e-mail, phone) of three professional references who can address candidate's qualifications.

Review of applications will begin October 13, 2017 and search will remain open until the position is filled, with a start date of July 1, 2018.

Applications must be submitted via Interfolio to https://apply.interfolio.com/42576 Tulane University is an Affirmative Action/Equal Employment Opportunity Employer.

Please contact any member of the search committee if you have additional questions.

- Dr. Caz Taylor (caz@tulane.edu, committee chair)
- Dr. Tim Mclean (tmclean1@tulane.edu)
- Dr. Emily Farrer (efarrer@tulane.edu)

Animal Physiological Ecologist

The Department of Ecology & Evolutionary Biology at Tulane University invites applications for a tenure-track faculty position at the Assistant Professor level conducting physiological research addressing

— / —

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

---

UBath ResTech EvolutionaryGenomicsMicrobes

We are excited to be recruiting a Research Technician to work on a project focused on the genetic basis and evolution of social, developmental, and life-history traits in a microbe (a social amoeba). The project will combine high throughput measurements of traits with genome sequencing to understand the genetic basis to variation in natural populations. The technician will be required to work independently and will oversee several different technical components requiring different skill sets.

The technician will support all aspects of the project, including culturing of strains, performing phenotyping assays, the preparation of genomic DNA samples, DNA (Sanger) sequencing, genome sequencing, and the processing of data sets.

The successful candidate will have a university degree in biology and relevant experience with laboratory based research in biology, including knowledge of basic molecular biology. Previous experience with microbiological techniques is desirable.

The position is fixed-term of 12 months and available to start as early as September 2017, but earlier or later start dates may be possible, subject to negotiation and approval.

For further information and to apply please see: https://www.bath.ac.uk/jobs/Vacancy.aspx?ref=SF5059 This is a collaborative project, offering opportunities to interact and work with colleagues both in Bath and at other institutions.

For an informal discussion about the role, contract and salary issues, and the project details please contact Prof Jason Wolf via email: j.b.wolf@bath.ac.uk (telephone or Skype consultations can be arranged)

jason@evolutionarygenetics.org

UBritishColumbia ChairInBiodiversity

UBC President's Excellence Chair in Biodiversity Studies

The Biodiversity Research Centre at the University of British Columbia, in Vancouver, Canada, invites applications for the President's Excellence Chair in Biodiversity Studies. We welcome applications from diverse candidates working in any area of biodiversity research and on any organisms or ecosystems. Candidates are expected to have an innovative and integrative research program that would extend and complement existing faculty strengths in conservation biology, ecology, evolutionary biology, microbial evolution, physiology, and systematics. We are especially interested in candidates with a track record of effective societal engagement. The appointment is expected to be at the rank of Associate or Full Professor, according to the qualifications of the candidate. Review of applications will begin in the fall and will continue until the position is filled (for full consideration, please submit materials by September 18, 2017).

For more information, please see:

https://academic.ubc.ca/sites/vpa.ubc.ca/files/documents/ubc_presidents -excellence-chair-biodiversity-studies-ad.pdf

Katie Beall <brcadmin@biodiversity.ubc.ca>

UCalifornia Davis ViralEvolution

The Diaz-Munoz Lab at the University of California, Davis is looking for a SENIOR FLU GURU (PROJECT SCIENTIST). The Diaz-Munoz Lab studies the social lives of viruses, with a current focus on coinfection and reassortment in segmented viruses (cystoviruses and influenza viruses). We have an evolutionary perspective and take an integrative approach to the study of virus-virus interactions using tools from genomics, environmental microbiology, classical virology, genetics, and ecology.

The successful candidate will work on an NIH-funded project that experimentally examines reassortment in human and avian influenza viruses using high-throughput sequencing. While the position is to work on a specific project, creative contributions to the ongoing project and future offshoots are expected and encouraged. The successful candidate will also, in coordination with the PI, manage influenza virus-related aspects of the lab. Excellent interpersonal and communication skills are essential, as the lab is a diverse team in terms of scientific and personal backgrounds.

Required Qualifications: (summary of qualifications below, see official posting for details) - Ph.D. in virology, microbiology, molecular-cell biology, immunology or related fields - More than 5 years of experience post-PhD (see postdoc ad if <5 yrs post-PhD) - Experience with cell culture, animal virus culture and standard virology techniques - Experience working in BSL2 (or higher) containment - Experience with standard genetics lab techniques (e.g. RT-PCR, electrophoresis)

Preferred Qualifications (one or more) - Experience with influenza virus culture - Experience with single cell techniques - Molecular cloning or genetic engineering experience - Microscopy experience - Experience with RNA and protein detection techniques - Research or university-level coursework in evolution and ecology

UC Davis is a leading research institution with over $750 million dollars in research funding and top-tier faculty. The campus is a diverse, supportive community with UC Davis named top college for women in STEM (Forbes), first in the world for campus sustainability (GreenMetric), and a top college for economic diversity and upward mobility (NY Times). The City of Davis is a vibrant, livable, family-friendly community. It was ranked best small town for cycling (Bicycling Magazine) and hosts one of the best farmer's markets in the nation (American Farmland Trust). Davis has a privileged position between Sacramento, Napa Valley, and the Sierra Foothills with the San Francisco Bay Area and Lake Tahoe just a drive away.

Interested candidates should submit the following materials via the UC Davis Jobs posting https://-recruit.ucdavis.edu/apply/JPF01623: 1. A cover letter briefly describing: why you are interested in working in the lab, relevant experience, research interests, and a list of contact information for three references 2. Curriculum Vitae 3. 1-2 relevant publications (can be links if open access) 4. (Optional) One page Statement of Contributions to Diversity.

Apply by July 15, 2017 for full consideration. Applications will be reviewed until the position is filled. People from underrepresented and underserved communities are especially encouraged to apply (for Realz).

samdiazmunoz@UCDAVIS.EDU

UCambridge EvolutionaryDynamicsEarlyCancer

Research Associate (postdoc)

CRUK Cambridge Center, University of Cambridge, UK

We are seeking a motivated postdoc interested in the dynamics of somatic variants in healthy and precancerous tissues. The post will involve developing quantitative models (both simulations and theory) of clone dynamics in rapidly cycling tissues and applying these models to deep sequencing data sets generated from longitudinal blood samples collected over a 20-year period.

This full-time position is for a three year fixed term. Start date is somewhat flexible.

Informal enquiries are strongly encouraged, and should be directed to Jamie Blundell at jrb75@cam.ac.uk.

For further information about the position see

http://www.jobs.cam.ac.uk/job/14398/ or the lab website < http://blundelllab.com/ >

Application deadline: 19th September 2017.

– Jamie Blundell web: blundelllab.com twitter: @jrblundell < https://twitter.com/jrblundell >

Jamie Blundell <jrb75@cam.ac.uk>

UFlorida StAugustine LabTech MarineScience

Whitney Laboratory for Marine Bioscience, University of Florida, St. Augustine, Florida: Lab Technician

The Schnitzler lab at the Whitney Laboratory for Marine Bioscience seeks candidates for a full-time molecular laboratory technician. The laboratory technician will lead and assist with the care and maintenance of our lab organism, the colonial marine hydroid Hydractinia. This includes maintenance and cleaning of aquarium tanks for the hydroids, regular feedings, and water changes. Following protocols for spawning and maintaining developing embryos and performing microscope-aided dissections is also required. The laboratory technician will be responsible for daily water quality care (monitoring pH, salinity, nitrite levels, etc.) and daily animal care. The laboratory technician will order all necessary supplies and equipment for the lab, maintain equipment, keep track of purchases and their status in an online system, maintain chemical and equipment inventory, and handle both receiving and returning orders when necessary. Other duties include preparing the lab for EH&S inspections, managing biohazardous wastes, and preparing stock solutions and reagents. In addition to carrying out these daily tasks, the technician will develop and carry out molecular and cellular biology techniques and protocols and manage and analyze resulting data, including maintaining a detailed online laboratory notebook. Techniques will include DNA and RNA extraction and quantification, molecular cloning, preparation and purification of plasmid DNA, in situ hybridization, gene manipulation and gene editing techniques (RNAi, morpholinos, CRISPR/Cas9), microinjection and electroporation of embryos, standard and quantitative PCR, epifluorescence and confocal microscopy.

A minimum of a BachelorÂ¹s degree in a biological science with college level coursework in genetics, molecular biology and/or cellular biology is required with a MasterÂ¹s degree preferred. Experience with maintaining and feeding of marine organisms is preferred. At least 6 months experience working in a molecular, cellular biology or genetics laboratory environment is required. Experience with some of the molecular and cellular biology techniques listed above is required. A flexible schedule and availability to work on some weekends is preferred. The candidate must be able to work efficiently, effectively, and independently, have great organizational and communication skills, work well in a group, and be willing to train others.

Preferred start date is late August or early September 2017. Interested applicants should submit a curriculum vitae, a letter of interest detailing how their background prepared them for each of the requirements of this position, and the names of three potential references.

Submit applications here: http://explore.jobs.ufl.edu/cw/en-us/job/501859/ops-laboratory-technician Application must be submitted by 11:55 p.m. (EDT) on 11 August 2017 for full consideration.

Dr. Christine Schnitzler Assistant Professor, Biology Whitney Laboratory for Marine Bioscience University of Florida http://www.whitney.ufl.edu/christineschnitzler/ Christine Schnitzler <christine.schnitzler@whitney.ufl.edu>

UGlasgow ResAssist Growth-Lifespan

Research Assistant/Associate

Reference Number 018228 Location Gilmorehill Campus / Main Building College / Service COLLEGE OF MVLS Department RI BIODIVERSITY ANIMAL HEALTH & COMPMED Job Family Research And Teaching Grade 6/7 Position Type Full Time Salary Range 27,629 - 31,076/33,943 - 38,183

You will contribute to a project investigating the mechanisms underlying the trade-off between growth and lifespan in order to understand how early growth conditions can influence ageing and longevity, using captive zebra finches. The focus will particularly be on the somatotrophic axis, mitochondrial function and telomere dynamics.

Working with Professors Pat Monaghan and Colin Selman

Specifically, the job requires expert knowledge in. and experience of: Measuring hormones in small avian blood samples; agarose gel electrophoresis, using quantitative PCR; other basic molecular biology techniques including DNA extraction; advanced data analyses, writing scientific papers. Previous experience of working on mitochondrial function would also be beneficial.

Closing date 6th Aug. For more details see Glasgow University website https://udcf.gla.ac.uk/it/iframe/jobs/

Pat Monaghan Regius Professor of Zoology College of Medical, Veterinary and Life Sciences Room 4-26, Graham Kerr Building University of Glasgow Glasgow G12 8QQ

++141 330 6640

Secretary Lorna Kennedy ++141 330 5975 email Lorna.Kennedy@glasgow.ac.uk

Pat Monaghan <Pat.Monaghan@glasgow.ac.uk>

UNottingham 1yrTeaching EvolutionaryEcology

A part time, 10 month position is becoming available to cover my teaching (evolutionary ecology and related content) at the University of Nottingham while on sabbatical next year. It is being advertised to internal (University of Nottingham) candidates only, until 18th July, but is likely to be advertised on jobs.ac.uk after that. Advertisement follows.

Teaching Associate (part time, fixed term) Life Sciences Location: University Park Salary: 29,301 to 38,183 per annum pro-rata depending on skills and experience. Salary progression beyond this scale is subject to performance.

Applications are invited to the above role. The primary purpose of the role will be to undertake undergraduate teaching and provide advice as a member of the Biology teaching team within an established programme of study. The role holder may also contribute to curriculum development in the School.

Teaching duties will include the delivery of Lectures, Tutorials, Supervision of field and laboratory work, and the assessment of student performance in each of these. In particular, the role holder will deliver the teaching of an existing member of academic staff (Dr Andrew MacColl). The role will include delivery of content in the following areas: Biodiversity (field course), Evolutionary Ecology, Parasitology, and Statistical analysis of biological data, as well as supervision of Honours project work in related areas. In addition to the delivery of existing content, the role holder will be involved in the development of new teaching and assessment practices in these areas and disseminating these practises within the School/Faculty.

Candidates must hold a PhD or equivalent in Zoology, Evolutionary Biology, Ecology or relevant subject area or an equivalent professional qualification. Experience of delivery and assessment of teaching in a Higher Education setting is a requirement and it is desirable that candidates be supported by a Higher Education teaching qualification (or working towards). Candidates must have relevant experience in the specific areas of content to be delivered. Recent experience in module convenorship, use of Moodle (or similar online learning environment) are highly desirable.

This part time role (18.12 hours per week) is available fixed term from 1 September to 31 May 2018.

Informal enquiries may be addressed (Dr. Andrew MacColl, andrew.maccoll@nottingham.ac.uk) Please note that applications sent directly to this Email address will not be accepted.

The School of Life Sciences holds an Athena Silver SWAN Award, in recognition of our commitment to supporting and advancing women's careers in the life sciences (STEMM). You can read more about this initiative at http://www.nottingham.ac.uk/lifesciences/documents/athena-swan-silver-award.pdf Associate Professor of Evolutionary Ecology School of Life Sciences University of Nottingham University Park Nottingham NG7 2RD, U.K. Tel: +44 115 951 3410 http://ecology.nottingham.ac.uk/AndrewMacColl/index.php Andrew.Maccoll@nottingham.ac.uk

---

UOklahoma AncientDNA TechnicianPosition

Lab/Research Technician III - Job Number: 171743

Laboratories of Molecular Anthropology and Microbiome Research

Department of Anthropology

University of Oklahoma

Job type: Full time + benefits

Apply by: Open until filled

Start date: August 2017, open to negotiation

University of Oklahoma's Laboratories for Molecular Anthropology and Microbiome Research (LMAMR.ORG) is seeking a laboratory technician to conduct studies in anthropological genomics and proteomics under Dr. Courtney Hofman. The research technician will be involved in generating and analyzing molecular datasets from archaeological and museum samples. The technician will work in LMAMR's 6-room ISO-6 ancient DNA laboratory and well-equipped modern lab to prepare samples for high throughout DNA sequencing. The technician will also share responsibility for day-to-day lab operations, including laboratory administration and data organization. Experience with high throughput DNA sequencing is preferred. Ability to communicate clearly, work independently, and interact collaboratively is essential. More information about the research activities of LMAMR and Dr. Hofman can be found at lmamr.org and courtneyhofman.com.

The University of Oklahoma is a Carnegie-R1 comprehensive public research university known for excellence in teaching, research, and community engagement. The University of Oklahoma enrolls over 30,000 students and has more than 2,700 full-time faculty members in 21 colleges. Norman is a culturally rich and vibrant community located just outside Oklahoma City. With outstanding schools, amenities, and a low cost of living, Norman is often cited in "best places to live" rankings. The greater Oklahoma City metropolitan area has a population of over 1.25 million residents and offers all of the culture, dining, entertainment, and amenities typical of a modern metropolis.

Please apply with a cover letter and CV at:

https://ou.taleo.net/careersection/2/jobdetail.ftl?job=171743&tz=GMT%2B02%3A00 Lab/Research Technician III < https://ou.taleo.net/careersection/2/jobdetail.ftl?job=171743&tz=GMT%2B02%3A00 > ou.taleo.net Click the link provided to see the complete job description.

"Hofman, Courtney A." <courtney.hofman@ou.edu>

URegina ComputationalBiol

Luther College at the University of Regina invites applications for a tenure-track position in Computational Biology at the Assistant Professor level, starting July 1, 2018, subject to budgetary approval. We are seeking an individual who can investigate various complex biological problems, addressing hypothesis-driven biological questions using computational approaches. Applicants within the numerous sub-fields of computational biology, including, but not limited to genomics, bio-modelling, evolutionary biology, and dynamic systems, will be considered. Applicants should have a completed PhD, a strong commitment to quality teaching, the ability to teach introductory, as well as more advanced, undergraduate courses in Biology, and a productive research record. Teaching experience and post-doctoral experience are assets.

Luther College is a federated college of the University of Regina; candidates must identify strongly with the vision and mission of the College, a small, multidisciplinary institution federated with a medium-sized comprehensive University. Further information about the College is available at www.luthercollege.edu/university, and about the University of Regina at www.uregina.ca . The successful candidate will also be a member of the University of Regina's Dept. of Biology. Numerous opportunities exist for research collaborations with members of the Dept. (https://www.uregina.ca/science/biology/), the Institute for Environmental Change and Society (IECS), the soon to be commissioned Institute for Microbial Systems and Society (IMSS), and other units. IECS (http://www.iecs-uregina.ca/) contains equipment for proteomics and genetics research, stable isotope analysis, confocal microscopy, and more. IMMS contains equipment for high throughput DNA sequencing, microbial culturing, plate readers, and more. Additionally, the Biology Dept. and IMSS have close connections with the Saskatchewan Disease Control Laboratory, which is located adjacent to campus.

Candidates must express a clear interest in the smaller context of a community-involved College, where spiritual and humanistic concerns and diversity are highly valued. Applications should include a curriculum vitae, outlining disciplinary interests and professional qualifications; if possible, a teaching dossier demonstrating ability in undergraduate teaching; a research dossier with evidence of an active research program; photocopies of transcripts; and the names and contact information of three referees. A statement explaining the candidate's specific interest in teaching at Luther College at the University of Regina should be included. The deadline for applications is October 31, 2017. Applications should be sent to:

Dr. Franz Volker Greifenhagen, Academic Dean Luther College, University of Regina, 3737 Wascana Parkway Regina, SK S4S 0A2 dean@luthercollege.edu

In accordance with Canadian immigration requirements, this advertisement is directed to Canadian citizens and permanent residents. Luther College is committed to employment equity and encourages applications from all qualified candidates including women, indigenous people

dean@luthercollege.edu

UTexas Austin IntegrativeBiology

The University of Texas at Austin invites applications for a tenure-track faculty position at the Assistant Professor level in the Department of Integrative Biology. We wish to hire an exceptional candidate whose research focuses broadly on ecological questions. Interdisciplinary applicants are especially encouraged to apply. The candidate's research can incorporate field experiments, lab experiments, and/or theory and can involve any group of organisms. We expect this to be the first in a series of hires strengthening the areas of plant biology, microbial biology, behavior and physiology, and computational biology. A PhD or equivalent is required at the time of appointment.

We are a vibrant and inclusive community, and we seek candidates who are interested in contributing to diversity and equal opportunity within higher education.

Applicants should submit the following items via Interfolio at https://apply.interfolio.com/43206: i) a cover letter with contact information (ii) a CV, (iii) a research statement, (iv) a teaching statement, (v) up to 5 reprints/preprints, and (vi) names of three individuals who will write letters of recommendation. Note that letters are not required for initial consideration; candidates will be notified if letters are needed. Applications received prior to August 31, 2017 will be assured of full consideration. For additional information about the department, see https://integrativebio.utexas.edu . The University of Texas at Austin, as an Equal Opportunity/Affirmative Action Employer, complies with all applicable federal and state laws regarding nondiscrimination and affirmative action. The University is committed to a policy of equal opportunity for all persons and does not discriminate on the basis of race, color, national origin, age, marital status, sex, sexual orientation, gender identity, gender expression, disability, religion, or veteran status in employment, educational programs and activities, and admissions.

Caroline Farrior <cfarrior@utexas.edu>

UTexas Austin ResTech EvolutionImmunity

University of Texas at Austin: Technician. The Bolnick lab at the University of Texas at Austin is searching for a technician to assist with an NIH-funded study of the genetic basis of anti-helminth immunity in fish. The technician will join an active research lab (https://bolnicklab.wordpress.com) that is part of the intellectually dynamic Department of Integrative Biology at the University of Texas at Austin (https://-integrativebio.utexas.edu). Previous work by the Bolnick lab identified naturally evolved variation in resistance to a severe cestode parasite (Weber et al 2017 American Naturalist; Weber et al 2017 Proceedings of the National Academy of Sciences). The technician will join an ongoing study evaluating the genetic and immunological basis of stickleback suppression of cestode growth, and cestode elimination. With supervision and training from the project postdoc, and with help from UT undergrads, the technician will be responsible for generating next generation sequencing data for RNAseq and ddRADseq and genome sequences. Additional duties may include (1) assisting with fish care, (2) conducting experimental infection assays, (3) characterizing immune phenotypes via flow cytometry and histology, and (4) experimental genetic manipulations to confirm candidate genesâ euro phenotypic effects. The technician will also assist with maintaining a stocked and organized laboratory. Some field research on Vancouver Island, British Columbia, will also be an option.

The position is for up to 5 years, subject to annual renewal based on performance. The technician is requested to start work at the University of Texas in fall 2017. The salary range is $32,000-$36,000 (depending on experience), with benefits.

Applicants should electronically submit a single pdf file containing the following, in order: 1) Coverletter, including a summary of research experience and career goals 2) CV 3) List of three references, with contact information (email, telephone, and mailing address). We will request letters directly from these references, after identifying top candidates.

Qualifications: At a minimum individuals must have a BS or BA degree in biology or a closely related field, with experience in molecular genetics research. A MA is preferred. Prior experience with next generation sequencing (especially RNAseq or RADseq) library preparation and/or analysis is especially valuable.

The application file should be emailed to Dr. Daniel Bolnick (danbolnick@austin.utexas.edu). Include the subject line “Immune Genetics Technician Application: <YOUR NAME>”. Applications must be received by August 21, 2017 for full consideration, though the position is open until filled. For questions about this position, please email danbolnick@austin.utexas.edu or yestuart@utexas.edu.

The University of Texas is an Equal Opportunity Employer. Applicants with questions about disability services can privately discuss their application with the University of Texas Disability Services Office (http://sites.utexas.edu/disability/). Dual career couples may consider also applying for a second concurrent Lab Technician position in the Bolnick lab (https://bolnicklab.files.wordpress.com/2015/10/parallel-evolution-technician-ad.pdf) or a postdoctoral position in the Bolnick lab (https://bolnicklab.files.wordpress.com/2015/10/postdoctoral-position.pdf) or a postdoctoral position in the Matz Lab (http://www.bio.utexas.edu/research/matz_lab/matzlab/welcome.html)

Dr. Daniel I. Bolnick

Professor Department of Integrative Biology Chair, Graduate Program in Ecology Evolution and Behavior One University Station C0990 University of Texas at Austin Austin, TX 78712

512-471-2824 fax 512-471-3878

Lab website: https://bolnicklab.wordpress.com danbolnick@austin.utexas.edu

---

UTexas Austin Tech StickleBackEvolution

University of Texas at Austin: Technician.

The Bolnick lab at the University of Texas at Austin is searching for a research technician. The technician will join an active research lab (https://bolnicklab.wordpress.com) that is part of the intellectually dynamic Department of Integrative Biology at the University of Texas at Austin (https://integrativebio.utexas.edu). The employee will participate in an NSF-funded study of natural selection underlying (non)parallel phenotypic and genetic divergence. Previous work on lake-stream population pairs of threespine stickleback fish (Stuart et al., 2017, Nature Ecology and Evolution) suggests that there is a continuum of parallelism in lake-stream divergence, from highly parallel to partly parallel to antiparallel. The technician will join an ongoing study evaluating the genetic targets of natural selection in these lake-stream pairs. With supervision and training from the project postdoc, and with help from UT undergrads, the technician will be responsible for (1) obtaining phenotypic data from >2000 experimental F2 hybrid and wild fish, (2) extracting and sequencing (using ddRADseq techniques) DNA from >4000 experimental F2 hybrid and wild Fish, (3) next generation sequencing to characterize the fish gut microbiota, and (4) using bioinformatics methods to process the sequence data. The technician will also likely take part in field research on Vancouver Island, British Columbia, Canada in spring 2018.

The position is for 15 months. The technician is requested to start work at the University of Texas in mid to late Fall 2017. The salary range is $32,000-$36,000 (depending on experience), with benefits.

Applicants should electronically submit a single pdf file containing the following, in order: 1) Coverletter, including a summary of research experience and career goals 2) CV 3) List of three references, with contact information (email, telephone, and mailing address). We will request letters directly from these references, after identifying top candidates.

Qualifications: At a minimum individuals must have a BS or BA degree in biology or a closely related field, with experience in molecular genetics research. Preferred qualifications include experience with next generation sequencing library preparation and/or analysis. Candidates with Masters degrees are encouraged to apply. Good organizational skills are required.

The application file should be emailed to Dr. Daniel Bolnick (danbolnick@austin.utexas.edu) and Dr. Yoel Stuart (yestuart@utexas.edu). Include the subject line “ Parallel Evolution Technician Application: <YOUR NAME>”. Applications must be received by August 21, 2017 for full consideration, though the position is open until filled. For questions about this position, please email danbolnick@austin.utexas.edu or yestuart@utexas.edu.

The University of Texas is an Equal Opportunity Employer.

Dr. Daniel I. Bolnick

Professor Department of Integrative Biology Chair, Graduate Program in Ecology Evolution and Behavior One University Station C0990 University of Texas at Austin Austin, TX 78712

512-471-2824 fax 512-471-3878 danbolnick@austin.utexas.edu

Lab website: https://bolnicklab.wordpress.com danbolnick@austin.utexas.edu

UToronto 2 EEB Professorships

ECOLOGY AND EVOLUTION - Two Assistant Professorships

The Department of Ecology and Evolutionary Biology at the University of Toronto invites applications for two tenure-stream appointments in ecology and evolution. These appointments will be at the rank of Assistant Professor, with an expected start date of July 1, 2018.

We seek candidates who conduct conceptually driven research in ecology and evolution, especially those with research programs in disease and/or theory. We seek applications from candidates whose research program complements the research programs of the highly collaborative faculty currently in the department.

The successful applicants must have a PhD in a related field by July 1, 2018 or soon thereafter, with a record of sustained publications in top-ranked, field-relevant journals. The appointees will be expected to build an active, externally funded and internationally recognized research program. The successful candidates will also demonstrate excellence in teaching and contributions to the education and training of undergraduate and graduate students. Evidence of demonstrated excellence in research and teaching should be documented through the applicant's CV, publications, research and teaching statements, strong letters of reference from referees of high standing and where appropriate, course evaluations.

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

Salary to be commensurate with qualifications and experience.

All qualified candidates are invited to apply online. Applications must include a CV and statements of research and teaching interests combined into a single PDF file, plus three representative publications. Applicants should arrange to have three confidential letters of recommendation (signed and on letterhead) sent directly to: Professor Donald Jackson, Chair of Search Committee, Department of Ecology and Evolutionary Biology, 25 Willcocks Street, University of Toronto, Toronto, Ontario, M5S 3B2 Canada. Letters of reference may be e-mailed to chairsec.eeb@utoronto.ca. Deadline for receipt of applications, including reference letters, is September 13, 2017.

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

The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from racialized persons / persons of colour, women, Indigenous / Aboriginal People of North America, persons with disabilities, LGBTQ persons, and others who may contribute to the further diversification of ideas. As part of your application, you will be asked to complete a brief Diversity Survey. This survey is voluntary. Any information directly related to you is confidential and cannot be accessed by search committees or human resources staff. Results will be aggregated for institutional planning purposes. For more information, please see http://uoft.me/UP. All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority.

< http://mahlerlab.com/ >

Luke Mahler <luke.mahler@utoronto.ca>

UWashington ResScientist EvolutionaryGenomicsBehavior

A Research Scientist 1 position is available in the Snyder-Mackler lab < https://smacklab.csde.washington.edu/ > at the University of Washington in Seattle. Position is for 75-100% FTE depending on the need, and will last 12 months, with the possibility of renewal contingent on availability of funding. The Snyder-Mackler lab studies the relationship between behavior, the social environment, and the genome, with a focus on two nonhuman primate populations. We combine detailed behavioral and demographic information with genomic and epigenomic data sets. Current projects focus on the gene regulatory mechanisms linking the social environment to aging and resilience in rhesus macaques, the genomic signature of early life social adversity, and the genomic and phenotypic consequences of high altitude adaptation in gelada monkeys.

As the lab manager, your duties will include the design, implementation, and analysis of genomics experiments. This includes next-generation library preparation for high throughput sequencing experiments; cell culture and experimental treatment; sample collection and DNA/RNA extraction; experimental design of genomics experiments including the development and optimization of novel protocols relevant to the Snyder-Mackler Lab's objectives; and managing day-to-day logistics of the lab including purchasing, coordinating visitors and their lab use, working with trainees, shipping/receiving, etc.

Requirements: Bachelor's degree in Biology, Psychology, Genetics, or a related field; at least 1 year experience in a research laboratory, and familiarity with fundamentals of molecular biology.

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

For more information about the lab and our work, see: https://smacklab.csde.washington.edu/ If interested, email resume, including contact information for two references, to Noah Snyder-Mackler, nsmack@uw.edu.

More information on the job and how to apply through the University of Washington can be found here: https://uwhires.admin.washington.edu/eng/candidates/default.cfm?szCategory=jobprofile&szOrderID=147196 The University of Washington is an Equal Opportunity/Affirmative Action/ADA Employer committed to providing employment opportunity without regard to an individual's age, color, disability, genetic information, gender, gender identity, national origin, race, religion, sexual orientation, or veteran status.

Noah Snyder-Mackler <nsmack@uw.edu>

YaleU BiodiverityWebDeveloper

Map of Life is seeking a Front-end Web Developer to join their international team and participate in the design, development, deployment, and maintenance of mol.org web applications and the API that support them. We require familiarity with Google Cloud Platforms (BigQuery, Cloud SQL, Cloud Datastore) and hosted platforms such as Google App Engine and CARTO. We require experience in developing responsive web applications in HTML5 and CSS3 on JavaScript frameworks such as Angular and React. For details see https://mol.org/careers . This is one of several positions starting fall/winter 2017/18 associated with the Yale Center for Biodiversity and Global Change (http://bgc.yale.edu), Map of Life (https://mol.org) and the Jetz Lab (http://jetzlab.yale.edu). To apply please send, in one pdf, a short cover letter, CV and contact info for three referees to michelle.duong@yale.edu. For questions or associated PhD opportunities contact walter.jetz@yale.edu. The final selection process will begin on 18 Aug 2017, but applications before this date are welcome and will be reviewed as received.

Environment: The interdisciplinary BGC program (http://bgc.yale.edu) connects biodiversity scientists from across campus. Yale has a thriving and growing community of young scholars in ecology, evolution and global change science in the EEB Department, the Yale Institute for Biospheric Studies, the Peabody Museum, and the Yale School of Forestry and Environmental Studies. The town is renowned for its classic Ivy League setting, 75 miles north of New York City.

"walter.jetz@yale.edu" <walter.jetz@yale.edu>

YaleU Biodiversity manager

Map of Life is seeking a qualified candidate to join their international team to help oversee the management (and analysis) of species occurrence information and associated metadata. The successful applicant will work with software engineers and research team to build, extend, support, and manage new databases driving biodiversity web and mobile applications. The ideal candidate will be a quick learner, self-driven, and detail oriented. We require experience in working with geospatial and biodiversity data and the PostgreSQL/PostGIS environment, and python and shell scripting skills. For more details see https://mol.org/careers . This is one of several positions starting fall/winter 2017/18 associated with the Yale Center for Biodiversity and Global Change (http://bgc.yale.edu), Map of Life (https://mol.org) and the Jetz Lab (http://jetzlab.yale.edu). To apply please send, in one pdf, a short cover letter, CV and contact info for three referees to michelle.duong@yale.edu. For questions or associated PhD opportunities contact walter.jetz@yale.edu. The final selection process will begin on 18 Aug 2017, but applications before this date are welcome and will be reviewed as received.

Environment: The interdisciplinary BGC program (http://bgc.yale.edu) connects biodiversity scientists from across campus. Yale has a thriving and growing community of young scholars in ecology, evolution and global change science in the EEB Department, the Yale Institute for Biospheric Studies, the Peabody Museum, and the Yale School of Forestry and Environmental Studies. The town is renowned for its classic Ivy League setting, 75 miles north of New York City.

"walter.jetz@yale.edu" <walter.jetz@yale.edu>

Other

Cairns VolunteerFieldAssistant

Volunteer field assistant

We are looking for field assistants to help monitor nests of a small bird, large-billed gerygone for PhD project (Australian National University, Canberra). The main objective of this research is to gain a better understanding of the breeding ecology of large-billed gerygone, and the coevolution between large-billed gerygone and little bronze-cuckoo. Research will be conducted in Cairns region, Queensland, Australia. We will be based in Cairns city, and travel to several sites in this area. Volunteer field assistants are needed from *15 Sep to 15 Nov, 2017*. The exact dates are flexible but need to be around this time.

Overall duties will include nest searching and filming, behavioral observations, and data entry. The large-bill gerygone build nests over the water, and the height of nests varies from 1m to 5m. The study site is rugged, hot, and venomous snakes and ticks are quite common. Working days are long, with early starts, six days a week. Therefore, applicants must have good physical fitness to walk along the creek with a heavy ladder, withstand harsh conditions at the site, and maintain an energetic attitude despite long hours in hot and humid conditions. Work schedules and duties will vary, so flexibility is necessary. Previous experience with fieldwork is highly desired, and handling eggs and chicks is also preferred, but a positive attitude is much more important than tons of field experience.

Food and housing will be provided, and assistants will enjoy fantastic wildlife viewing opportunities, proximity to Queensland rainforest and the surrounding area of Cairns. Please feel free to enquire with any questions related to the application process or on the project in general.

To apply, send a cover letter detailing interests, previous relevant field research experience, dates of availability and a CV to Hee-Jin Noh (hjnoh891@gmail.com).

hjnoh891@gmail.com

ESEB OutreachFunds Deadline Sep15

ESEB Outreach Fund

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

Applications for funding will be accepted for educational initiatives that promote evolution, translation of evolutionary material (books, films, and websites) intended for a general audience, public outreach seminars, public exhibitions, etc. Please note that scientific meetings are not supported by these funds. While most projects will be financed for a sum between 1000-1500 Euro, exceptions can be made if a strong argument is provided for additional funds.

Please use the application form, which can be found at http://eseb.org/prizes-funding/outreach-fund/. Applications will be accepted twice yearly (deadlines March 15, September 15) and should be submitted by email to Ute Friedrich (office@eseb.org; Subject: Outreach).

– Dr. Ute Friedrich ESEB Office Manager Email: office@eseb.org

European Society for Evolutionary Biology - eseb.org

ESEB <office@eseb.org>

Fish internal fertilisation answers

Dear All

Internal fertilisation in an egg-laying fish

Some months ago I asked whether anyone was aware of any records of internal fertilisation of eggs in normally egg laying fish species. What I meant by that was records of embryos inside the ovaries of normally oviparous females. Thank you to those who responded. Although there are quite a number of fish species with internal fertilisation (viviparous), it appears that records of this occurring in species that normally lay eggs are extremely rare. The only well documented one that I have found is in the Japanese cottid fish Hemilepidotus gilberti, in which the embryos fail to develop properly, see:

Hayakawa, Y., Munehara, H., 2001. Facultatively internal fertilization and anomalous embryonic development of a non-copulatory sculpin Hemilepidotus gilberti Jordan and Starks (Scorpaeniformes: Cottidae). J. Exp. Mar. Biol. Ecol. 256, 51- 58.

and

Hayakawa, Y., Munehara, H., 2003. Comparison of ovarian functions for keeping embryos by measurement of dissolved oxygen concentrations in ovaries of copulatory and non-copulatory oviparous fishes and viviparous fishes. 295, 245- 255.

Best wishes Andrew MacColl

Associate Professor of Evolutionary Ecology School of Life Sciences University of Nottingham University Park Nottingham NG7 2RD, U.K. Tel: +44 115 951 3410 http://ecology.nottingham.ac.uk/AndrewMacColl/index.php Andrew.Maccoll@nottingham.ac.uk

Help with kSNP3 problem

REQUEST FOR HELP WITH kSNP3 PROBLEM During the last year many of you have contacted me about problems with kSNP3 when trying to annotate genomes. The problem appears to be the result of NCBI discontinuing the use of GI numbers in sequence files as of a year ago.

Shea Gardner, who was the author of kSNP3 (and its earlier versions), died last year at the end of February. I am confident that Shea would have dealt with this problem promptly and efficiently. Sadly, I am a much less skilled perl programmer than was Shea, and I have been unable to solve the problem.

I have been able to determine that, provided that the reference genome files use the new style header (>accesion_number) rather than the old-style header (>gi|number), the problem is confined to the annotate_SNPs_from_genbankFiles3.pl script. Despite the lack of gi numbers in the new-style header kSNP3 still downloads the full genbank files that are to be used for annotation.

Fortunately, it is not necessary to run the entire kSNP3 program in order to test the correct operation of the annotate_SNPs_from_genbankFiles3.pl script.

If you are willing to try to fix annotate_SNPs_from_genbankFiles3.pl please email me (barryghall@gmail.com) and I will happily send you everything you need to have a go at fixing it.

With thanks in advance, Barry G. Hall barryghall@gmail.com July 19, 2017

“Barry G. Hall” <barryghall@gmail.com>

Hydropsyche pellucidula caddisfly samples

My laboratory is seeking specimens of the European caddisfly Hydropsyche pellucidula (Trichoptera: Hydropsychidae) for a phylogenetics study. Either larvae or adults would be satisfactory for our purposes, as would DNA samples from specimens that have been identified with confidence. Only a few individuals are required and I can pay for postage. Please drop me a note if you think you can help.

Thanks,

Jeff

Dr. Jeffrey M. Marcus

Associate Professor

Department of Biological Sciences

University of Manitoba,

Winnipeg, MB, R3T 2N2

CANADA

Jeffrey.Marcus@umanitoba.ca

Morinda-noni fruit needed

Dear all,

We are currently conducting some work on the microbiota of Drosophila sechellia. We had been sourcing their host fruit morinda/noni (Morinda citrifolia) from PB Medicinal Herbs in the US, but unfortunately they have temporarily stopped producing it.

Does anyone know of an alternative supplier of fresh morinda please? Google searching has proved (ahem) fruitless.

Thanks in advance, and best wishes,

Zen Lewis and Chloe Heys

Dr Zenobia Lewis Senior Lecturer, Director of Studies, Biological Sciences

@Zen_of_Science

Room G53, Ground Floor, Biosciences Building

School of Life Sciences University of Liverpool Liverpool L69 7ZB UK

+44(0) 151 795 4384

“Lewis, Zenobia” <Z.Lewis@liverpool.ac.uk>

Opinions On ThermalCyclers

Hello all,

I have a grant to purchase 4 thermal cyclers for my group. It was originally envisioned that this would be a set that could be daisy-chained together (e.g. Eppendorf MasterCyclers), however, these are all very large units and space is a major constraint for us. We have settled on 3 other models with smaller footprints but would like to solicit opinions/reviews from anyone who has experience with them (particularly in terms of ease of use, reliability, and overall longevity).

1) BioRad T100

2) ABI/Life Technologies SimpliAmp

3) PCRMax AlphaCycler4 (seems to be the only tetrad unit on the market- I am especially interested in anyone with experience in this system as it doesn't seem to be very common in North America).

Please send responses to kaela.beauclerc@ontario.ca

Any replies will be compiled and posted.

Thanks in advance! Kaela Beauclerc Wildlife Research and Monitoring Section Ontario Ministry of Natural Resources and Forestry

"Beauclerc, Kaela (MNRF)" <Kaela.Beauclerc@ontario.ca>

Soil Sampling In Alaska

Hi,

I am reaching out to obtain soil samples from an elevational gradient in Alaska. I would need soil samples from grasslands located at altitudes of 1000m, 2000m and 3000m AMSL (if 3000m is not possible then altitudes of 500m, 1000m and 2000m would be fine as well). For each grassland, eight replicate samples of about 300g of soil should be taken at 10-20cm depth. If possible, thermologgers (which I will provide) should be burried for 1 year at the 3 elevation sites. Shipping of samples will be arranged and all costs will be covered by my lab. Considering the involved sampling effort, co-authorship on a publication resulting from this work will be offered.

Contact me if you are interested in helping out or if you need further details!

Thanks in advance,

Max Ballhausen

– Dr. Max-Bernhard Ballhausen Freie Universität Berlin Plant Ecology/Ãkologie der Pflanzen Altensteinstr. 6 D- 14195 Berlin Germany

Ludo Muller <ludo_muller@yahoo.com>

Teaching famous experiments

We're generating a list of studies that had major impacts on the fields of evolutionary biology or ecology, AND that COULD plausibly be replicated (at least in part) by undergraduate students with professorial guidance over the course of a semester.

Even if the original study had design flaws, please add it to our list.

If you have ideas for this list, please email me.

Also, we'll have a table at ESA in Portland (Table E in the exhibit hall) the week after next, and we'd love for you to come by and talk to us about your ideas.

We'll be happy to share the completed list (and more) with anyone who's interested.

Best, Tim

Tim Parker Co-organizer, TTEE (Tools for Transparency in Ecology and Evolution) Chair, Department of Biology Interdisciplinary Program in Environmental Studies Whitman College Walla Walla, WA 99362 USA +1.509.526.4777 parkerth@whitman.edu http://people.whitman.edu/ ˜ parkerth/ "parkerth@whitman.edu" <parkerth@whitman.edu>

Tympanidaceae project samples

I am Luis Quijada and currently I have been granted to develop a project in Tympanidaceae family and related (Ascomycetes, Leotiomycetes) in the harvard herbarium. The project will start in October and is focussed in sampling different types of forest to link the identification of specimens in the family with DNA barcodes to monitoring this group in which some members produce forest disease. Tympanidaceae family is composed by the genera: Lahmia, Claussenomyces, Collophora, Durandiella, Grovesiella, Holwaya, Micraspis, Myriodiscus, Pragmopora, Tympanis (and related). If you know this genera , or you work in forest disease and usually go to sampling, or have access to herbarium collections and would like to collaborate in some way in the project please write email to lquijull@gmail.com

Best wishes,

Luis

Luis Quijada <lquijull@gmail.com>

USunshineCoast Vol KoalaConservation

Volunteer Position - Koala research using detection dogs

I am seeking a dedicated field assistant for the 2017 field season (start of August to end of October) in the Frere Lab at the University of the Sunshine Coast, Queensland, Australia. This is a fantastic opportunity to get involved in innovative research and gain new skills. This research is conducted as part of the Detection Dogs for Conservation Program (https://www.usc.edu.au/DDC), which uses specially trained detection dogs to study and protect koalas.

The field assistant will be helping me organise and conduct surveys of koala habitat (i.e. bushland vegetation) with a detection dog specially trained on the odour of koala scats. We will be searching for koalas and their scats and recording habitat characteristics in the Moreton Bay, Sunshine Coast, Noosa, Gympie and Fraser Coast Council regions of south-east Queensland.

This research forms part of a PhD project studying the distribution, abundance and health status of koalas in rehabilitated vegetation and is part of a long-term study of koala behaviour, ecology and genetics.

Timeframe: 3 months (start of August to end of October 2017)

Location: The Moreton Bay, Sunshine Coast, Noosa, Gympie and Fraser Coast Council regions of south-east Queensland.

About: Office-based duties include contacting private landholders, community groups and government bodies to organise surveys of their properties; and data entry and processing. In the field, assistance will be required to operate field equipment whilst the handler instructs the dog to search the bases of trees for koala scats. The assistant will help to record data in data sheets and data loggers; collect, label and organise koala scat samples; take photos; and record features of observed koalas. Other tasks include laboratory sample preparation and assisting with dog training and testing, as required.

Weather permitting, days in the field can be consecutive, long and tiring in variable environmental conditions. Some of the fieldwork will involve overnight stays at various locations in south-east Queensland. For these trips, suitable accommodation will be arranged at no expense to the assistant. This is an unpaid, volunteer position and the successful candidate will need to make his/her own way to Brisbane or the Sunshine Coast. However, food and accommodation will be covered once in the Sunshine Coast.

The volunteer will be covered by University insurance.

Responsibilities:

* Helping organise field work * Recording site locations on a GPS * Taking photos * Recording features of observed koalas * Timing the koala habitat surveys with a stopwatch * Recording data in data sheets and data loggers * Collecting, labelling and organising koala scats * Assisting in genetic sample preparation and processing * Data entry and processing * Assisting with dog training and testing, as required

Qualifications: The ideal volunteer will be a recent graduate with a science background and a genuine interest in threatened species monitoring and conservation. This position is well-suited to recent graduates of environmental science, environmental management, ecology, zoology, genetics or similar fields looking to gain additional analytical and field experience.

He/she must:

* Be 18 years or older * Have a positive attitude * Love to learn * Pay attention to detail and be thorough * Listen and follow instructions * Possess basic computer skills * Be flexible and patient * Have great organisational skills * Be comfortable performing menial, repetitive tasks * Have a high work ethic * Be fluent in English * Be both willing and comfortable with engaging with the community * Be willing to make the full 3-month commitment * Have prior field research experience * Be prepared to work long, consecutive days, including weekends * Be comfortable working in the Australian bush (hot days, snakes, ticks) * Maintain a good mood when tired, hot, cold, wet, hungry, bitten by mosquitoes, etc.

We live and work in close quarters so mature and respectful candidates are required.

If interested, please email Natalie.Dowling@research.usc.edu.au with the subject line RESEARCH ASSISTANT by Friday 7th July 2017. Please include in the email:

1. Letter of interest 2. CV 3. Email contacts for 2 references

Looking forward to hearing from you.

Cheers, Natalie Dowling PhD Candidate University of the Sunshine Coast Sippy Downs, Australia www.celinefrerelab.com Natalie Dowling <Natalie.Dowling@research.usc.edu.au>

Videos from Evolution2017

If you missed the 2017 Evolution conference in Portland or want to revisit talks from the meeting, visit the Evolution 2016 youtube channel: goo.gl/L2eMpS.

There are approximately 400 presentations recorded with playlists (*goo.gl/XrgM3w < http://goo.gl/-XrgM3w >*) that group the talks by keywords. For an index of the talks with links to their specific video, visit the youtube station guide: goo.gl/c4Sjt5

There are also over 30 posters from the conference available for more detailed viewing on FigShare: goo.gl/pi19dN

Thank you to the conference organizers for such a great meeting, Howard Rundle for supporting and finding funding for the video recording initiative, the presenters that had their research documented to share with the broader community and the 55 student volunteers that video recorded and uploaded all of these talks.

- Emily Behrman and Rohini Singh,

Video Recording Coordinator Volunteers

Emily Behrman Ph.D. Candidate Schmidt Lab Department of Biology University of Pennsylvania 433 S University Ave Philadelphia, PA 19104

Bemily@sas.upenn.edu http://www.emily-behrman.com "bemily@sas.upenn.edu" <bemily@sas.upenn.edu>

VisualizingGenomicData Sep11-15

Visualizing genomic data: techniques and challenges.

The advent of Next Generation Sequencing technologies has allowed the rapid production of massive amounts of genomic data, and created a corresponding need for new tools and methods for visualizing and interpreting these data in order to extract relevant biological information.

Visualizing genomic data requires more than simply plotting data. It requires a decision: what message should be conveyed by a particular plot? And, it often presents a choice: which methodologies should be used to represent the results in an easy, clear and accurate way to the users? Interpretation and visualization of genomic data, often consisting of thousands to billions of data points, and extracting biological meaning remains a serious challenge.

We will run a workshop on Genomic Data Visualization and Interpretation (Sept 11-15, 2017; https://www.physalia-courses.org/courses-workshops/-course14/) https://www.physalia-courses.org/courses-workshops/course14/ with the twin scientists Dr. Malachi Griffith (Malachi's website http://-www.malachigriffith.org) and Dr. Obi Griffith (Obi's website http://www.obigriffith.org), who lead a combined research group (The Griffith lab) at the McDonnell Genome Institute at Washington University. They will be joined by Mr. Zachary Skidmore, a staff scientist in their group and expert in genomic visualization. The Griffith lab's research is focused on developing methods of applied bioinformatics for genomic data analysis, personalized medicine and improved cancer care. They have participated in dozens of genomic studies from the earliest sequencing of full-length human genes and whole genomes, initial surveys of the mutational landscape of multiple cancer subtypes, and some of the first proof-of-principle applications of sequencing to cancer precision medicine. They have a strong commitment to developing open-source tools and knowledgebases for cancer gene and variant interpretation including pVAC-seq (github.com/griffithlab/pVAC-Seq https://github.com/griffithlab/pVAC-Seq), CIViC (http://civicdb.org), DGIdb (http://dgidb.org), and DoCM (http://docm.info). They are also the creators of GenVisR (bioconductor.org/packages/release/bioc/html/GenVisR.html https://bioconductor.org/packages/release/bioc/html/-GenVisR.html), a Bioconductor package, which provides a user-friendly, flexible and comprehensive suite of tools for visualizing complex genomic data for multiple species of interest. In this Workshop we will explore a number of best-in-class visualization tools, and we will provide working examples that demonstrate important principles of omic interpretation strategies.

Participants are encouraged to bring their own experimental design ideas and data from recent experiments to discuss with the team of instructors who have collectively participated in hundreds of diverse data analysis projects.

Here we have the possibility to discuss this topic with them:

* You are both leading the Griffith Lab - could you please tell us about the different research topics of your group? How has the combination of your different bioinformatics skills and knowledge been important in accomplishing scientific objectives and key results?

Our lab's activities can be divided into four broad categories: cancer genomics studies, personalized medicine efforts, bioinformatics tool development, and educational efforts such as this workshop. Our group conducts data analysis of a wide array of data types. Major sources of data include whole genome, exome and RNA-seq. We are also involved in many projects that involve a wide variety of custom gene panel assays. We are increasingly working with T-cell receptor (TCR) sequencing and cell-free DNA (cfDNA) sequence data. We don't focus on a particular cancer but have many projects involving AML, lung, head and neck cancer, liver cancer, and breast cancer. To help translate results from these next generation sequencing assays to clinical application we develop open source tools and online resources for interpretation of data in a personalized genomics context. These include the drug-gene interaction database (http://www.dgidb.org), the database of curated mutations (http://www.docm.info), the personalized Variant Antigens by Cancer Sequencing (pVAC-seq) pipeline (github.com/griffithlab/pVAC-Seq

— / —

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

Volunteer AustralianDesertZebraFinch

Field assistant position (Australian desert, zebra finch)

What for: Helping on my PhD research on foraging movements of zebra finches in the wild. In this project, a series of experiments will be conducted testing how zebra finches use their landscape to forage. Reproduction will also be monitored in a long-term study area with nest boxes. The field work will essentially take place in the morning (from sunrise to after lunch).

Where: Accommodation in Fowlers Gap Research station, 110km north from Broken Hill, NSW, Australia.

How long: 1st September to 10th December 2017 (longer if you want)

For you if you are: Not afraid of harsh conditions (cold at night, hot during the day, isolated, presence of wild animals) Enjoy team work Happy to do repetitive tasks over a long period of time Fluent in English (or knowledge of English and fluent in Italian or Portuguese) Previous experience in bird handling is welcome (capture, morphological measuring and PIT-tagging) Interested in learning how to handle small birds (the zebra finch)

Costs: Accommodation and inland travel costs will be covered.

If you would like more information, feel free to contact me at caterina.funghi@live.com.

If you are interested in volunteering, please send a cover letter to caterina.funghi@live.com in which you specify your interest and whether you had previous experience in the field.

Caterina Funghi <caterina.funghi@LIVE.COM>

PostDocs

AberystwythU CoastalGeneFlow

Post-doctoral Research Associate - Ecostructure Institute/Department: Institute of Biological, Environmental and Rural Sciences Salary: 32,958 per annum Duration: Fixed term until 3 September 2020 FT / PT: Full Time Weekly Hours: 36.5 Interview Date: September 2017 Closing Date: 28/08/2017 Ref No: 1515

We are seeking to appoint a Postdoctoral Research Associate (PDRA) to join an energetic and enthusiastic team of investigators working on a project entitled 'Climate change adaptation through ecologically sensitive coastal infrastructure (Ecostructure)'. Ecostructure is an interdisciplinary project, part-funded by the European Regional Development Fund through the Ireland Wales Cooperation Programme 2014-2020 which aims to raise awareness of eco-engineering solutions to the challenge of coastal adaptation to climate change by providing developers and regulators with accessible tools and resources.

The successful applicant will investigate the Impact of artificial structures on dispersal and gene flow of native and non-native species inhabiting the Irish Sea coasts of Ireland and Wales. Additionally, they will be expected to communicate their results to stakeholders in industry, government and coastal communities. We aim to appoint an enthusiastic, highly motivated individual whose laboratory and field skills are complemented by good communication and reporting skills.

To make an informal enquiry, please contact Dr Joe Ironside at jei@aber.ac.uk.

Un o'r 4 prifysgol uchaf yn y DU a'r orau yng Nghymru am fodlonrwydd myfyrwyr. (Arolwg Cenedlaethol y

Myfyrwyr 2016) www.aber.ac.uk Top 4 UK university and best in Wales for student satisfaction (National Student Survey 2016) www.aber.ac.uk jei@aber.ac.uk

ANU Canberra BiogeographyBiodiversity

Australian_National_Uni.biogeography.biodiversity

A postdoctoral position is available at the Australian National University to study how dispersal, disturbance and density-dependent processes interact to drive spatial patterns of genetic diversity. This position is an exciting opportunity for a highly-motivated postdoctoral researcher with experience in evolutionary ecology, biogeography and / or population genomic analyses. The project will inform core ecological and evolutionary theory, and will contribute to improving strategies for conserving biodiversity in the face of rapid environmental change.

The Australian National University is the top-ranked university in the Southern Hemisphere, and 20th globally (QS 2017). Canberra is an easy-living city of ~400,000 people, with all the benefits of a city but none of the traffic, and is the capital city of Australia. Some of the world's most beautiful beaches are a short drive away, as are the Snowy Mountains.

The successful applicant will be based in the Fraser lab group (see www.ceridwenfraser.com). Research in this group is assessing the influence of environmental conditions, including past and future environmental change, on global patterns of biodiversity, with a particular focus on Australasian and Antarctic ecosystems. The project's specific focus and approach will depend on the skills and interests of the successful applicant - this is a unique opportunity to play a role in designing a project that makes the most of your existing skills, as well as allowing you to gain new skills and explore exciting new research directions.

The position is for two years (part-time possible) initially, with possibility of extension. Applications close on 20 August 2017.

For more information, see http://jobs.anu.edu.au/cw/en/job/517341/postdoctoral-fellow-in-biogeography-biodiversity and http://www.ceridwenfraser.com/single-post/2017/07/20/Postdoc-position-available Ceridwen Fraser <ceridwen.fraser@anu.edu.au>

CornellU AvianEvolution

The Cornell Lab of Ornithology invites applications for our Edward W. Rose Postdoctoral Fellowships. These competitive postdoctoral fellowship awards (www.birds.cornell.edu/postdoc) support innovative, independent research by early career scholars of exceptional promise. Multiple Rose Fellow positions are available annually, with applications due on September 8. All Rose Fellows join a vibrant community of more than a dozen concurrent postdocs within the Rose Postdoctoral Program and interact with many other scholars across a wide range of disciplines.

These Rose Postdoctoral Fellowship awards support individuals pursuing cutting-edge scholarship, while fostering intellectual interaction with multiple Lab programs and Cornell scholars. Any area of inquiry related to the Lab's mission "to interpret and conserve the earth's biological diversity through research, education, and citizen science focused on birds" is appropriate. Potential applicants are encouraged to learn more about the Cornell Lab and our formal programs in Bioacoustics, Bird Population Studies (avian ecology), Citizen Science, Conservation Science, Communication, Education, Evolutionary Biology, Information Science, Macaulay Library (animal behavior), Multimedia Productions, and Public Engagement in Science. Activities involving research and/or outreach spanning several of these areas are particularly encouraged, and therefore each postdoctoral scholar may be co-mentored by two senior Cornell scholars. Projects that foster links to people and units from across Cornell University are likewise welcome. Potential applicants are encouraged to contact the most relevant faculty and staff at the Lab to brainstorm about areas of mutual interest and synergistic projects. We are especially interested in supporting the independent research of individuals who can bring new ideas, approaches, and connections to the Lab, while simultaneously leveraging our existing tools, data, and expertise in science, education, and communication.

Each Rose Postdoctoral opportunity spans up to 24 months via two consecutive year-long appointments at the Lab. Located at the Imogene Powers Johnson Center for Birds and Biodiversity in the 220-acre Sapsucker Woods sanctuary, the Cornell Lab of Ornithology is a vibrant unit within Cornell's University's College of Agriculture & Life Sciences. More than 200 faculty and staff work at the Lab within our 10 mission-driven programs. Our management and staff are committed to the highest standards of ethics and excellence in all areas of our work.

These appointments provide a competitive salary, Cornell health and other benefits, and funds to help support the Scholar's research and other professional needs. Start dates are usually flexible within the year following the application. Interested applicants should visit the Annual Rose Postdoctoral Fellowship Competition web site(www.birds.cornell.edu/postdoc) for more information about the overall Program and about the Rose Fellow selection process.

The application package consists of a cover letter, CV, two-page research proposal, pdfs of up to three representative publications, and names and contact information for three references. Applicants must have received their PhD before beginning their postdoctoral appointment at Cornell. Application materials should be sent as a single pdf file to the attention of Sue Taggart (SET2@cornell.edu). Applications for the multiple positions available in 2018 will be accepted until September 8, 2017. The selection committee is chaired by Dr. Irby Lovette (IJL2@cornell.edu), Fuller Professor of Ornithology and Associate Director for Academic Affairs at the Lab.

Edward W. Rose, known by family and friends as "Rusty," joined the Lab's Administrative Board in 1993 and served as its Chairman from 2004 to 2014. Rusty was a brilliant man who inspired everyone at the Lab, not only through his infectious laugh but even more by asking tough questions, expecting excellence, and seeking global impact. Rusty had a deep conservation ethos which he exemplified both in his own actions and through his support of the Cornell Lab and kindred institutions. He was among the Lab's most enthusiastic promoters of early career scientists, and he always relished learning about their discoveries and accomplishments. Rusty passed away in January 2016, but his legacy endures in many contexts, including the Edward W. Rose Postdoctoral Fellowship Program which brings together the Lab's entire postdoctoral community. Through the generosity of Rusty and his wife Deedie, together with that of fellow board members Larry and Nancy Fuller, Russ and Carol Faucett, and Imogene Powers Johnson, the Lab shall award multiple Edward W. Rose Postdoctoral Fellowships annually.

Cornell University is an innovative Ivy League university and a great

— / —

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

---

EmoryU TheoreticalEvolutionaryGenetics

Up to two postdoctoral positions in theoretical evolutionary genetics are available in Daniel Weissman's group at Emory University.

I* am especially looking for people who are interested in developing new approaches for learning the evolutionary dynamics of viral and microbial populations from large-scale sequencing. I've been lucky enough to start collaborations with some great experimental and observational groups, but now there's way more to be done than I can handle by myself. The current projects range from fairly well-defined ones to ones where the big challenge is even figuring out what questions to ask, so postdocs would be able to reliably build a track record while also thinking about new directions that they could use to start their own careers as independent researchers. While data analysis is the most urgent need in the group right now, I'm also very happy to hire people who would prefer to focus more on pure theory, including but not limited to evolution on fitness landscapes and the interaction between adaptation and spatial structure and their effects on genetic diversity. Ideally, everyone in the group gets to do a mix of theory and analysis.

If you're interested and would like to hear more about the specifics, please email me. Successful applicants will have a PhD and a strong publication record in evolutionary theory, theoretical physics, statistics, or a related field. I am particularly interested in candidates with a track record of scientific creativity and independent thinking. Review of applications will begin immediately and will continue until the positions are filled. Please send your CV, a brief description of your research experience and interests, and a list of three references to dbweissman@gmail.com.

Emory University is one of the world's leading research universities, with top-ranked programs in Population Biology, Ecology, and Evolution and Biomedical Engineering. The outstanding School of Medicine and Rollins School of Public Health and the nearby Georgia Institute of Technology provide ample opportunities for collaborations. The hired postdoctoral scientists will benefit from unique resources available at Emory, including the Center for Disease Control, which is located on Emory Campus. Emory is located within a leafy neighborhood in the heart of Atlanta and offers a high quality of life.

People from underrepresented backgrounds are especially encouraged to apply. Emory University is an Equal Opportunity/Affirmative Action employer.

Thank you, Daniel Weissman Assistant Professor Physics, Associated Assistant Professor of Biology Emory University http://weissmanlab.github.io *Sorry, I just can't write this whole thing in the third person and the passive voice.

Daniel Weissman <dbweissman@gmail.com>

Estonia HumanGenomics

Hello,

please find here (http://www.ebc.ee/NEWS/2017/-ResearchFellow_population_genetics_2017091 5.pdf) a call for a Postdoctoral position at the Estonian Biocentre in Tartu. The position is funded by a research project aimed at analysing 2500 high coverage Estonian human genomes using haplotype-aware methods such as chromopainter, fineStructure, Globetrotter, PCAdmix and the like. The candidate is welcome to expand and improve this line of research, based on his/her personal interests within the field of human population genetics.

Previous practical experience on any of the above mentioned approaches is highly recommended. Deadline for the application is 15^th September 2017.

The Estonian Biocentre Evolutionary Biology unit aims at reconstructing human's evolutionary history through modern and ancient DNA genome sequences. Its research experienced growing international press coverage and all the sequenced data are freely accessible (www.ebc.ee/free_data) to the scientific community.

Please circulate to potential candidates and encourage them to get in touch for further info.

Best and thank you,

Luca Pagani

Senior Researcher,

Estonian Biocentre

Riia 23b, 51010, Tartu, Estonia

###Copy/Paste version of the call linked above###

Research Fellow in Population Genetics (Postdoctoral level) Evolutionary biology workgroup, Estonian Biocentre, Tartu, Estonia.

Coordinator: Dr. Luca Pagani

Deadline: 15.09.2017 (please get in touch if you cannot make the deadline)

Salary: 33,632 euro (gross salary, approx. 26,369 euro after taxes).

Duration: The advertised position is funded for 24 months and can be extended up to April 2021.

Duties and responsibilities Carrying out research activity and co-supervise two PhD students in the fields of human Population Genetics and Biological Anthropology within the Mobilitas Pluss funded project "Unravelling the Estonian genome: the whole is greater than the sum of its parts" (see description below).

Research project short description: Recent advances in the field of ancient human genetics showed that the gene pool of Estonians, as elsewhere in Europe, is the sum of various evolutionary histories that met in the region after the Ice Age. Each of these human groups, however, carried different genetic variants with potentially different consequences on the physiology and genetic makeup of modern Estonians. With the present project the whole genome sequences of 2500 modern Estonians recently generated at the Estonian Genome Centre will be subdivided into their ancestral components. These components will be screened for their burden of genetically causative variants (from a catalogue of GWAS and literature hits). Given the uniqueness of modern Estonian genomes, this approach will shed light on the evolutionary bases that form the present disease burden in the region.

Required qualifications: PhD Bioinformatics, Biostatistics, Human Evolutionary Genetics or related subjects.

Required skills: Advanced programming skills in at least one of the following languages are mandatory: R, Perl, Python, C++;

Required language skills: English

Starting on 01.10.2017 as earliest

Workload: 1,0

Application documents and notification of results: In order to be considered for the position, the candidate must submit to the Estonian Biocentre (postal address: Riia 23b, 51010 Tartu, Estonia OR email to: lp.lucapagani@gmail.com) the following documents: 1) a letter of application/motivation 2) a curriculum vitae; 3) a copy of a document (including its annexes) which shows the candidate to hold the required qualification (authorized translation into Estonian or English if the credential is not in one of these languages), or proof of thesis submission if the PhD has yet to be defended. A candidate can be required to submit the original or a certified copy of the document (including its annexes) showing the candidate to hold the required qualification; 4) a list of relevant publications; 5) other materials considered relevant by the candidate.

Additional information: Luca Pagani: lp.lucapagani@gmail.com or Merilin Raud: merilin@ebc.ee

Notification of results: The candidate will be notified of selection results within two weeks from the application deadline.

Luca Pagani <lp.lucapagani@gmail.com>

Hawaii RevisionaryMolluscanSystematics

Postdoctoral Researcher Revisionary Molluscan Systematics

Malacology - Bernice Pauahi Bishop Museum, Honolulu, HI

An NSF funded postdoctoral position in revisionary molluscan systematics is available in the Department of Malacology at the Bernice Pauahi Bishop Museum (BPBM) under the supervision of PI Dr. Norine W. Yeung and collaborating investigators (Hayes and Slapcinsky).

We are seeking a highly motivated, well organized, and creative candidate with a proven record of training and achievement in morphology-based taxonomic revisionary work on invertebrates, preferably gastropods, that includes molecular phylogenetics. The candidate should be eager to integrate additional biodiversity informatics tools and approaches into their research.

Candidates should also have the following:

- A strong publication record following from their PhD (published papers, in press, or submitted)

- Creativity, independence, and a strong desire to learn new skills and mentor students and junior researchers

- Excellent written and oral communication skills

The candidate will join a team of national and international researchers interested in understanding the evolutionary patterns and processes that generate and maintain biodiversity, particularly of Pacific island land snails. Ongoing research into the systematics, evolution, and conservation of Pacific island land snails includes some of the most diverse and iconic families in the Hawaiian Islands. The target of our current funding is the Achatinellidae, which include the iconic, but endangered Oahu tree snails (Achatinella spp.), and 12 other genera within five subfamilies. The chosen candidate will take on a well circumscribed, taxonomically focused aspect of the project, which will assist in meeting the overall objectives of the award.

The postdoc will also be heavily involved in training and outreach components of the project, including; 1) Training students from underrepresented groups in STEM in modern taxonomy, museum studies, nomenclature, anatomical dissection, integrative molecular and morphological phylogenetics, microscopy, scientific presentation and publication, and 2) Producing digital identification guides of extant Hawaiian achatinellids that will include information on biology, taxonomy and evolution, and developing museum exhibits for the National Museum of Natural History, BPBM, and the Florida Museum of Natural History.

The preferred start date is January 1, 2018, and funds are available for at least two years, possibly longer, pending suitable progress.

Initial informal inquiries via email are strongly encouraged and should be directed to Dr. Norine Yeung, but all applicants will be required to submit an application consisting of: (1) a cover letter describing their interests, (2) a curriculum vitae, (3) a 1 page statement of research experience that explains your background, specific interest in the project, and (4) the names and contact information for at least three professional references. Application materials should be sent as a single PDF document via email to Dr. Norine Yeung (nyeung@hawaii.edu).

Closing date for receipt of complete applications is October 1, 2017.

Kenneth A. Hayes Howard University Department of Biology 415 College Street NW, EE 332 Washington, DC 20059 Phone: 202-806-6926 Fax: 202-806-4564 Web: http://hayeslab.weebly.com/ "kenneth.hayes@Howard.edu" <kenneth.hayes@Howard.edu>

MaxPlanck Odense EvolutionOfHumanAging

Postdoc position in Citizen Science and Evolution of Human Aging

The Department of Biology and Max Planck Odense Center on the Biodemography of Aging invite application for a position in human aging research working on a citizen science project. The position is funded within the Open Data Experimentarium (ODEx) and will initially run for a period of 13 months, starting September 2017 or soon thereafter. Application deadline: 15 August 2017.

Human life expectancy rises by about two years per decade. Despite intensive aging research we have only a limited understanding of the underlying aging process that allows such lifespan extensions. Are longer lives simply achieved by delaying aging, or has the wear and tear process behind aging slowed? Such fundamental questions will be studied by the difference between perceived age (how old one looks) and chronological age (how old one is) as a biomarker. The core of project builds on a citizen science project, AgeGuess.org, in which more than 3750 citizen scientists currently participate. The citizen scientists have uploaded over 4700 facial images and guessed an impressive 200000 times the age on the images, analyzing this data and expanding the project by launching targeted campaigns and publicly outreaching will be the main task of the post-doc.

Job description The successful applicant will be expected to work on a citizen science project, AgeGuess.org, by conducting and publishing international research in the field of human aging research with focus on biomarkers of aging comparing chronological and perceived age, and statistical analysis of such data collected by citizen scientists. We also expect the applicant to be centrally involved in outreach activities and launching targeted campaigns to increase the involvement of citizen scientists in the project.

The applicant will work in a multi-disciplinary, international team of biodemographers, evolutionary biologists, health-scientists, economists, computational biologists, and biostatisticians.

Major requirements - A PhD in natural, health, technical or social sciences or comparable - Research in the mentioned disciplines, preferably across disciplines, with a strong quantitative component - A proven interest in the fundamentals of human aging - Experience in teaching and outreach activities - Grant writing experience.

It is expected that the new postdoc participates in undergraduate and postgraduate teaching and in supervising of students and researchers.

Other requirements - Excellent communication and interpersonal skill - Excellent statistical and analytical abilities - A computer language such as R, Python, or similar is required. Applicants from computer science are particularly welcome. - Fluent English language skills - Ability to work independently as well as in multidisciplinary teams - A strong team player.

Further information can be obtained from the work package leader, Associate Professor Ulrich Steiner, telephone +45 6550 2753, e-mail: usteiner@biology.sdu.dk.

"usteiner@biology.sdu.dk" <usteiner@biology.sdu.dk>

Mexico HumanGeneticBiobank

Postdoc positions available at LANGEBIO, Mexico: The Mexican Biobank Project

You are invited to apply to work on the Mexican Biobank project which aims to build one of the largest genetics biobanks in Latin America and to build capacity in big data science in medical genomics in admixed populations. The project is funded through CONACYT and the Research Councils UK (RCUK) and integrates teams in Mexico (LANGEBIO), the UK (Oxford) and the US (Standford). The project will generate genetic data on 10,000 Mexican individuals with linked demographics and medical data, and measure antibody titers on a panel of approximately 20 pathogens that are naturally circulating in the Mexican population.

This resource will provide research apportunities in population genetics and genetics of complex traits in an admixed population, and the opportunity to study the genetic determinants of seropositivity to many common pathogens in Mexico.

We are seeking two exceptional postdocs to work in data analysis and opportunities for training are available across the expertise of the team. Analyses include data quality control, phasing, imputation, association analysis and population genetics analyses including natural selection and distribution of deleterious alleles. You will be working with data generated from genotyping arrays but also from sequencing studies. You will be closely surpervised by Dr. Andres Moreno from the National Laboratory of Genomics for Biodiversity (LANGEBIO) in Mexico, with expertise in population genetics of admixed populations; and Dr. Selene Fernandez, with an expertise in genomics and bioinformatics of non-coding RNA. In addition, the project will also be closely supervised by Dr. Alexander Mentzer and Mexican researcher Dr. Adrian Cortes, based at the Wellcome Trust Centre for Human Genetics, Oxford University, with expertise in genetics of complex diseases and immunogenetics, as well as Dr. Carlos Bustamante from Stanford University and Dr. Christopher Gignoux from UC Denver.

This is a great opportunity for advanced trainees to get access to one of the most comprehensive and innovative datasets in Biomedical Data Science from Latin America and build and independent scientific career in medical and/or population genetics where strong quantitative and computational skills are required. LANGEBIO is one of the leading institutions in genomic research not only in Mexico but also internationally (www.langebio.cinvestav.mx). The applicant will have full access to the local infrastructure at LANGEBIO and the Genomics Core Facility (www.langebio.cinvestav.mx/labsergen), the Moreno laboratory (www.morenolab.org), as well as the extended collaborative network in the UK and USA. Previous experience working with large genomic datasets, statistical genetics and computational skills including one or more scripting or programming languages (e.g. R, Perl, Python, C, Java) and complete familiarity in working in a Linux/Unix environment is desired.

Laboratorio de Servicios Genomicos LABSERGEN | LANGEBIO www.langebio.cinvestav.mx Explora nuestra variedad de metodos disponibles para tus necesidades de secuenciacion masiva.

Human Population Genomics Lab www.morenolab.org We are a young research team interested in human diversity and population genetics. We are applying genomic and computational tools to answer research questions about ...

LANGEBIO www.langebio.cinvestav.mx About Langebio In our website you will find information about our research activities, graduate program, and technology services that our institution offers.

If you are interested please send 1) a copy of your CV 2) copy of your most relevant publications (up to three) 3) a one-page letter of intent describing your research interests and why you would like to join the project and 4) two letters of recommendation to andres.moreno@cinvestav.mx Competitive salaries will be offered according to demonstrated experience and CV. Funds are available to support both positions for two years starting early 2018 ideally. The positions will remain open until filled.

____

Consuelo Quinto Cortes

Laboratorio de Genomica Evolutiva Humana y de Poblaciones LANGEBIO http://www.morenolab.org Consuelo DayzÃº Quinto Cortés <consuelo.quinto@cinvestav.mx>

MonashU AdaptiveDynamicsModeller

Postdoctoral Position in the Centre for Geometric Biology Monash University Australia

Professor Dustin Marshall is seeking an experienced theoretical biologist experienced in Adaptive Dynamics modelling.

As the postdoctoral researcher, you will use adaptive dynamics modelling approaches to explore the drivers and consequences of body size evolution. Working with other researchers in the Centre for Geometric Biology, you will parameterise models based on empirical findings and provide advice of key tests of model predictions.

You will further be expected to maintain consistently high research output in the form of quality publications, supervision of students, development and submission of grant proposals to external funding agencies, contribute more generally to communicating the research activities of the group, and participation in appropriate career development activities.

Your application must address the selection criteria.

Other job-related information

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

- Travel to other campuses for undergraduate teaching and to conduct training may be required from time to time. - The taking of leave may be restricted during peak periods of work

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

Dustin Marshall, Professor, School of Biological Sciences, +61 3 9902 4449

Dr. Liz Morris Administration Manager Centre for Geometric Biology School of Biological Sciences Monash University Clayton, Vic 3800 Australia Mob: +61 3 404 069 210 Email: Liz.Morris@monash.edu

Liz Morris <liz.morris@monash.edu>

MonashU ZooplanktonEvolution

Postdoctoral Position in the Centre for Geometric Biology, Monash University Australia

Professor Dustin Marshall is seeking an experienced zooplankton biologist.

As the postdoctoral researcher, you will use quantitative approaches to explore the drivers and consequences of body size evolution in zooplankton. Working with other researchers in the Centre for Geometric Biology, you will have expertise in growing and studying zooplankton to test theory about energy dynamics.

You will further be expected to maintain consistently high research output in the form of quality publications, supervision of students, development and submission of grant proposals to external funding agencies, contribute more generally to communicating the research activities of the group, and participation in appropriate career development activities.

Your application must address the selection criteria.

Other job-related information

- This role is a full-time position; however, flexible working arrangements may be negotiated. - Travel to other campuses for undergraduate teaching and to conduct training may be required from time to time. - The taking of leave may be restricted during peak periods of work

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

http://careers.pageuppeople.com/513/cw/en/job/-561073/researc h-fellow-biological-sciences-life-history-empiricist Enquiries

Dustin Marshall, Professor, School of Biological Sciences, 03 9902 4449

Dr. Liz Morris Administration Manager Centre for Geometric Biology School of Biological Sciences Monash University Clayton, Vic 3800 Australia Mob: +61 3 404 069 210 Email: Liz.Morris@monash.edu

Liz Morris <liz.morris@monash.edu>

MountSinai NewYork PopulationGenetics

A computational postdoctoral fellow position is available immediately in Statistical Genetics, Human Genetics and/or Population Genetics in Dr. Ron Do’s lab. The Do lab is in the Charles Bronfman Institute for Personalized Medicine, Department of Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai, New York, New York.

The Charles Bronfman Institute for Personalized Medicine is an interdisciplinary institute to advance personalized health and health care. One of the institute’s key resources is the BioMe electronic health record (EHR)-linked Biobank, an ancestrally diverse population of >34,000 individuals recruited from throughout New York City. BioMe has a longitudinal design and captures and full spectrum of common and rare biomedical phenotypes. BioMe is also rich in genetic data, including genome-wide array genotypes, and exome (N ~34,000) and whole genome (N ~15,000) sequencing data.

Dr. Do’s lab focuses on determining the genetic and biological bases of complex disease. The group pursues these interests by utilizing approaches from statistical genetics, population genetics, human genetics and genetic epidemiology.

Current lab research areas include: (1) Causal inference of biomarkers with complex disease; (2) Identification of biological processes of complex disease using functional data; (3) Inferring the strength and mode of natural selection for complex disease; (4) Rare variant association studies using sequencing data; (5) Data mining in electronic health records.

The successful candidate will have the opportunity to work on large-scale cutting-edge sequencing, genotyping and high-throughput functional data. Importantly, the candidate will have substantial input to the specific nature of their research project.

Lab members will benefit from collaborations with neighboring labs in the Charles Bronfman Institute for Personalized Medicine, the Center for Statistical Genetics, and the Icahn Institute for Genomics and Multiscale Biology.

The term for this position is for 3 years with possibility of an extension depending on successful progress and available funding. A competitive salary, benefits and travel opportunities will be offered commensurate with experience and qualifications.

Job Qualifications: 1. Candidates should have a Ph.D., M.D. or equivalent doctorate in statistical genetics, population genetics, computational biology and/or human genetics.

2. Candidates should have proficiency in programming (e.g. Perl or Python) and statistical computing (e.g. R).

3. Candidates should have a track record of scientific productivity and/or leadership.

Please send inquiries via email to ron.do@mssm.edu. Informal inquiries are welcome.

Ron Do, Ph.D. | Assistant Professor in Genetics and Genomic Sciences | The Charles Bronfman Institute for Personalized Medicine | The Center for Statistical Genetics | The Icahn Institute for Genomics and Multiscale Biology | Icahn School of Medicine at Mount Sinai | Website: http://labs.icahn.mssm.edu/dolab/ "Do, Ron" <ron.do@mssm.edu>

MPIO Seewiesen EvolutionCognition

The Max Planck Institute for Ornithology (MPIO) in Seewiesen (located near Starnberg, about 50 km from Munich) is an internationally renowned research institution with more than 200 employees working in four departments and nine research groups. The research group of Comparative Cognition (Dr. Auguste von Bayern) runs a research station in collaboration with the Loro Parque Fundación (LPF) on Tenerife, Spain. In this regard, a third-party funded grant is offered, financed by the “Animal Minds Project e.V.”, and invites applications for

1 Postdoctoral grant in Comparative Cognition.

We are interested in the evolution and mechanisms of complex cognition in birds (parrots and corvids) using a comparative approach.

Access to the greatest parrot collection in the world comprising over 350 (sub)species of parrots and a laboratory with over 40 trained parrots (touch screen, exchange paradigm etc.) of 4 species (and further corvid species in Germany) allows comparative cognitive studies at a new scale and on a new large-brained model system. The work will focus on socio-cognitive abilities of parrots in relation to ecology/life history both in the laboratory and in the breeding station of the LPF. Other topics might be covered additionally as the postdoc will be responsible for coordinating and mentoring a team of (post)graduate students working on different projects. The position includes opportunities to teach at the Ludwig-Maximilians-University, Munich.

Applicants should hold a PhD in animal cognition or experimental/developmental psychology, and have a minimum of two years of Postdoc research experience in animal cognition and/or developmental psychology of human children. Good statistical skills in relevant subjects are desirable. High self-motivation and ability to work independent and in a team are an absolute must. Additionally, the position requires team-leading skills, good organization and time management skills and writing proficiency. Basic knowledge of Spanish is helpful.

The starting date will be summer/autumn 2017 but no later than 30th of September 2017. The position is available initially for two years but can be extended subject to satisfactory performance. For further information, please do not hesitate to contact Dr. Auguste von Bayern e-mail: avbayern@orn.mpg.de.

The monthly stipend will be € 2,325.- and will be paid directly through the “Animal Minds Project e.V.”.

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

Please submit a cover letter (describing your research interests, experience and goals), your CV, copies of degree certificates and a list of three references as one single PDF preferred via e-mail to: personal@orn.mpg.de

or via mail to:

Max Planck Institute for Ornithology

Human Resources Department

Eberhard-Gwinner-Str.

D-82319 Seewiesen

Deadline for applications: 07.08.2017

"anastacia.k@web.de" <anastacia.k@web.de>

Munich EvolutionImmuneSystems

The Parmenides Foundation offers one partial senior stipend and three partial stipends of up to 3 years for theoretical investigations into the Population genetics of transitional organisations between prokaryotes and eukaryotes. Candidates are expected to have demonstrated excellence in population genetics of non-standard genetic systems (such as in the origin of life and elsewhere). Send CV and publication list to Carsten Freitaeger, email carsten.freitaeger@parmenides-foundation.org by July 20.

Thank you!

Carsten

Parmenides Stiftung Kirchplatz 1 82049 Pullach Tel +49.89.4520935.0 Skype: Parmenides.Foundation carsten.freitaeger@parmenides-foundation.org

I am writing you as a representative of Parmenides Foundation in Munich, Germany. We are a rather small non-profit organisation with research concentrated on all aspects of thinking. One of our fellows, Prof. Eors Szathmary, is looking to fill a post-doc position within the research team of one of his EU grant projects. Could you please be so kind and post our post-doc position offer on your website (evoldir). The position and candidate profile as we would like to have it posted on your website:

A thematic Parmenides fellowship is open at the Parmenides Center for the Conceptual Foundations of Science (Munich, Germany) under the supervision of Prof. Eors Szathmary. The successful candidate will carry out his/her own research agenda in the fields described below. The position is for a minimum of 1 year to a maximum of 3 years. The successful applicant will receive a stipend of 2500 EUR per month (net). The proposed project can start as soon as a suitable candidate is identified, but not later than the 1st January, 2014.

Origin and evolution of adaptive immune systems: The project will involve the development of a conceptual framework and detailed evolutionary scenario to place the origin and evolution of adaptive immune systems in the framework of the major evolutionary transitions. Individual steps of the evolutionary pathway will be investigated with the help of mathematical and simulation models.

We seek applicants with an interest in both theoretical evolutionary biology and immunology, with experience in using a range of computational, bioinformatics and mathematical techniques to answer evolutionary questions. The ideal candidate will have 5+ years of postdoctoral experience, a track record in publishing in international scholarly journals and fluency in English. Past experience in the supervision of MSc/PhD students is an advantage.

Candidates should submit an application consisting of a CV with full list of publications, a motivation letter (1 page) and a proposed workplan (max 3 pages).

The deadline for applications is 15^th December, 2013. Applications should be sent by email to Eors Szathmary, szathmary.eors@gmail.com. Please do not hesitate to contact me, if you have any questions about my request or the position to be filled. Thank you.

Kind regards, Carsten Freitager

Carsten Freitager Projektmanagement Parmenides Stiftung Kirchplatz 1 82049 Pullach Tel +49.89.4520935.0 Fax +49.89.4520935.31 Mobil +49.173.5403274 carsten.freitaeger@parmenides-foundation.org

Carsten Freitäger <carsten.freitaeger@parmenides-foundation.org>

NortheasternU GenomicsComputationalBiol

A postdoctoral position is available in the laboratory of Dr. Kathleen Lotterhos at Northeastern University. The postdoc will also be mentored by Sam Yeaman at the University of Calgary. The successful candidate will be part of an NSF-funded project to study the behavior of genome scans across a range of genomic architectures, from monogenic to highly polygenic. The successful candidate will be expected to generate a large set of realistic simulations, evaluate various types of statistical methods for analyzing genomic data, and manage a diverse team of developers and collaborators.

Qualifications Applicants will be expected to develop and lead projects. Candidates are required to have a Ph.D. in Evolutionary Genetics, Statistics, Computational Biology (bioinformatics), or related disciplines. A computing background is required, especially experience with Unix, and knowledge in one or several programming languages (R/BioConductor, Python, C/C++, etc). Candidates should demonstrate a strong track record of publication; have strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team.

Additional Information The appointment is for 24 months. Start time is flexible, with a desired start after August 1.

The Lotterhos Lab is based at the beautiful in Nahant campus north of Boston (NUMSC). The NUMSC has a strong research presence in evolution and ecology research and there are many opportunities for interaction and collaboration both there and in the greater Boston area. More information about our lab's research can be found here: https://sites.google.com/site/katielotterhos/home. The successful candidate will also have opportunities to travel to Calgary and work with Yeaman. We welcome applications from candidates with diverse educational backgrounds.

To apply, please prepare a CV, cover letter, references, and one peer-reviewed publication and upload them at this site: https://neu.peopleadmin.com/postings/49443 Kathleen E Lotterhos Assistant Professor Department of Marine and Environmental Sciences Northeastern University Marine Science Center, Room 113 430 Nahant Rd Nahant, MA 01908 Phone: 781.581.7370 ext 304

"k.lotterhos@northeastern.edu"
<k.lotterhos@northeastern.edu>

OIST Japan InsectEvolutionAndGenomics

The Okinawa Institute of Science and Technology Graduate University (OIST) is a model for change in education and research with the best international graduate students, working side by side with world-class faculty in modern well-equipped laboratories. Beautifully situated on the island of Okinawa, OIST relies on a cross-disciplinary approach, with an emphasis on creativity and exchange, to offer unique, individualized graduate training. OIST is a university with no departments, eliminating artificial barriers between people working in different fields, but many nationalities, with students and faculty being attracted from all over the world. Concentrating initially on Neuroscience, Molecular Sciences, Mathematical Sciences, Environmental and Ecological Sciences and Physical Sciences, OIST is bringing some of the best brains in the world to Okinawa to transform the way science and education is done in the global academic world.

Position summary:

The Evolutionary Genomics Unit is seeking for a postdoctoral researcher with background in ecology and evolution, and with ability to analyze high throughput sequencing data. The researcher will work around on one or more of these promising topics: molecular evolution of the symbiosis between insects and microorganisms, molecular phylogenetic of insects and their microorganisms, historical biogeography of termites.

Position:

The Evolutionary Genomics Unit is a research group recently established at OIST with interests in evolution of insects in general. Our main research topics include molecular evolution of the symbiosis between insects and microorganisms, molecular phylogenetic of insects and historical biogeography of termites. We address all these themes using high throughput sequencing. OIST possesses cutting edge sequencing facilities, equipped with high throughput sequencing, including Illumina Hiseq 2500, Hiseq 4000, Miseq, and PacBio. We are looking for a postdoctoral candidate with extensive experience in high throughput sequencing and who is keen to work on one of our insect models: cockroaches or termites. The candidate is expected to work in collaboration with members of the Evolutionary Genomics Unit, and she/he will be given relative independence to develop her/his own research within the frame of the Unit's research agenda.

Some possible research topics include, but are not restricted to:

- Studying the role of termite gut microorganisms in soil-feeding termites using metagenomic analyses. Many species of termites feed on soil but they are not studied as intensively as wood-feeding termites. Metagenomics can help us understanding the function of these microorganisms.

- Studying the evolution of genome reduction in the cockroach endosymbiont Blattabacterium. Most cockroaches are associated with Blattabacterium, a bacterium that recycles nitrogen wastes and provides amino acid to their host. The number of genes varies between strains of Blattabacterium, and one question is therefore what are the factors responsible of gene erosion in some strains?

- Studying the historical biogeography of termites using molecular phylogenies. Termites are distributed worldwide and often make up a large part of animal biomass in the tropics. We are studying the origin of their distribution using mitochondrial genome phylogenies, to determine the timing and direction of their spread across the globe.

- Studying the coevolution between termites and their microorganisms. The gut of termites host 1000s of bacterial species participating to the degradation of wood and other organic compounds. Gut bacteria are inherited from parents, or are acquired by transfer from other sources. We aim to determine the respective role of vertical inheritance versus horizontal transfer in shaping the termite gut bacterial communities.

Working Location:

Onna-son, Okinawa, Japan

Responsibilities:

1. Carrying out lab experiments
2. Data analysis
3. Writing papers
4. And possibly carrying out fieldwork

Qualifications:

(Required)

1. Ph.D. in Biological Science, with relevant research experience
2. Proficiency in written and spoken English
3. Good track record of publications
4. Ability to analyze high throughput sequencing data
5. Highly motivated and with strong social skills

(Preferred)

1. Previous fieldwork experience, especially of insect sampling
2. Experience with insect breeding

Term:

Full-time, fixed term appointment for 1 year, with possibility of renewal for up to a total of 3 years.

Working hours:

9:00-17:30 (Discretionary)

Compensation:

In accordance with the OIST Employee Compensation Regulations

Benefits:

- Relocation, housing and commuting allowances
- Annual paid leave and summer holidays
- Health insurance (Private School Mutual Aid http://www.shigakukyosai.jp/), welfare pension insurance (kousei-

— / —

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

---

Omaha 2 ConservationNGS

SUMMARY

Omaha's Henry Doorly Zoo & Aquarium Department of Conservation Genetics based in Omaha, Nebraska, is seeking two post-doctoral researchers with interest/expertise in the generation and analysis of next-generation sequencing data of lemurs, tortoises, and other taxa from Madagascar.

RESPONSIBILITIES AND DUTIES include the following. Other duties may be assigned.

The successful applicant will be proficient in the construction genomic libraries and in solution hybridization methodologies for high throughput sequencing as well as all relevant analysis of large datasets, and manage next-generation sequence workflows.

The researchers will be responsible for development, implementation, and support of software applications related to variant detection and interpretation from high-throughput experiments involving multiple species of lemurs, tortoises, and taxa from Madagascar.

Assembly of whole genomes is in-progress, but will likely require additional analysis pertinent to specific research projects. Interested candidates should be highly motivated, organized, independent, and have extensive experience with molecular genomics and bioinformatics, and be able to efficiently write and revise manuscripts. Data on a variety from a variety of species has already been generated, thus candidates will be able to quickly start analysis and manuscript preparation.

Travel to Madagascar to support the field programs of Omaha Zoo and the Madagascar Biodiversity Partnership is required for a minimum of five week intervals twice a year.

Basic Qualifications:

Applicants should hold a PhD in bioinformatics, computer science, molecular genomics or related field and have more than one year of experience in high-throughput genome sequence analysis. Applicants should be experienced at software related to next generation sequencing data and be able to manipulate genomic data for phylogenetics and phylogeography. Our group's focus is large-scale sequencing for phylogenetics, phylogeography and evolutionary studies of lemurs, tortoises and other taxa from Madagascar. Thus, previous experience in genome assemblies, annotation and analysis of a variety of next generation sequencing (NGS) pipelines is preferable. The ideal candidates will be independent, highly motivated, productive, and able to work effectively in a team with members from a variety of diverse backgrounds, and have outstanding written and verbal communication skills. The successful applicants must be interested in interdisciplinary science and field research and have a solid publication record that illustrates ability to conduct novel, independent research.

Preferred Qualifications

Candidates should have 3+ years of experience in molecular biology, genetics, or bioinformatics. The position requires proficiency in programming (perl or python) and bash scripting using Linux operating systems. Applicants are also expected to be familiar with bioinformatics tools, be able to implement complex computational pipelines, incorporate genomics databases and have extensive and creditable laboratory experience with constructing genomic libraries. The applicants will need to work closely with two full time technicians to manage NGS lab work, as well as with a full time bioinformatician. While in Madagascar the researchers will work with a variety of Malagasy graduate students, and is expected to assist with the progression of a variety of projects, and assist with completion of their degrees and peer-reviewed manuscripts. Based on all these above duties requires candidates with excellent interpersonal skills, and the ability to train and teach both national and international audiences is necessary. Candidates must also be able to jump between a variety of projects, based on needs of the research group.

Time Frame

These positions will be part of an on-going team of rotating postdoc fellows. One of the positions is expected to begin approximately September 2017, while the second is expected to start in January 2018. Initial appointment will be for two years, with possibility to extend to three years.

Application

Please submit your CV with the contact information for 3 professional references, a letter describing your interests and goals, and copies of a few publications. Please apply at: http://www.omahazoo.com/careers/

Learn more at: https://madagascarpartnership.org/
Genetics Department <genetics@omahazoo.com>

Omaha 2 NGS Conservation

SUMMARY

Omaha's Henry Doorly Zoo & Aquarium Department of Conservation Genetics based in Omaha, Nebraska, is seeking two post-doctoral researchers with interest/expertise in the generation and analysis of next-generation sequencing data of lemurs, tortoises, and other taxa from Madagascar.

RESPONSIBILITIES AND DUTIES include the following. Other duties may be assigned.

The successful applicant will be proficient in the construction genomic libraries and in solution hybridization methodologies for high throughput sequencing as well as all relevant analysis of large datasets, and manage next-generation sequence workflows.

The researchers will be responsible for development, implementation, and support of software applications related to variant detection and interpretation from high-throughput experiments involving multiple species of lemurs, tortoises, and taxa from Madagascar.

Assembly of whole genomes is in-progress, but will likely require additional analysis pertinent to specific research projects. Interested candidates should be highly motivated, organized, independent, and have extensive experience with molecular genomics and bioinformatics, and be able to efficiently write and revise manuscripts. Data on a variety from a variety of species has already been generated, thus candidates will be able to quickly start analysis and manuscript preparation.

Travel to Madagascar to support the field programs of Omaha Zoo and the Madagascar Biodiversity Partnership is required for a minimum of five week intervals twice a year.

WORKSKILLS: Strong people skills, detailed oriented, willingness to learn and contribute, follow directions, meets deadlines

Basic Qualifications:

Applicants should hold a PhD in bioinformatics, computer science, molecular genomics or related field and have more than one year of experience in high-throughput genome sequence analysis. Applicants should be experienced at software related to next generation sequencing data and be able to manipulate genomic data for phylogenetics and phylogeography. Our group's focus is large-scale sequencing for phylogenetics, phylogeography and evolutionary studies of lemurs, tortoises and other taxa from Madagascar. Thus, previous experience in genome assemblies, annotation and analysis of a variety of next generation sequencing (NGS) pipelines is preferable. The ideal candidates will be independent, highly motivated, productive, and able to work effectively in a team with members from a variety of diverse backgrounds, and have outstanding written and verbal communication skills. The successful applicants must be interested in interdisciplinary science and field research and have a solid publication record that illustrates ability to conduct novel, independent research.

Preferred Qualifications

Candidates should have 3+ years of experience in molecular biology, genetics, or bioinformatics. The position requires proficiency in programming (perl or python) and bash scripting using Linux operating systems. Applicants are also expected to be familiar with bioinformatics tools, be able to implement complex computational pipelines, incorporate genomics databases and have extensive and creditable laboratory experience with constructing genomic libraries. The applicants will need to work closely with two full time technicians to manage NGS lab work, as well as with a full time bioinformatician. While in Madagascar the researchers will work with a variety of Malagasy graduate students, and is expected to assist with the progression of a variety of projects, and assist with completion of their degrees and peer-reviewed manuscripts. Based on all these above duties requires candidates with excellent interpersonal skills, and the ability to train and teach both national and international audiences is necessary. Candidates must also be able to jump between a variety of projects, based on needs of the research group.

Time Frame

These positions will be part of an on-going team of rotating postdoc fellows. One of the positions is expected to begin as soon as possible, while the second is expected to start in January 2018. Initial appointment will be for two years, with possibility to extend to three years.

Application

Please submit your CV with the contact information for 3 professional references, a letter describing your interests and goals, and copies of a few publications. Please apply at: http://www.omahazoo.com/careers/ Learn more at: https://madagascarpartnership.org/ Must be legally entitled to work in the USA. Visa sponsorship is not available.

From: Genetics Department Sent: Monday, June 19, 2017 3:18:21 PM To: Golding@McMaster.CA Subject: EvolDir -for announcement section

Job Title: Postdoctoral Fellow - Madagascar Biodiversity Genomics

Date Position Opens: June 19, 2017

— / —

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

---

OregonStateU PopulationGenomics

DEADLINE: July 31^st 2017

POSTDOCTORAL RESEARCH ASSOCIATE - The O'Malley lab at Oregon State University (OSU) invites applications for a Postdoctoral Researcher (Post Doc) in Population Genomics. The Post Doc will hold a leadership role among a larger research team evaluating the population structure of Albacore tuna (Thunnus alalunga). This research is funded by the Saltonstall-Kennedy Grant Program and will be conducted in collaboration with NOAA's Southwest Fisheries Science Center (SWFSC).

The primary responsibilities for this position include coordinating with the SWFSC to obtain previously collected tissue samples, working with OSU's Center for Genome Research and Biocomputing (CGRB) to direct the next generation sequencing library preparation, performing data analyses using the CGRB's computational infrastructure, and synthesizing the results in a peer-reviewed manuscript.

The Post Doc will be a member of OSU' Department of Fisheries and Wildlife and the Coastal Oregon Marine Experiment Station.

This position is located at the Hatfield Marine Science Center in Newport, Oregon.

ONLINE APPLICATION: To review posting and apply, go to https://jobs.oregonstate.edu. Apply to posting #P01414UF. Closing Date: 07/31/17. OSU is an AA/EOE. Email questions to: Kathleen.omalley@oregonstate.edu

Kathleen O'Malley, Associate Professor

Oregon State University, Hatfield Marine Science Center

Coastal Oregon Marine Experiment Station

2030 SE Marine Science Drive, Newport, Oregon 97365

ph: (541) 961-3311 fax: (541) 867-0345

marinegenomics.oregonstate.edu

"O Malley, Kathleen G" <Kathleen.OMalley@oregonstate.edu>

PrincetonU MammalianEvoDevo

A Postdoctoral position is available in the laboratory led by Ricardo Mallarino, Department of Molecular Biology, Princeton University (www.mallarinolab.org). The lab focuses on uncovering the genetic and developmental mechanisms by which form and structure are generated during vertebrate embryogenesis. We combine the study of emerging and traditional model organisms to explore questions relating to patterning and evolution of novelty in the mammalian skin. The lab uses a variety of approaches, including experimental embryology, genetics, genomics, imaging, and mathematical modelling to uncover gene function and understand mechanisms of evolutionary change.

The lab is currently focusing on two model systems: striped rodents and gliding mammals. Available projects include:

- Spatial control of genes implementing stripe patterns
- Molecular mechanisms of stripe pattern specification
- Comparative genomics and evolution of pigment patterns
- Molecular mechanisms of gliding membrane formation and evolutionary genomics of gliding

While the position entails working on one of these areas, the candidate is expected/encouraged to take a leading role in the conceptual and experimental design of the project. In addition, there will be significant opportunities for pursuing original ideas that fall within the general focus of the lab.

Applicants with a strong background in developmental biology, genetics/genomics, and/or molecular/cell biology are encouraged to apply. A Ph.D. in these disciplines is preferred, but candidates holding a Ph.D. in other areas that have strong laboratory and/or bioinformatics skills will also be considered. Prior experience with experimental embryology, cell/tissue culture, and microscopy would be very beneficial. However, necessary training will be provided for a motivated candidate. Excellent oral and written communication skills and the ability to work independently or in collaboration are essential.

To apply for this position please submit a CV, a cover letter describing research interests, and contact information for three references who can comment on your research to rmallarino@princeton.edu. Applications will be reviewed promptly until the position is filled. Princeton University is an equal opportunity employer and complies with applicable EEO and affirmative action regulations.

Ricardo Mallarino <rmallarino@oeb.harvard.edu>

RadfordU MathematicalBiologyEducation

Postdoctoral Position in Mathematical Biology Education

A postdoctoral position is available with the Quantitative Undergraduate Biology Education and Synthesis (QUBES) project (https://qubeshub.org), with investigators at Radford University, the University of Pittsburgh, the College of William and Mary, Unity College, and the BioQUEST Curriculum Consortium (http://bioquest.org).

Project: In brief, the project aims to facilitate greater penetration of quantitatively rigorous curriculum and experiences in undergraduate biology programs across the country. As part of the larger project, QUBES develops and supports online Faculty Mentoring Networks that partner geographically distributed faculty who wish to incorporate more quantitative approaches in their teaching with a mentor who has expertise and experience doing just that. The focal idea is to provide support, guidance, and faculty development *during* the implementation and assessment of curricular change rather than just before. Read more about the Faculty Mentoring Networks and the larger project here: www.qubeshub.org .

Position: The postdoctoral research position, funded by a grant from the National Science Foundation, will be involved in curriculum development, faculty development, web communications, and assessment of the

QUBES Faculty Mentoring Networks. The position will include teaching responsibilities in the Department of Biology at Radford University, providing opportunities for implementing and assessing innovative curriculum first-hand. The work will be supervised most directly by Dr. Jeremy M. Wojdak at Radford University, but will include close interactions with the Project Director, Dr. Sam Donovan at the University of Pittsburgh, and Dr. Kristin Jenkins, the Executive Director of BioQUEST.

Qualifications/ Requirements: Applicants must have a Ph.D. in the biological sciences or a related field, preferably including experience/expertise in biological mathematics or statistics. Preference will be given to applicants that have demonstrated a strong interest in undergraduate STEM education. Indications of interest in STEM education include participation in professional development programs (e.g., FIRST IV, HHMI Teaching Fellows program, or participation in CIRTL, or coursework in education/pedagogy), experience with outreach (e.g., GK12 project, directing REU program or summer program for high school students), or publications on undergraduate education projects.

We desire applications with strong verbal and written communication skills, good social and organizational skills, and a robust work ethic. Familiarity with statistics (R or equivalent) and the analysis of educational or program assessment data is desirable, as is experience working with diverse faculty and student populations.

Benefits and Opportunities: This is an excellent opportunity for a recent Ph.D. with career interests in science education - by the nature of the mentoring network project, the postdoctoral researcher will have frequent opportunities to connect and interact with a wide swath of faculty interested in quantitative biology education across the country. This position will allow the postdoctoral researcher to gain meaningful teaching experience and robust professional development as an instructor. The project team has a wealth of experience in STEM education pedagogy, scientific publishing, and grant writing, and training in these areas will be available.

Salary will be commensurate with experience, and includes Radford University's competitive benefit package. The candidate will initially be hired for one year, with an annual extensions possible contingent on performance. Grant funding will provide support for travel to conferences and project team meetings.

Radford University is a comprehensive, midsize public university nestled in the New River Valley along the foothills of the Blue Ridge Mountains. Radford provides a diversity of outstanding undergraduate and graduate academic programs for approximately 10,000 students. Renowned for teaching excellence and a focus on strong faculty/student bonds, the innovative use of technology in the learning environment and a vibrant student life on a beautiful campus, Radford University offers many opportunities to engage both faculty and students in teaching, research, and public service as scholars and citizens. Our faculty is proud of our students and their accomplishments. We seek new colleagues who will work to promote their development and help them pursue their aspirations as well as contribute to our versatile and collegial intellectual community. Additional information about the university can be found at http://www.radford.edu .The surrounding region affords a diversity of cultural and recreational

— / —

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

---

RoyalBotGardens UK CropGenetics

JOB VACANCY

POSTDOCTORAL RESEARCH FELLOW POSITION IN CROP GENETICS

Apply here: https://careers.kew.org/vacancy/research-fellow-in-crop-genetics-318593.html Kew is the world's leading botanic gardens, at the forefront of plant and fungal science, a UNESCO World Heritage Site and a major visitor attraction. We want a world where plants and fungi are understood, valued and conserved - because our lives depend on them. We use the power of our science and the rich diversity of our gardens and collections to provide knowledge, inspiration and understanding of why plants and fungi matter to everyone. Kew's Millennium Seedbank at Wakehurst Place in West Sussex hosts the world's most biodiverse seed bank containing seeds from almost 40,000 plant species, including many crop wild relatives.

We are currently seeking a research geneticist to join an international agricultural research and development project linking industrial and academic research partners in the UK and Ethiopia. Our innovative interdisciplinary project aims to improve livelihoods for Ethiopian smallholder farmers by transforming the productivity and quality of a traditional Ethiopian grain legume crop, the white lupin.

Your role will be to conduct genetic research into the control of alkaloid content, a key seed and forage quality trait. Using high-throughput genome sequencing approaches, you will identify the gene(s) governing alkaloid production and develop molecular tools for use in plant breeding.

Educated to doctoral level, you will be required to demonstrate proficiency in genetic research in plant or animal systems and a capacity to effectively query large genomic datasets. You will have proven track record in publishing research in respected international scientific journals. You should be able to interact effectively with both industry and academic collaborators, and be willing to co-supervise research students. You will also make contributions to the overall running of the Science Directorate commensurate with the grade of the post.

Salary will be 30,000 - 32,760 per annum pro rata, depending on skills and experience. Benefits include competitive annual leave allowance, excellent pension, a flexible benefits scheme, as well as a great working environment.

For full details on this role please visit our website link https://careers.kew.org/vacancy/research-fellow-in-crop-genetics-318593.html from our website.

Informal enquiries can be addressed to Dr Matthew Nelson via m.nelson@kew.org.

Closing date: 16 July 2017

We are committed to equality of opportunity and welcome applications from all sections of the community. We guarantee to interview all disabled applicants who meet the essential criteria for the post.

Matthew Nelson <M.Nelson@kew.org>

RutgersU PopulationGenomics

Postdoctoral position in Population Genomics at Rutgers University

Seeking qualified applicants for a NIH funded postdoctoral position with Andrew Kern in the Department of Genetics and the Human Genetics Institute of New Jersey at Rutgers University. I'm looking for a colleague who will work with me on applying machine learning methods that we have developed to population genomic datasets. The initial contract will be for 1 year, with the option to extend to multiple years.

The ideal candidate would hold a Ph.D. and have a record of research achievement in population genetics, evolutionary biology, phylogenetic/phylogeography, computational biology, computer science, statistics, or a related field. A background in comparative/population/evolutionary genomics is of course highly desirable. The candidate should have experience programming in python (but any scripting language is fine), have experience with cluster computing environments, and have some familiarity with C/C++ (although this is negotiable).

More information about the Kern lab can be found here: http://kernlab.rutgers.edu . More information about the department can be found here: http://genetics.rutgers.edu/. The lab is located on the Busch campus of Rutgers University, in central New Jersey, and is in easy commuting range to New York City.

Review of applications will begin immediately and continue until the position is filled. The position could begin as early as August, 2017. Interested candidates should submit an electronic version of their CV along with a cover letter describing their qualifications and relevant experience to Andrew Kern (kern@biology.rutgers.edu)

Andrew Kern Associate Professor of Genetics Rutgers University website: http://kernlab.rutgers.edu email: kern@biology.rutgers.edu

Andrew Kern <Kern@dls.rutgers.edu>

SibFU Russia ForestGenomics 2

Call for a postdoc in genomics and bioinformatics!

09.07.2017

A postdoctoral position (for 1 year with potential extension for 2 more years) is available at the Siberian Federal University (SibFU) in the Laboratory of Forest Genomics in Krasnoyarsk (Russia) focusing on studying genomes of Siberian conifer species and their major phytopathogens.

Job description

- Teaching: lecturing in a Master's program "Genomics and Bioinformatics";

- Research: work on the main project of the laboratory ≪Genomics of the key boreal forest conifer species and their major phytopathogens in the Russian Federation≫ supervised by Prof. K.V. Krutovsky;

- Coaching and/or mentoring: Bachelor and Master Degree students.

Posdoc fellow positions requirements: * To qualify for the postdoc position, the applicant must have a PhD or similar degree in Biology, Computer Science, Mathematics, Informatics or Biophysics; * Experience with the NGS techniques: genome and transcriptome assembly and annotation, RNA-seq, phylogenetic analysis, candidates with strong skills in bioinformatics and computer programming are also considered; * Fluent English, at least B2 (ALTE); * At least 3 WoS / Scopus publications in the last 3 years (2014-2016).

Salary

The salary of the appointed researcher will be 120 000 RUR per month (equivalent of ˜2000 euro).

Official application deadline:

July 31, 2017

What we offer:

- The results obtained in our laboratory are unique, only a few laboratories in the world conduct research on the complete genomes of conifers, thus, there is a good opportunity to get original results and publish them in high-quality journals;

- There are two sequencing machines - Illumina HiSeq 2000 and MiSeq in our Laboratory, equipment for manipulating with nucleic acids, a cluster for high-performance computing, a server for processing genomic data with 3 TB of RAM;

- The master's program on Genomics and Bioinformatics was established in 2016 at the related department of the SibFU, where you can practice teaching and giving lectures;

- Comfortable and inexpensive housing in the residence hall at the SibFU campus;

- Reimbursement of travel expenses for relocation (one-way flight tickets).

Please, contact:

Putintseva Yuliya, Research Associate at the Laboratory of the SibFU Center for Genomic Research, tel.: +7 913 527 79 96, e-mail: yaputintseva@mail.ru

Natalia Oreshkova, Research Associate at the Laboratory of the SibFU Center for Genomic Research, tel.: +7 (391) 249-46-25, e-mail: oreshkova@ksc.krasn.ru

Anastasia Garmash, Manager of International Recruitment Office, tel.: +7 (391) 206-25-13, e-mail: agarmash@sfu-kras.ru for further information.

Application Procedure

The following documents must be attached to the application:

- Academic curriculum vitae in English;

- Passport copy;

- Copies of the academic degree and academic title;

- Statement of Intent to participate in the Postdoc Fellowship program;

- Motivation letter;

- The list of publications in international peer-reviewed journals;

- A brief description of research merits and action plan in English;

- Contact information of two persons whom may be asked to give a statement of the candidate;

- Consent to personal data processing.

To see more details and submit your application, please, click here.

Thank you.

Prof. Dr. Konstantin (Kostya) V. Krutovsky

Department of Forest Genetics and Forest Tree Breeding

Georg August University of Gottingen

Busgenweg 2, D-37077 Gottingen, Germany

E-mail: kkrutov@gwdg.de

http://www.uni-goettingen.de/en/414626.html http://essm.tamu.edu/people/faculty/adjunct-faculty/-krutovsky-konstantin http://genome.sfu-kras.ru/en/-krutovsky +49-(551)-393-35-37 (off.)

+49-(551)-39-83-67 (fax)

"Krutovsky, Konstantin" <konstantin.krutovsky@forst.uni-goettingen.de>

StellenboschU AvianEvolution

Post-doctoral Research Fellowship - The evolution of seabird detection to infrasound

A postdoctoral research position is available at Stellenbosch University (duration 3 years) to work on a collaborative project examining the evolution of aural structures in seabirds and their potential role in detecting infrasound (https://seabirdsound.wordpress.com/-about/)

This specific postdoctoral project will focus on exploring the mechanisms that may underlie seabird infrasound detection. The project will use advanced 3D imaging techniques to visualize and measure sensory organs in a variety of seabird species. The data will be examined within a phylogenetic framework and integrated with spatial modelling and geophysical components of a larger international collaborative project. Aural structural data will also be used to model theoretical frequency sensitivity of infrasound detection by seabird sensory organs.

The project and postdoctoral position is part of a larger project (funded by a Human Frontier Science Program grant) that brings together the fields of geophysics (hosted by Jelle Assink, Royal Netherlands Meteorological Institute, The Netherlands), behavioural ecology (Samantha Patrick, University of Liverpool, UK), physiology (Susana Clusella-Trullas, Stellenbosch University, South Africa) and spatial modeling (Mathieu Basille, University of Florida, USA).

The position will require a PhD in biological sciences, preferably comparative anatomy or physiology, or a related field (e.g. evolutionary physiology). The candidate should have experience and creative insights into microscopy methods (e.g. TEM/SEM, fluorescence microscopy, 3D imaging and analysis), a strong background in advanced statistics (e.g. multivariate analyses; geometric morphometrics) and a proven track-record for publishing research in high quality peer-reviewed literature. Desirable criteria include knowledge of and advanced programming in the R statistical environment.

The applicant will be based in the CL*I*M*E laboratory of Susana Clusella-Trullas (http://clusellatrullas.blogspot.co.za/), Department of Botany and Zoology at Stellenbosch University, South Africa, but must be able to work as part of a close collaborative team and be willing to spend short periods of time at all four institutions involved. The post is full time and fixed term for 36 months and candidates would start on 1st October 2017.

To apply

Applications should consist of an academic CV, cover letter and brief description (300 words) of three key published papers that show skills relevant to this post and particularly novel results. Applications and further enquiries should be directed to S. Clusella-Trullas (sct333@sun.ac.za).

Review of applications begins August 1st 2017 and will close as soon as a suitable candidate has been found.

Susana Clusella-Trullas Associate Professor - Physiological Ecology Department of Botany and Zoology & Centre for Invasion Biology Stellenbosch University Private Bag X1 - Stellenbosch 7602 South Africa Tel: +27 21 808 3974

http://clusellatrullas.blogspot.co.za/ https://scholar.google.co.za/citations?user=i0T9UOsAAAAJ&hl=en https://www.researchgate.net/profile/Susana_Clusella-Trullas "Clusella-Trullas, S, Prof <sct333@sun.ac.za>" <sct333@sun.ac.za>

TempleU ComputationalEvolutionaryGenomics

Position —— NIH-funded postdoctoral research positions in computational and evolutionary genomics are immediately available in the laboratory of Sergei Pond at the Institute for Evolutionary Genomics and Medicine at Temple University (iGEM, igem.temple.edu). We have a diverse portfolio of NIH-funded projects with the unifying theme of using statistical methods and scientific computing to power comparative analyses of sequence data. Examples of current projects include molecular epidemiology and transmission network inference of viral pathogens, computational immunomics, developing tools for high throughput analysis of viral genomic data, and general software and methodology development for quantifying sequence evolution (e.g., HyPhy and Datamonkey). —

Our team offers a vibrant work environment with excellent opportunities for collaborative efforts, independent accomplishments, and a robust work-life balance. Ideal candidates will have completed a PhD program with a strong background in one of the following (this list is not exhaustive): sequence analysis, genomics, bioinformatics algorithm development, big data analytics, statistical inference, viral pathogen evolution, or molecular epidemiology. We are looking for an invididual with a high level of enthusiasm, the ability to set goals and carve out independent research niches, and the desire to transition to an independent research career. NIH-funded positions are immediately available for a duration of 2-5 years. Positions offer a competitive salary and full fringe benefits.

To apply, please send a CV, a brief statement of research interests, and names and contact information of three individuals who can provide references to spond@temple.edu.—

Environment —— Key areas of focus for the newly established Institute for Evolutionary Genomics and Medicine at Temple University are the development and dissemination of computational tools that are essential for advancing modern biomedical research and enabling precision and personalized medicine. Teams in iGEM have pioneered and continue to maintain popular software tools and platforms, including MEGA (megasoftware.net), and HyPhy (www.hyphy.org), which jointly account for up to 40% of scientific citations worldwide in their field and have well over a hundred thousand users. Web services provided by iGEM (e.g., datamonkey.org) process tens of thousands of complex analysis requests monthly delivering free high-throughput computational facilities to researchers worldwide.

Compliance Statement —– In the performance of their functions as detailed in the position description employees have an obligation to avoid ethical, legal, financial and other conflicts of interest to ensure that their actions and outside activities do not conflict with their primary employment responsibilities at the institution. Employees are also expected to understand and be in compliance with applicable laws, University and employment policies and regulations, including NCAA regulations for areas and departments which their essential functions cause them to interact. To obtain additional information about Temple University please visit our website at www.temple.edu. Temple University's Annual Security and Fire Safety Report contains statistics, policies, and procedures related to campus safety and can be found at: http://www.temple.edu/safety/asfr/ .You may request a copy of the report by calling Temple University's Campus Safety Services at 215-204-7900.

"stephanie.spielman@temple.edu"
<stephanie.spielman@temple.edu>

TempleU ComputTheoEvolutionaryGenomics

The Schraiber Lab at Temple University is hiring postdocs! We embrace the full stack of computational genomics: pen and paper theory, statistical methods development, and application to data. An ideal candidate would be well versed in population genetics, statistics and/or programming, as well being independent and comfortable directing their own research. We are currently focused on the use of ancient DNA for understanding demography and natural selection. Empirically, we mainly study human evolution using publicly available datasets and animal domestication through collaborations with some of the best ancient DNA labs in the world. We are also interested in theoretical methods more broadly, particularly with a focus on linking evolution and functional genomics (e.g. gene expression, chromatin accessibility, DNA-protein interactions, etc.). We are embedded in the Center for Genetics and Genomics (CCGG) as well as the Institute for Genomics and Evolutionary Medicine (iGEM). Between iGEM and CCGG, a postdoc would be able to interact with a variety of people at the forefront of computational evolutionary genomics, including Sudhir Kumar, Jody Hey, Blair Hedges, Ananias Escalante, Masatoshi Nei, Sergei Pond, David Liberles, Rachel Spigler, Matt Helmus, Jocelyn Behm and Rob Kulathinal. CCGG offers training opportunities for postdocs interested in careers in both academia and industry. Temple University is also well situated in the Northeast United States, which is currently a hotbed of evolutionary genetics research, making it an ideal location for a postdoc to forge connections and collaborations. Interested applicants should send a CV and a brief (i.e. one paragraph) statement of interest to Joshua Schraiber (joshua.schraiber@temple.edu).

"tug85527@temple.edu" <tug85527@temple.edu>

UArizona ProteinEvolutionBioinformatics

Postdoc position: long-term trends in protein evolution

A postdoc position is available with PI Joanna Masel (http://eebweb.arizona.edu/faculty/masel) at the University of Arizona in Tucson. A popular tourist destination surrounded on all four sides by mountainous national and state parks, Tucson is a vibrant city of nearly a million people with an attractive climate. The EEB department was ranked in the top 10 by US News & World Report.

We recently found that genes of different ages encode proteins with different computationally predictable structural properties, forming an extraordinarily long-term trend. This project will use bioinformatics techniques to discover whether these long-term trends are really a consequence of evolution by descent with modification that continues for long periods of time in a consistent direction. More details of the project, including preprints of preliminary findings, are available upon request.

Techniques used may include phylostratigraphy (assigning ages to gene families), ancestral sequence reconstruction, and porting macroevolutionary techniques for studying speciation and extinction to the study of gene duplication and loss. A high level of statistical sophistication is required throughout.

Excellent computer programming skills are strongly preferred, ideally with bioinformatics / genomics and statistics experience. Exceptionally strong candidates who come from a more experimental background within evolutionary biology, and who now wish to retrain as bioinformaticians, will also be considered. A background in evolutionary biology is also strongly preferred, although again, exceptionally strong computational scientists from highly quantitative backgrounds outside evolutionary biology will also be considered. Statistical knowledge, and knowledge about protein structure and folding, are advantages. Start date is negotiable, and the position is renewable, with funding secured through July 2020.

Contact Joanna Masel at masel@u.arizona.edu for more information and to apply.

masel@email.arizona.edu

UBath BacterialEvolution

Postdoc - SF5014 Research Associate (Fixed Term), Bath - UK

Biology & Biochemistry Salary: Starting from 32,004, rising to 38,183 Placed On: Thursday 29 June 2017 Closing Date: Thursday 13 July 2017 Interview Date: To be confirmed Reference: SF5014 A NERC-funded postdoctoral research associate position is available for a highly motivated research scientist to analyses a wide range of genomic data related to population structure and evolution of pathogenic bacteria.

The successful candidate is expected to have a PhD degree in a relevant area of biology (microbiology, genetics or bioinformatics), a good publication record and strong interest in microbial genomics and evolution. Applicants must be familiar with Unix environments, proficient in scripting languages, and with experience in high throughput sequence analysis of microbial genomes and metagenomics data.

The position is offered on a full-time, fixed-term (up to 7 months) basis in the laboratory of Dr Jaime Martinez-Urtaza at the Milner Center for Evolution, Department of Biology and Biochemistry, University of Bath. Informal enquires are welcome and should be directed to Dr Jaime Martinez-Urtaza (J.L.Martinez-Urtaza@bath.ac.uk).

Key Responsibilities include:

-Manage and analyse large-scale whole-genome sequencing datasets

-Perform analysis on datasets generated by next generation sequencing platforms

-Integrate sequence data with environmental/epidemiological data

-Liaise with collaborators and coordinate projects

-Train group members

-Develop new methods to analyse sequence data

Essential Skills:

-PhD in microbiology, population genetics, molecular evolution, computer science, or bioinformatics

-Experience working with next generation sequence data and/or large datasets

-Ability to program in either Perl or Python

-Experience with bacterial genomics, genome annotation, phylogeny and metagenomics

-Outstanding personal initiative and communication skills

-Strong publication record in peer-reviewed journals

-A desire to learn, to innovate and to move out of their comfort zone

The following recent publication has direct relevance to this project:

Martinez-Urtaza et al. 2016. Is El Niño a long-distance corridor for waterborne disease? Nat Microbiology. 1, 16018.

The University of Bath and our Department are committed to equality of opportunity. We particularly encourage applications from under-represented groups, including women.

More info: https://www.bath.ac.uk/jobs/-Vacancy.aspx?ref=SF5014 Contact:

Dr Jaime Martinez-Urtaza Reader in Infection and Immunology The Milner Centre for Evolution Department of Biology and Biochemistry University of Bath Bath BA2 7AY United Kingdom

J.L.Martinez-Urtaza@bath.ac.uk +44 (0)1225 384292

Ronnie Gavilan <ronniegavilan@gmail.com>

UCalifornia Berkeley ComputationalGenomics

Postdoctoral Scholar at Nielsen Group, UC Berkeley

The University of California's Conservation Genomics Consortium is a cross-campus effort to leverage recent developments in genomics for conservation efforts in California. The Consortium has launched the CALeDNA project (http://www.ucedna.com), aimed at collecting and analyzing environmental DNA in California. To fully take advantage of the data generated by the project, new computational methods are needed for analyzing Next Generation Sequencing (NGS) data in the context of taxonomic assignment and ecological modeling. This Postdoc position will work on developing and applying new computational and statistical methods for species assignment, new methods for analyzing biases associated with sequencing technologies and PCR, and new methods for testing ecological hypotheses using large geospatial DNA data.

See aprecruit.berkeley.edu/apply/JPF01425 for more information.

"rasmus_nielsen@berkeley.edu"
<rasmus_nielsen@berkeley.edu>

UCalifornia Davis VirusEvolution

The Diaz-Munoz Lab at the University of California, Davis is looking for a PHAGE WIZARD or FLU WIZARD (POSTDOCTORAL SCHOLARS). The Diaz-Munoz Lab studies the social lives of viruses, with a current focus on coinfection and reassortment in segmented viruses (cystoviruses and influenza viruses). We have an evolutionary perspective and take an integrative approach to the study of virus-virus interactions using tools from genomics, environmental microbiology, classical virology, genetics, and ecology.

The successful candidate will be passionate about the study of viruses, evolution, or microbiology and possess experience working with bacteriophages or eukaryotic viruses as demonstrated by scientific papers. While the position may entail working on specific projects, creative contributions to the ongoing project are expected. Wizards are encouraged to lead original projects within the lab's focus to develop their own careers. Strong preference will be given to candidates skilled in techniques distinct and complementary to those currently in the lab (e.g. single cell, cloning or genetic engineering, RNA and protein detection, microscopy experience). Excellent interpersonal and communication skills are essential, as the lab is a diverse team in terms of scientific and personal backgrounds.

Required Qualifications: -Ph.D. in virology, microbiology, molecular-cell biology, immunology, genomics, evolutionary biology, or related fields -Less than 5 years post-Ph.D. experience (see project scientist ad if >5 yrs post-PhD) -Experience with cell culture, eukaryotic virus culture, and standard virology techniques OR Experience with bacterial and bacteriophage culturing and standard microbiology techniques

UC Davis is a leading research institution with over $750 million dollars in research funding and top-tier faculty. The campus is a diverse, supportive community with UC Davis named top college for women in STEM (Forbes), first in the world for campus sustainability (GreenMetric), and a top college for economic diversity and upward mobility (NY Times).

The City of Davis is a vibrant, livable, family-friendly community. It was ranked best small town for cycling (Bicycling Magazine) and hosts one of the best farmer's markets in the nation (American Farmland Trust). Davis has a privileged position between Sacramento, Napa Valley, and the Sierra Foothills with the San Francisco Bay Area and Lake Tahoe just a drive away.

Interested candidates should submit the following materials as a single PDF to Dr. Sam Díaz-Muñoz samdiazmunoz@ucdavis.edu.

1. A cover letter briefly describing: why you are interested in working in the lab, relevant experience, research interests, and a list of contact information for three references 2. Curriculum Vitae 3. 1-2 relevant publications (can be links if open access) 4. (Optional) One page Statement of Contributions to Diversity.

Apply by August 1, 2017 for full consideration. Applications will be reviewed until the position is filled. People from underrepresented and underserved communities are especially encouraged to apply (for Realz).

Samuel L. Díaz Muñoz, Ph.D. Assistant Professor, Department of Microbiology and Molecular Genetics Faculty Scholar, Center for the Advancement of Multicultural Perspectives on Science (CAMPOS) University of California, Davis samdiazmunoz@ucdavis.edu http://-

sociovirology.org samdiazmunoz@ucdavis.edu

UCalifornia LosAngeles StatisticalGenomics

Postdoctoral fellow at UCLA in statistical and computational genomics

We are looking for a highly-motivated postdoctoral fellow to work with Prof. Sriram Sankararaman in the Departments of Computer Science and Human Genetics at UCLA. We have broad research interests: ranging from statistical inference and machine learning algorithms and application of these tools to problems in medical and population genomics. We develop statistical model and machine learning algorithms to understand evolutionary processes as well as genetics of complex traits and in applying these methods to large-scale datasets to answer biological questions.

An ideal candidate will have strong background in statistics and computation, programming skills, and population genetics with an ability to perform independent research. Potential projects include, but are not limited to: 1. Computational methods to study admixture at diverse time-scales and its impact on phenotype. 2. Methods for analyzing genomic time series. 3. Inferring demographic history from genome sequences. 4. Methods for genetic analysis of complex traits. 5. Algorithmic and inferential challenges that arise in these problems.

Our lab is tightly integrated with a vibrant research community in bioinformatics, population and medical genetics at UCLA. We collaborate closely with many other labs in computer science (Eskin, Halperin), human genetics (Pasaniuc, Freimer, Flint, Sul) and population genetics (Lohmueller). Further, we are part of the Institute for Quantitative and Computational Biosciences at UCLA (https://qcb.ucla.edu).

Candidates must hold a Ph.D. in computer science, statistics, bioinformatics, biostatistics, computational biology, or a related quantitative field and have a strong publication record. The position is available for 1 year and may be continued for an additional year contingent on successful progress and available funding. The expected start date is fall 2017 but is flexible.

Interested candidates should email Sriram Sankararaman (sriram@cs.ucla.edu) with their CVs, research statements and names of references.

Sriram Sankararaman <sriram@cs.ucla.edu>

UCambridge 2 Evolutionary Theory

Two post-doctoral research associate positions in the Department of Zoologe are available to work with Professor Rufus Johnstone on mathematical and computational modelling of the evolution of inheritance and life history.

—

Position 1, Evolution and inclusive inheritance

Available from 8 August 2017 for up to 31 May 2019.

The position is part of the world's largest project to expand our understanding of evolution. The Extended Evolutionary Synthesis project, involving a multi-national, interdisciplinary consortium of 51 world-renowned experts, with funding from the John Templeton Foundation, aims to explore new ways to think about and understand evolutionary phenomena.

The PDRA will work on modeling three mechanisms of inclusive inheritance: (i) social transmission (exploring how social learning and teaching changes across the life-cycle), (ii) epigenetic inheritance (investigating how maternal investment and resource transmission impacts on subsequent health and development), and (iii) ecological inheritance (considering how environmental modulation and niche construction generate group differences in behaviour). There is, however, scope for the focus of the modelling to reflect the interests of the candidate.

Duties will include developing models, using a combination of game theoretical and adaptive dynamic techniques, possibly supplemented by individual-based simulations, and analysing and writing up the results.

Further info: http://www.jobs.cam.ac.uk/job/14268/

—

Position 2, Life history evolution

A post-doctoral research associate position in Department of Zoology, located in Central Cambridge on Downing Street, is available from 7 August 2017 or as soon as possible thereafter for up to eighteen months, to work with Professor Rufus Johnstone on mathematical and computational modelling of life history evolution in banded mongooses.

The PDRA will work on integrating trans-generational costs of reproduction into models of life history evolution, and exploring the strategies that breeders may adopt to ameliorate these costs. We are interested in i) the circumstances under which selection favours parents that incur costs themselves in of trans-generational damage on their offspring, ii) how this trade-off modulates investment in other life history traits, and iii) how investment in shielding of young, and consequently offspring quality and subsequent life history, may be expected to change with parental age. There is, however, scope for the focus of the modelling to reflect the interests of the candidate.

This work will be carried out as part of a NERC-funded project, in collaboration with Dr Jon Blount and Prof Michael Cant at the University of Exeter, who will be collecting data on trans-generational costs of reproduction in wild banded mongooses, which will be used to inform development of the models and to test their predictions.

Further info: http://www.jobs.cam.ac.uk/job/14199/

—

Informal enquiries can be directed to Rufus Johnstone, raj1003@cam.ac.uk.

"A.L.W.Kuijper@exeter.ac.uk"
<A.L.W.Kuijper@exeter.ac.uk>

UCork Ireland EvolutionaryGenomics

We are looking for an ambitious and competent senior post-doctoral fellow to work on dissecting the genomic basis of anadromy and migration-related traits in brown trout. The post-doc will interact with an international team (funded by an ERC Starting Grant to T Reed) involving ecologists, physiologists, population and quantitative geneticists, and modellers. S/he will be responsible for the generation and analysis of genomic data (e.g. RAD-seq) and RNA data (e.g. RNA-seq) and is expected to have excellent English and bio-informatics skills (proven experience with interpretation of output from recent novel statistical approaches and software programs). The primary role of the post-doc will be analysis of next-gen sequencing data and association/QTL mapping, but there is scope also for a range of additional population genomic and quantitative genetic sub-projects, under the common umbrella of understanding the evolution and genetic architecture of flexible migration strategies in fish.

Candidates should have a strong publication portfolio in molecular ecology/evolutionary type journals. A background in evolutionary biology, ecology, or conservation/wildlife/fisheries biology would be preferable, although applicants from other backgrounds (e.g. human genetics, microbiology, agriculture) will be considered. Molecular lab experience a plus, but not a must.

The fellow will work at the University of Cork, one of Ireland's largest and most successful universities. The research would be conducted in the School of BEES which consists of 21 faculty (including 3 holders of current ERC grants), ca. 20 postdocs and 50 PhD students across Zoology, Ecology, Plant Sciences and Geology. Cork is situated on the south coast of Ireland, 2.5 hours from Dublin, is served by an international airport, has a population of about 200,000, and is on the doorstep of some of the most beautiful coastline in Europe.

The project will involve collaborations with colleagues from the Marine Institute of Ireland and Queens University Belfast, and we also collaborate widely with groups from across Europe and the US.

Applicants should send their CV, a letter of intent describing the candidate's motivation, qualifications, skills, and experience relevant to this position, and contact information for three references to treed@ucc.ie, before Sept 9th 2017. Expected start date somewhere between October and December 2017. Post is for 2 years, with possibility of 1.5 year extension thereafter.

For more info on our research, see here: http://fisheye.ucc.ie/ Tom Reed <treed@ucc.ie>

"Reed, Thomas" <treed@ucc.ie>

UEastAnglia EvolutionaryGenomics

Postdoc position in Evolutionary Genomics

The research group of Simone Immler at the School of Biological Sciences, University of East Anglia is looking for a postdoctoral researcher to fill a position in bioinformatics and population genomics. The project is funded by a Starting Grant from the European Research Council (ERC).

The successful candidate will be an integral member of the team with responsibility to develop and test theoretical and analytical frameworks and perform bioinformatics analyses on existing NGS datasets from experimental projects in the zebrafish. The candidate will develop analytic and simulation tools implementing these frameworks using scripted and/or compiled languages, and will have the opportunity to work closely with collaborators and bioinformaticians when developing frameworks and tools. The candidate will also work with other team members to interpret related datasets from a variety of sources. There will be ample opportunity for the candidate to pursue their own research questions related to the larger team goals.

The School of Biological Sciences benefits from close interactions with other Schools within UEA, including the Schools of Chemistry and Pharmacy and the Norwich Medical School. UEA is also part of the Norwich Research Park that includes the Norfolk and Norwich University Hospital, the Institute of Food Research, the John Innes Centre and the Earlham Insitute.

More information about the School of Biological Sciences UEA can be found at:

http://www.uea.ac.uk/bio/ Qualification requirements * PhD in Evolutionary Genomics, Bioinformatics, or Population Genetics * Research experience with genomic experimentation * Research experience with developing and applying bioinformatics analyses * Research experience with developing analytic concepts for NGS datasets * Demonstrable experience with tool development in Perl or Python * Demonstrable communication skills in English language * Excellent report writing and presentation skills. * Good time management and organisational skills. * Good interpersonal skills.

Desirable additional skills * Research experience with population genetics theory * Research experience with NGS datasets

* Statistical analysis with R * Programming in C or C++

For informal enquiries please contact PI Simone Immler (s.immler@uea.ac.uk) and check out our webpage (http://www.ieg.uu.se/evolutionary-biology/immler/)

The application deadline is currently set for 10th of August 2017 or until filled. To apply for the position please use the following link:

https://myview.uea.ac.uk/webrecruitment/pages/vacancy.jsf?vacancyRef=RA 1423

Simone Immler <S.Immler@uea.ac.uk>

UExeter 2 MicrobialEvolution

Two (theoretical and experimental) postdoctoral positions, Microbial Ecology and Evolution, University of Exeter

We are recruiting two Research Fellows to participate in an interdisciplinary project combining experimental microbial ecology/evolution (position 1) and mathematical modelling (position 2). Both positions are available from 1st October 2017 for the period of 3 years. Our research will consider laboratory communities of devastating human fungal pathogens that kill more people than tuberculosis, malaria or breast cancer, focusing on Candida species. We will quantify how microbial community composition is determined by the metabolism, genetics and physiology of individual players, establishing principles by which microbial composition affects antimicrobial resistance.

The successful applicants will be working in the lab of Professor Ivana Gudelj, Biosciences, University of Exeter.

Position 1 (empirical): Applicants will possess a PhD in a related field of study and ideally have a mix of skills including evolutionary biology, microbiology and molecular biology laboratory techniques, experimental design and statistics, and analysis of next generation sequence data.

Position 2 (theoretical): Applicants will posses a PhD in a quantitative discipline (mathematics, physics, engineering or computer science) and ideally be familiar with ordinary differential equations, their use in modelling, analysis (Dynamical Systems techniques) and simulation.

More information about the project and how to apply can be found at:

Position 1: https://jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/run/ETREC107GF.open?VACANCY_ID=385921JBQC&WVID=3817591jNg&LANG=USA Position 2: https://jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/run/ETREC107GF.open?VACANCY_ID=730355JBQC&WVID=3817591jNg&LANG=USA Closing date is 20th August 2017

“Gudelj, Ivana” <I.Gudelj@exeter.ac.uk>

UFlorida QuantitativeMovementEvolution

We are seeking a postdoctoral researcher highly trained in quantitative movement ecology (statistical and mechanistic models) to fulfill a position of Postdoctoral Associate at the University of Florida's Fort Lauderdale Research and Education Center in Davie, Fl. The candidate will work in a large international project funded by the Human Frontier Science Program, investigating the use of infrasound by seabird. The candidate will be in charge of developing a comprehensive movement ecology framework to investigate movement of seabirds in relationship to the infrasoundscape on the open sea using a hierarchy of environmental cues at multiple nested scales. Lead PI is Dr. Samantha Patrick, from the Seabird Ecology Group (University of Liverpool, UK); co-PIs are Dr. Susana Clusella-Trullas (Stellenbosch University, South Africa), Dr. Jelle Assink (Royal Netherlands Meteorological Institute, the Netherlands) and Dr. Mathieu Basille (University of Florida, USA). See below for the general project summary. The candidate will be located at the University of Florida's Fort Lauderdale Research and Education Center in Davie, Fl, under the supervision of Dr. Basille. The project covers 3 years of postdoctoral research in each institution, and all postdoctoral researchers will tightly work together, including several extended stays at collaborators' institutions.

The postdoctoral researcher will be primarily in charge of developing statistical and mechanistic models to investigate movement of seabirds in relationship to the infrasoundscape. The postdoctoral researcher will also be largely involved in hiring and supervising a Master's student for this project, as well as training lab members (including graduate students) in state-of-the art techniques in movement ecology.

Preferred Qualifications: A PhD is required as well as strong mathematical and programming skills. Advanced knowledge of R and SQL (PostGIS) is expected. Experience in Movement Ecology is highly desirable. Strong publication record in peer-reviewed journals in Quantitative Ecology or Biostatistics is highly desirable. Previous experience with Linux systems preferred.

To apply: Please follow the instructions at UF Career http://explore.jobs.ufl.edu/ (job number 502790)

General project summary:

Seabirds have the longest migrations on earth and can travel 8 million km in a lifetime, yet how they navigate across a seemingly featureless ocean is still one of the greatest puzzles in nature. Evidence from mammalian and insect systems shows that animals adjust their behavior in response to infrasound and a handful of studies have suggested pigeons may use infrasound for navigation. These low frequency sound waves can propagate over hundreds of kilometers, creating "hills" and "valleys" of an infrasoundscape that birds may use to navigate, like a topological map. When combined with meteorological and oceanographic models, these maps can be modeled to create real time soundscapes that individual seabirds could use in movement decisions over spatial scales. By combining a network of 60 international atmospheric infrasound and hydro-acoustic monitoring stations that detect signals from around the globe with a database of over 15,000 seabird movement tracks, we will have a unique opportunity to explore the role of atmospheric and oceanic infrasound in navigation, respectively for aerial and aquatic species. The mechanisms allowing animals to detect low frequency sound has been identified in other taxa, and our study will examine how seabird sensory organs may capture infrasound. The development of an innovative movement framework grounded in landscape ecology will allow us to assess determinants of large-scale movement, notably the effect of infrasound in directing migration and commuting trips in the open ocean. Furthermore, novel biologging devices, which can detect sound and meteorological parameters, will be used to simultaneously capture movement, infrasound and weather conditions to examine individual movement decisions at fine scale. Finally, interspecific comparisons will assess the relative importance of infrasound for seabird navigation, with respect to phenotypical and phylogenetic differences, thus offering a complete assessment of the physiology, behavior and physics underpinning the use of infrasound in navigation.

–

Mathieu Basille

basille@ufl.edu | http://ase-research.org/basille +1 954-577-6314 | University of Florida FLREC

≪ Le tout est de tout dire, et je manque de mots Et je manque de temps, et je manque d'audace. ≫ - Paul ÃÂluard

This message is signed to guarantee its authenticity. For a true private correspondence, use my public key to encrypt your messages:

http://mathieu.basille.net/pub.asc

— / —

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

UGothenburg TreeOfLife

A 2-year post-doc position is now available at the University of Gothenburg, Sweden, on building the tree of life from molecular sequences using the tree-building platform SUPERSMART (http://www.supersmart-project.org/). If you have a strong background in computational biology, molecular phylogenetics, bioinformatics, computer science, or related field, and you are interested in a new challenge, then welcome to apply by August 20th.

For more information on the position and how to apply please visit: http://www.gu.se/english/about_the_university/job-opportunities/vacancies-details/?id=1015 Best wishes

Alex

Alexandre Antonelli, PhD Professor in Systematics and Biodiversity Director, Gothenburg Global Biodiversity Centre < http://www.ggbc.gu.se > Wallenberg Academy Fellow < https://www.wallenberg.com/kaw/en/research/history-can-tell-us-how-sensitive-species-are-climate-change > | Future Research Leader < https://www.euraxess.se/jobs/funding/ssf-individual-grants-future-research-leaders > Young Academy of Sweden < http://www.sverigesungaakademi.se/ > | Royal Society of Arts and Sciences < http://www.kvvs.se/ > co-PI, Biodiversity and Ecosystem services in a Changing Climate < http://www.becc.lu.se/ > Scientific Curator, Gothenburg Botanical Garden < http://www.botaniska.se/ > Science advisor, Universeum Science Centre < https://www.universeum.se > Chairman and co-Founder, BioNote < http://bionote.xyz/ >

Delivery address: Gothenburg Global Biodiversity Centre Box 461, SE-405 30 Göteborg, Sweden Visiting address: University of Gothenburg < http://www.gu.se > Dept of Biological and Environmental Sciences < http://www.bioenv.gu.se > Carl Skottsbergs gata 22B, Göteborg, Sweden

Lab homepage < http://antonelli-lab.net/ > | Twitter < https://twitter.com/antonelli_lab > | Google scholar < https://scholar.google.se/citations?user=KYbhJxMAAAAJ&hl=en > | Facebook < https://www.facebook.com/alexandre.antonelli.7 > E-mail: alexandre.antonelli@bioenv.gu.se Phone: + 46 (0) 703 989570

Alexandre Antonelli <alexandre.antonelli@bioenv.gu.se>

UHelsinki ModellingPhenotypicEvolution

Post-doc in mathematical modelling on phenotypic evolution and embryonic development:

1.Job/project description:

The postdoc could choose between three main research projects:

a. Mathematical modeling of phenotypic evolution in populations with embryonic development.

b. Mathematical modeling of gene network and embryonic development evolution.

c. Mathematical modeling of organ development and their evolution in mammalian teeth or Drosophila wing.

The actual project will be chosen together with the candidate depending on his/her interests and skills.

The research will take place in the Isaac Salazar-Ciudad's group in the Center of Excellence in Experimental and computational developmental biology of the Biotechnology Institute of the University of Helsinki.

The job is for 1 year and renewable for 1 extra year.

2. Background:

The process of embryonic development is now widely acknowledged to be crucial to understand evolution since any change in the phenotype in evolution (e.g. morphology) is first a change in the developmental process by which this phenotype is produced. Over the years we have come to learn that there is a set of developmental rules that determine which phenotypic variation can possibly arise in populations due to genetic mutation (the so called genotype-phenotype map). Since natural selection can act only on existing phenotypic variation, these rules of development have an effect on the direction of evolutionary change.

Salazar-Ciudad's group is devoted to understand these developmental rules and how these can help to better understand the direction of evolutionary change. The ultimate goal is to modify evolutionary theory by considering not only natural selection in populations but also developmental biology in populations. For that aim we combine mathematical models of embryonic development that relate genetic variation to morphological variation with population models. The former models are based on what is currently known in developmental biology.

Salazar-Ciudad's group is in close collaboration with Jukka Jernvall's group and other groups within the center of excellence in experimental and computational developmental biology. The center includes groups working in tooth, wing, hair and mammary glands development. In addition to evolutionary and developmental biologists the center of excellence includes bioinformaticians, populational and quantitative geneticists, systems biologists and paleontologists.

"The Academy of Finland's Centres of Excellence are the flagships of Finnish research. They are close to or at the very cutting edge of science in their fields, carving out new avenues for research, developing creative research environments and training new talented researchers for the Finnish research system."

3. Requirements:

The applicant must hold a PhD in either evolutionary biology, developmental biology or, preferably, in evolutionary developmental biology (evo-devo). Applicants with a PhD in theoretical or mathematical biology are also welcome.

Programming skills or a willingness to acquire them is required.

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

4. Description of the position:

The fellowship will be for a period of up to 1+1 years (100% research work: no teaching involved).

Salary according to Finnish postdoc salaries.

5. The application must include:

-Motivation letter including a statement of interests

-CV (summarizing degrees obtained, subjects included in degree and grades, average grade).

-Summary of PhD project, its main conclusions and its underlying motivation.

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

isaac.salazar@helsinki.fi

No official documents are required for the application first stage but these may be required latter on.

6. Deadline:

There is no specific deadline, the position will be filled as soon as a suitable candidate is found.

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

Brun-Usan M, Marín-Riera M, Grande C, Truchado-Garcia M, Salazar-Ciudad I. A set of simple cell processes is sufficient to model spiral cleavage. Development. 2017 Jan 1;144(1):54-62.

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

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

8. Interested candidates should check our group webpage:

http://www.biocenter.helsinki.fi/salazar/index.html
The center of Excellence webpage:

http://www.biocenter.helsinki.fi/bi/-evodevo/ECDev.html "Salazar, Isaac" <isaac.salazar@helsinki.fi>

UHohenheimStuttgart CropPopulationQuantGenomics

The research group 'Crop Biodiversity and Breeding Informatics' invites applications for the position of a

Research Associate in Crop Plant Population and Quantitative Genomics (3 + 3 years)

We offer a position for a research associate to develop quantitative approaches for the characterization and utilization of plant genetic resources in (pre-)breeding programs of field crops. Our group works with landraces and wild relatives of major (barley, maize) and minor crops (quinoa and amarant) to characterize their evolution and to identify useful variation for breeding (http://evoplant.uni-hohenheim.de). Possible topics are the integration of population and quantitative genomics methods in plant genetic resource utilization (e.g., via genomic selection), or the exploration of evolutionary concepts like genomic conflicts or host-pathogen coevolution in the context of plant breeding (e.g.,—https:/-

/dfg-spp1819.uni-hohenheim.de/en/117512). We have access to a high performance computing infrastructure, a lab for molecular work and excellent facilities for field trials.

We seek a creative, motivated and mature scientist with a track record of scientific publications in either population, quantitative or evolutionary genetics, plant breeding or bioinformatics. Experience in large-scale data analysis of omics data (with e.g. R or Python), communication and team skills are required. An interest in method development, genomics tools and/or plant research is highly advantageous. The position offers the possibility to develop an independent research program. We therefore expect that applicants are willing to attract independent funding from national and international sources and to advise student projects.

The successful applicant will be initially appointed for three years with the possibility of extension for another three years. The starting date can be as early as 1 October 2017. Salary will be according to the German government salary scale (TV-L E13 or A13 Akademischer Rat auf Zeit) and depends on previous experience, age and marital status. The position involves 4 hours of teaching per week during the semester (entirely in English), which includes lecturing, student supervision and course administration in the agricultural sciences and crop science study programs. Programs for career training and teaching at universities ("Baden-Württemberg Zertifikat für Hochschuldidaktik") are available and an academic qualification via Habilitation is possible.

The University of Hohenheim is located on a beautiful campus in the city of Stuttgart, South Germany, which has a high quality of life. We participate in national and international networks of academic research and plant breeding (public and private). Examples are the Hohenheim Competence Unit of Plant Breeding, the Tübingen-Hohenheim Regional Research Alliance: Yield stability in dynamic environments (http://regio-alliance.uni-hohenheim.de/en/1670), or the DFG-funded Priority Program SPP1819 "Rapid Evolutionary Adaptation" (https://dfg-spp1819.uni-hohenheim.de). A university-wide co-working environment for research groups in the area of big data and digitization is currently set up to facilitate collaboration.—The University of Hohenheim is an equal opportunity employer; female researchers are strongly encouraged to apply.

Informal inquiries about the position can be using the contact information below. Formal applications that include a CV, a statement of motivation and the contact information of at least two references should be uploaded as single PDF document at this link: http://-evoplant.uni-hohenheim.de/jobs . Application deadline: 7 September 2017

Contact: Dr. Karl Schmid Professor of Crop Biodiversity and Breeding Informatics Institute of Plant Breeding, Seed Science and Population Genetics (350) University of Hohenheim Fruwirthstrasse 21, D-70599 Stuttgart Tel: +49 711 459-23487 Email: karl.schmid@uni-hohenheim.de Web: evoplant.uni-hohenheim.de

Karl Schmid <karl@minzer-schmid.de>

UIceland LichenPopulationGenomics

The Institute of Life and Environmental Sciences at the School of Engineering and Natural Sciences at the University of Iceland, seeks applicants to fill a full Post Doc position in the research domain of Biology, with emphasis on population genomics and gene expression in lichens.

Field of work The candidate will work on population genomics and gene expression of Peltigera lichens. The project will be carried out with the research groups of professor Ãlafur S. Andrésson and Silke Werth (University of Graz). The project is funded for two years by the Icelandic Research Fund and is entitled Impact of genome and long-term acclimatization on gene expression and phenotypic traits of lichen symbioses. The candidate will work on population genomics and gene expression of Peltigera lichens. The following skills are essential for the task: Excellent analytical skills with respect to population genetic analyses, familiarity with lichen biology, physical ability and experience to perform field work, and excellent manuscript writing skills. Basic knowledge of Linux programming/scripting is an advantage.

Qualification requirements Applicants should have a doctorate in the field of population biology and genetics or comparable. A solid background in population genetics, terrestrial ecology, analytical methods and statistics, together with field and laboratory experience, is required.

How to apply The successful applicant is expected to start the appointment as early as possible.

The following papers are needed. Please send them in one pdf file: - A letter of motivation - Certificates attesting to education (PhD or equivalent) - List of publications - CV - Contact information for 3 references

All applications will be acknowledged and applicants will be informed of the appointment when a decision has been taken.

The salary for the position will be in accordance with the current collective wage and salary agreement between the Union of University Teachers of Iceland and the Minister of Finance.

Appointments to positions at the University of Iceland are made in consideration of the Equal Rights Policy of the University of Iceland.

At the School of Engineering and Natural Sciences, 360 people are employed in research and teaching. The School offers an international environment, with the number of international employees and students increasing each year. Currently 25% of all employees and postgraduate students are international. There are around 2300 students at the School, divided into six faculties, thereof are 350 graduate students and 150 doctoral students. Research institutes at the school are the Science Institute that divides into the Institute of Earth Sciences and Institute of Physical Sciences, Institute of Life and Environmental Sciences, Engineering Research Institute and the Institute for Sustainability Studies which is an interdisciplinary institute and belongs to the five schools of the University of Iceland.

The University of Iceland is the largest teaching, research and science institute in Iceland and is ranked among the top 250 universities in the world by Times Higher Education.

Information on the University of Iceland and Relocation Service is found here: http://english.hi.is/-university/international_office . *Further information* For further information contact Prof. Ãlafur S. Andrésson, tel (+354) 525 4627, osa@hi.is or Silke Werth, silke.werth@uni-graz.at

Deadline The application deadline is through the 30th July, 2017

Please apply through the University of Iceland website: https://ugla.hi.is/radningar/index.php?sid=2448&starf=225 "Werth, Silke (silke.werth@uni-graz.at)" <silke.werth@uni-graz.at>

UIllinois EvolutionarySystemsBiologySymbiosis

A postdoctoral position is available in the department of Plant Biology, in the School of Integrative Biology, at the University of Illinois in Urbana-Champaign. PIs Heath (plant-microbe coevolution), and Marshall- Colon (plant systems biology) are looking for a highly motivated postdoc to work on a NSF-funded project aimed at understanding the molecular underpinnings of highly efficient nitrogen-fixing symbioses between legume (Medicago truncatula) and rhizobia. This project takes a systems genetics approach to integrate information from the bacterial genome with gene expression and metabolite data to build "symbiosis networks." Network comparisons will identify key factors underlying high-quality partnerships for plants. Postdocs will work closely with both Heath and Marshall-Colon to receive cross-disciplinary training in metabolomics, transcriptomics, genomics, network modeling and evolution.

The duties of the project postdoc will include some laboratory work but will focus more on computational biology including bioinformatic and statistical analyses, developing new network modeling approaches, and writing manuscripts.

Expertise in some or all of the following areas is desired: Bioinformatics, Statistical modeling, Genomics, Metabolomics, Trait Mapping, Evolution.

Strong candidates will also possess the following attributes:

- A strong publication record from their PhD (papers published, in press, or submitted).

- Creativity, independence, and the desire to learn new things.

- Excellent communication skills, both written and oral.

All candidates must have received a Ph.D. in a relevant field. The position is available for 2 years, with the first year as a probationary period, and will include a competitive salary and full benefits. Application review will begin September 1, 2017 and will continue until the position is filled. Start date is flexible, but ideally January 2018. All materials should be submitted to the PIs below for consideration. Applications should include a brief cover letter, curriculum vitae, and the names and contact information for three references. Please put "postdoc application" in the subject line of your email!

Champaign-Urbana is a great college town midway between three major cities (Chicago, St. Louis, Indianapolis), with great food and drink, abundant culture, and affordable cost of living. University of Illinois and our labs are committed to a diverse workplace, and prospective postdocs of all races, genders, and sexual orientations are encouraged to apply.

Contact either PI regarding the position or application process. For further information about the Marshall-Colon and Heath labs, or the Plant Biology department at the University of Illinois, visit the faculty page at: http://www.life.illinois.edu/plantbio/faculty.htm Amy Marshall-Colon and Katy Heath

Department of Plant Biology

University of Illinois

amymc@illinois.edu

kheath@illinois.edu

UKansas PopulationModelling

Dr Daniel Reuman is recruiting into his lab in the University of Kansas Department of Ecology and Evolutionary Biology (EEB). At least 3 years of funding are available to carry out modelling pertaining to spatial population dynamics and analysis of large spatial population data sets. The postdoc will join an interdisciplinary team consisting of Reuman, three postdocs and one student currently in the Reuman lab, collaborators in EEB and in the Math Department at KU, and collaborators at several institutions in the USA and UK. Funding is from the NSF Mathematical Biology program and the James S McDonnell Foundation.

In many hierarchical dynamical systems, "synchrony" between multiple fluctuating variables, i.e. correlations or other similarities in fluctuations between variables through time, is more important than the individual variables themselves. For instance, a neuron may fire only when its input neurons fire synchronously. Or the electrical grid may crash only when demands of multiple users become synchronized, producing total-usage spikes. Ecosystems can show this type of dependency on synchrony. Ecosystems include multiple trophic levels, with population signals from lower levels often being spatially aggregated to affect higher levels. For instance, a predator is only harmed if its prey are scarce over its whole hunting area. For systems of this type, it is primarily the synchronous components of signals that matter in the average signal that affects the next level - non-synchronous components tend to cancel in the spatial average. Thus synchrony is very important to ecosystems. Synchrony is found in organisms as diverse as mammals and protists, at distances up to thousands of kilometers. Synchrony relates to large-scale outbreaks and shortages and is important in conservation. In spite of the importance of synchrony in ecology, possible impacts of climate change on synchrony are little studied. Synchrony can also be transmitted through trophic interactions - e.g., a synchronized predator can induce synchrony in its prey. But the extent to which climate-induced changes in synchrony may cascade through species interaction networks via this mechanism, or influence spatial or other branches of ecology, is unknown. The postdoc will perform statistical and/or mathematical population modelling to address these questions, and will investigate connections to extinction risk models and to Taylor's law, a commonly applied empirical regularity in spatial ecology. The postdoc will be encouraged to develop his/her own projects within the goals of the funding grants.

We seek individuals from biological or physical-science backgrounds with skills and demonstrable interests in modelling and related areas. Experience with stochastic process modelling and Fourier or wavelet approaches is a plus. Experience with population models is a plus, as are computational skills, particularly if applied in a statistical or modelling context. A PhD or ABD in a related field is required. Applicants from underrepresented groups are encouraged.

The University of Kansas (KU) is a major research university with special strength in ecology and evolutionary biology. The EEB department has >40 permanent faculty working in a wide variety of theoretical and empirical areas, with National Research Council and Chronicle of Higher Education rankings in the top 10 in the USA. KU is located in Lawrence, Kansas, about 30 miles from Kansas City. Lawrence is a progressive and cosmopolitan university town with vibrant art, music, and sports scenes that has been ranked among the top ten college towns in the country for liveability.

See http://www.reumanlab.res.ku.edu/ for further information about the Reuman lab and links to past publications. Email reuman@ku.edu or call 785 864 1542 with questions. A start date during or before autumn 2017 is preferred. To apply, please send a CV, a cover letter of up to two pages, the names and contact information of two references, and one publication to reuman@ku.edu. Review of applications has begun. Position open until filled.

"Reuman, Daniel Clark" <d294r143@ku.edu>

ULiverpool UK ClimateDrivenEvolution

Genomics and epigenetics of climate-driven evolution University of Liverpool, UK Closing date 31st August

We are seeking a highly motivated individual to investigate how organisms respond to the impacts of climate-driven evolution. The project will make use of the keystone species Daphnia magna within large experimental mesocosms exposed to heat waves. You will be part of a team combining genomic, evolutionary biology and ecology to understand the relative importance of genetic and epigenetic changes for Daphnia adaptation. Your role will be the genomic and bioinformatic analyses of these populations. You should have a PhD degree in biology and excellent experimental and quantitative skills. The post is available until 30 August 2020.

A full job description is available at: http://tinyurl.com/y9cql48f Applications can only be accepted through the University of Liverpool site: http://tinyurl.com/yav2hsep Informal enquiries to s.paterson@liverpool.ac.uk

Steve Paterson, Stewart Plaistow and David Atkinson – Prof Steve Paterson Institute of Integrative Biology University of Liverpool Liverpool, L69 7ZB, UK Tel +44 151 795 4521 Fax +44 151 795 4408 Mob +44 797 024 7668 s.paterson@liv.ac.uk http://www.liv.ac.uk/genomic-research/ Twitter: @scottishwormboy

"S.Paterson@liverpool.ac.uk"
<S.Paterson@liverpool.ac.uk>

UManchester EvolutionaryPhysiology

Research Associate in Conservation Physiology

The University of Manchester - School of Earth & Environmental Sciences

Location: Manchester Salary: Â£31,076 to Â£33,943 Hours: Full Time Contract Type: Fixed-Term/Contract Placed on: 20th July 2017 Closes: 10th August 2017 Job Ref: 10400 â View Employer Profile

Closing Date : 10/08/2017. Employment Type : Fixed Term. Duration : 1 September 2017 until 31 August 2019. Faculty / Organisational Unit : Science & Engineering. School/Directorate : School of Earth & Environmental Sciences. Division : - Hours Per week : Full time. Salary : Â£31,076 to Â£33,943 per annum according to experience. Location : Oxford Road, Manchester. Job Reference : S&E-10400.

To support a growing partnership between the North of England Zoological Society (Chester Zoo) and the University of Manchester, we are recruiting a post-doctoral research assistant to deliver high-impact conservation science. This post will focus on developing and applying a novel and integrated macro-ecological tool kit for identifying the causes of, and for predicting, decline primarily in the critically endangered Grevy's zebra (Equus grevyi) but also in other species.

This full-time two-year post will work in collaboration with scientists from the University of Manchester, NEZS (Chester) zoo and additional stakeholders to undertake fieldwork to collect and evaluate environmental, behavioural and physiological data across populations of Grevy's zebra (and potentially other species) in East Africa. You will also work with these stakeholders to develop applied individual and population management recommendations in order to improve performance.

You will have experience with international fieldwork, analysing complex datasets and expertise in one or more of the following: endocrinology, analytical chemistry, social network analysis, spatial statistics, or ecological monitoring. You should hold a PhD in a relevant science discipline. The anticipated start date is 1st September 2017.

You will also become a Chester Zoo Conservation Fellow where you will receive an honorary membership to Chester Zoo for the duration of the research and will be encouraged to participate in Chester Zoo's public programmes and scientific communications to help establish Chester Zoo as a centre of excellence for animal welfare and conservation.

This role will involve international travel in challenging conditions.

As an equal opportunities employer we welcome applicants from all sections of the community regardless of gender, ethnicity, disability, sexual orientation and transgender status. All appointments are made on merit.

Please note that we are unable to respond to enquiries, accept CVs or applications from Recruitment Agencies.

Enquiries about the vacancy, shortlisting and interviews:

Name: Dr Susanne Shultz

Email: susanne.shultz@manchester.ac.uk

General enquiries:

Email: hrservices@manchester.ac.uk

Tel: 0161 275 4499

Technical support:

Email: universityofmanchester@helpmeapply.co.uk

Tel: 01565 818 234 To apply: https://www.jobs.manchester.ac.uk/-displayjob.aspx?jobid=13739 Susanne Shultz <susanne.shultz@manchester.ac.uk> Susanne Shultz <susanne.shultz@manchester.ac.uk>

UMichigan SpeciesDelimitiation

NSF Funded Postdoctoral Position

A two-year postdoctoral position is currently available in the Knowles Lab, in collaboration with Jeet Sukumaran and Craig Moritz, to work on statistical and conceptual issues regarding species delimitation. Specifically, the postdoc will work as part of the joint effort aimed at (i) developing a new approach that couples the multi-species coalescent with different diversification models for Bayesian statistical inference, with (ii) applications of genetic-based delimitation. Although the postdoc will not be required to program, the ideal candidate should have a quantitative background (e.g., experience with scripting and analysis of large genomic datasets) and conceptual interest in species delimitation. Given that the postdoc will be responsible for conducting analyses for extensively evaluating the general performance of the new modeling approach through simulated datasets, as well applications to existing datasets on Australian squamates, the postdoc should have experience conducting coalescent simulations. The postdoc will be based in Ann Arbor; however, as part of the collaborative project, will also be engaged in outreach activities that include workshops and public engagements in both the USA and Australia.

Please send CV and inquires to L. Lacey Knowles (knowlesl@umich.edu) briefly explaining your past experience with coalescent simulations and their application (e.g., phylogeographic, phylogenetics, species delimitation analyses), as well as your general proficiency with scripting and analysis of genomic data.

– L. Lacey Knowles Robert B. Payne Collegiate Professor Dept. of Ecology and Evolutionary Biology Curator of Insects, Museum of Zoology University of Michigan Ann Arbor MI 48109-1079

L Knowles <knowlesl@umich.edu>

UMontana WolbachiaEvolutionaryGenetics

Postdoctoral Positions Available Cooper Lab, University of Montana brandonscooper AT gmail

Postdoctoral scholars are sought to join the laboratory of Brandon S. Cooper in the Division of Biological Sciences at the University of Montana. Positions are funded by the NIH and expected to start on or after September 1; however, start dates are negotiable. Our group is focused on understanding the origin, spread, and maintenance of maternally transmitted Wolbachia bacteria in several (N ~ 20) Drosophila systems. We believe that the diversity of experiences and ideas that we each bring to the lab improves our ability to answer our questions. Thus, we encourage qualified individuals from all backgrounds to apply.

The positions - Postdoctoral research will be broadly focused on determining Wolbachia effects on host physiology and fitness that facilitate Wolbachia spread. Infections could be old and co-diverging with their hosts. In contrast, hybridization with sister species or horizontal transfer could lead to contemporary between-species Wolbachia spread. Once Wolbachia infect host lineages they often spread rapidly to high frequencies. For example, the wRi variant that infects D. simulans took over most of the Australian continent in about a decade. Yet how Wolbachia interact with their hosts to spread so rapidly remains mostly unknown. Postdocs will push back the frontiers of knowledge about the origin, spread, and maintenance of Wolbachia infections in Drosophila.

Desired skills - A variety of projects are available that will enable postdocs to leverage their existing expertise while learning new skills. For example, we would be equally happy to recruit evolutionary biologists with expertise in molecular genetics, cell biology, bioinformatics, and/or evolutionary genetics. Some projects will evaluate genomic variation, some will evaluate phenotypic variation, and others will assess cell-level variation in Wolbachia abundance. While our approaches are diverse, all projects seek to make progress towards our primary goal of understanding how Wolbachia infections spread to become common. Anyone interested should contact me directly (brandonscooper AT gmail).

The pay - Postdoctoral scholars will be paid according to the NIH stipend levels, which is currently $47,484 for first year postdocs. You can live quite comfortably on this salary with the reasonable cost of living in Missoula, MT. Postdocs will be initially appointed for one year, but up to three years of funding is available for postdocs making sufficient progress.

Our lab at UM - We share a new 5000 ft2 lab space with Zac Cheviron, Lila Fishman, Jeff Good, John McCutcheon, and Scott Miller, which generates an exceptional intellectual microenvironment. Several other labs interested in evolutionary genetics and host-symbiont interactions are nearby making UM a wonderful place for completing our goals. Postdocs will interact heavily with these labs in addition to our collaborators at other universities.

Life in Missoula - Missoula is located along the Clark Fork River in western Montana. Within minutes of our lab you can hike a mountain, float down a river, fly fish, or relax at any of the nearby breweries/coffee shops. We work hard, but we also enjoy life, and Missoula is a good place to do both.

brandonscooper@gmail.com

UOklahoma FloralEvolution

I have a postdoc position available in my lab at the University of Oklahoma to study the evolution of the flora of Oklahoma using sequence-based or modeling approaches. I am especially interested in the role ecological diversification has played in the evolution of the flora.

The major components of the job are field work and computer work to analyze sequence data and potentially perform distribution modelling (especially Linux and Python). Some lab work will be involved, but most sample preparation will be outsourced. Familiarity with programming or a strong desire to learn are necessary. There will also be the opportunity to help supervise undergraduate and high school researchers.

Description–

Job function:

1. Conduct botanical fieldwork in Oklahoma and other areas.
2. Perform DNA and RNA extractions and sample preparation for generation sequencing.
3. Analyze next generation sequencing data (using scripts and existing programs).
4. Mentor graduate and undergraduate students in the lab, at the computer, and in the field.
5. Conduct literature research and write up results for publication.

Experience:

Previous experience conducting botanical fieldwork.

Previous experience writing and publishing manuscripts.

Qualifications–

Required Education: PhD in botany, evolutionary biology, or a related field.

Previous experience conducting botanical fieldwork.

Previous experience writing and publishing manuscripts

Skills:

Ability to perform phylogenetic analysis of DNA/RNA sequence data.

Ability to communicate well with all lab members and collaborators.

Ability and desire to mentor graduate and undergraduate students

Certifications:

None

Advertised Physical Requirements:

Ability to walk and perform field work in extreme heat and wind.

Department Preferences:

Strong plant identification skills are preferred, but not required.

Scripting skills (especially python and/or R) are preferred, but not required.

Previous experience with analyzing next generation sequencing data is preferred, but not required.

Grant writing experience is preferred, but not required.

Feel free to e-mail me with any questions (abigail.j.moore@ou.edu). To apply, go to jobs.ou.edu, click on External Applicants–Staff Positions, and search for job # 171809. You will need to submit a cover letter, cv, and contact information for three references.

"Moore, Abigail" <abigail.j.moore@ou.edu>

UPennsylvania HumanGenomics

Postdoctoral fellowship in human genomics University of Pennsylvania, Perelman School of Medicine

Postdoctoral positions are available in Christopher Brown's lab in the Genetics Department at the University of Pennsylvania. Current research in the Brown lab is focused on identifying and characterizing non-coding variants that affect complex phenotypes. Successful applicants will have the opportunity to design their own projects relating to the genetics of gene expression regulation, eQTLs, or post-GWAS fine mapping and functional interpretation. The fellow will also have the opportunity to work as a part of the GTEx consortium and related projects.

Candidates with expertise in experimental or computational biology will be considered, but the ideal candidate will have significant wet and dry experience. Applicants must have an MD, PhD, or equivalent degree in genetics/genomics, evolutionary biology, bioinformatics, computational biology, or a related discipline. Candidates with backgrounds in statistics, computer science, physics, or other quantitative fields will be considered if they have experience with biological data. Experience with next-generation sequencing techniques and data, ChIP and related functional genomics techniques, and/or scientific programming are desired.

Applications (including CV, statement of research interests, and references) and informal inquiries should be emailed to Christopher Brown (chrbro@upenn.edu). Applications will be considered as they are received; positions are available now.

Christopher Brown Assistant Professor Department of Genetics University of Pennsylvania 538 Clinical Research Bldg 415 Curie Blvd Philadelphia, PA, 19104 chrbro@upenn.edu T: (215) 746-4049

casey6r0wn@gmail.com

UPorto EvolCooperativeBreeding 2

Correction: the application dates for the post-doc position below are from the 20/07-30/08. Please cite reference ICETA 2017-24

A post-doc position in Behavioural Ecology is available from mid-September for 1.5 years to study experimentally whether cooperative behaviour is influenced by sex-specific audience effects. The project will integrate a broader research program which investigates the potential role of social and sexual selection in the evolution and maintenance of cooperation in a colonial cooperative bird from Southern Africa, the sociable weaver. The successful post-doc candidate will integrate an international research group based in Portugal, France and South Africa and will be working closely with Rita Covas (CIBIO, University of Porto, Portugal), Claire Doutrelant (CEFE-CNRS, France) and Fanny Rybak (University of Paris-Sud, France). The project is based on acoustic and behavioural field experiments and requires spending an initial period of 4-6 months in the field. Previous experience with fieldwork, behavioural work and acoustics, as well as motivation to conduct behavioural experiments in field conditions are therefore essential prerequisites. Candidates are equally required to have solid knowledge of evolutionary ecology and preferably of cooperation and social evolution. Pre-application enquiries are encouraged and should be sent to rita.covas@cibio.up.pt , claire.doutrelant@cefe.cnrs.fr and fanny.rybak@u-psud.fr . More information about the project can be found at http://www.fitzpatrick.uct.ac.za/fitz/-research/programmes/longterm/soci ableweaver; https://cibio.up.pt/people/details/rcovas; https://-www.cefe.cnrs.fr/fr/recherche/ee/esp/777-c/152-claire-doutrelan t; http://www.cb.u-psud.fr/Fanny.htm The link to the official advert is http://www.eracareers.pt/-opportunities/index.aspx?task=global&jobId=92062 The application dates will be open from 20/07 a 03/08 2017. Applications must cite reference ICETA 2017-24 and include Curriculum Vitae (CV), motivation letter, copy of academic certificates, and contact details of two references, sent to: bolsas@iceta.up.pt

Rita Covas <rita.covas@gmail.com>

UTexas Austin 2 PopulationStatGenomics

Postdoctoral Research in Plant Population Genomics

The Juenger lab at the University of Texas at Austin is recruiting a postdoctoral position in population genomics to work on DOE funded research. The focus of the research is to explore the genetics and genomics of adaptation in switchgrass (Panicum virgatum), a native C4 perennial grass. The project is a multidisciplinary effort including ecologists, physiologists, genomic scientists and modelers. Our collaborative project is generating a number of exciting datasets ranging from high throughput phenomic descriptions of plant material to genome-scale polymorphism data. A major aim is to understand the natural diversity and evolutionary history of switchgrass. To this end, we have developed a diversity panel of hundreds of natural accessions that have been resequenced and are being utilized in common garden studies. The candidate will likely be involved in studies of demographic history, population structure, adaptive molecular evolution, and association studies of ecologically-important traits.

The position requires a PhD in Evolution, Population Genetics, Genomics, Plant Biology, or a related field. The ideal candidate will have experience in bioinformatics, population genomic modeling and inference, and statistical analyses of genome-wide polymorphism data. We are looking for highly motivated candidates with excellent communication skills, initiative, and enthusiasm for large collaborative team efforts. Our diverse research effort offers an ideal scenario for cross-disciplinary training, leveraging existing datasets and resources, leadership opportunities, a creative work environment, and avenues for applied impact in the development of sustainable biofuels.

Austin is the state capital of Texas, an inland city bordering the Hill Country. Home to the University of Texas, Austin is known for its eclectic live-music scene, sizeable tech sector, and SXSW Conference. Its many parks and lakes are popular for nearly year-round hiking, biking, swimming and boating. Austin boasts approximately 300 days of sunshine per year and is America's fastest growing city. https://hr.utexas.edu/prospective/austin We encourage applications from female, minority, and culturally diverse candidates. Please email all applications to bethaney.watson@austin.utexas.edu with the subject "Postdoctoral Application: population genomics". Applications should include a cover letter detailing experience and research interests, a current CV, and contact information for three professional references compiled in a single pdf file. Applicants can find additional information about the Juenger lab at https://sites.cns.utexas.edu/juenger_lab. Applications will be considered until the position is filled.

Postdoctoral Research in Statistical Genetics

The Juenger lab at the University of Texas at Austin is recruiting a postdoctoral position in statistical genetics to work on NSF and DOE funded research of native perennial C4 grasses. The candidate will be involved in projects exploring ecological and evolutionary genetics using switchgrass (Panicum virgatum) as a model system. The project involves a multidisciplinary team of investigators including ecologists, physiologists, modelers and genomic scientists. A major theme of the research is the study of gene-by-environment interaction, ecological and evolutionary tradeoffs, and the evolution of adaptive trait sets in natural plant populations. A central goal is to identify genes underlying local adaptation and ecotypic differentiation across species ranges. The Juenger lab has longstanding interests in quantitative genetics, gene-by-environment interaction, and the genetic architecture of ecologically important traits. Over the last decade we have developed a number of resources for studying quantitative genetics in perennial grasses include diversity panels, mapping populations, and common garden plantings. Our funded projects leverage existing gardens spanning 10 locations across the latitudinal species range of switchgrass (from Texas to South Dakota). The candidate will likely be involved in statistical genetic projects including genome-wide complex trait analysis (gREML), genetic mapping (outbred QTL and GWAS), and genomic selection in plant breeding. The position requires a PhD in Evolution, Population Genetics, Genomics, Statistical Genetics, Plant Biology, Plant Breeding or a related field. We are looking for highly motivated candidates with excellent communication skills, initiative, and enthusiasm for large collaborative team efforts. Our diverse research effort offers an ideal scenario for cross-disciplinary training, leveraging existing datasets and resources, leadership opportunities, a creative work environment, and avenues for applied impact in the development of sustainable biofuels.

— / —

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

UTexas Austin SticklebackEvolution

University of Texas at Austin: Postdoctoral Researcher.

The Bolnick lab (https://bolnicklab.wordpress.com/-) in the Department of Integrative Biology (https://-integrativebio.utexas.edu) at the University of Texas at Austin is searching for a postdoctoral researcher to participate in an NSF-funded study of parallel evolution in lake and stream threespine stickleback. For context, see http://tinyurl.com/y9gj8zdc). The duties of the postdoc are flexible, but we are particularly interested in someone able to contribute to analysis and publication of existing data on phenotypic, ecological, and genomic divergence among populations. There may also be opportunities, depending on applicant interest, to conduct field experiments on stickleback diversification, study the genetics of gut microbiome variation, or pursue other goals related to the evolution of lake-stream population differences.

The position is for one year. The start date is negotiable, but should be no later than June 1 2018, preferably earlier. There is an annual salary of $48,000 with benefits.

Applicants should electronically submit a single pdf file containing the following, in order: 1) Coverletter, including a summary of major research accomplishments and career goals 2) CV 3) Copies of 2 publications 4) List of three references, with contact information (email, telephone, and mailing address). We will request letters directly from these references, after identifying top candidates.

Qualifications: Ph.D. in Ecology, Evolution, Genetics, or a related field required. Strong skills in data analysis (preferably including genomic data) and writing are essential. Good organizational skills and the ability to work collaboratively on analysis and writing are required. Molecular genetics laboratory skills are preferred.

The application pdf file should be emailed to Dr. Daniel Bolnick (danbolnick@austin.utexas.edu) and Yoel Stuart (yestuart@utexas.edu), with a subject line "Parallel Evolution Postdoc Application: <YOUR NAME>". Applications will be considered until September 1, 2017. For questions about this position, please email danbolnick@austin.utexas.edu.

The University of Texas is an Equal Opportunity Employer.

Dr. Daniel I. Bolnick

Professor Department of Integrative Biology Chair, Graduate Program in Ecology Evolution and Behavior One University Station C0990 University of Texas at Austin Austin, TX 78712

512-471-2824 fax 512-471-3878 danbolnick@austin.utexas.edu

Lab website: https://bolnicklab.wordpress.com danbolnick@austin.utexas.edu

UToulouse ConservationGenomics

"We are looking for an ambitious and excellent postdoctoral fellow to work on the impact of habitat fragmentation on the genomic diversity of endemic trees of Madagascar. The hired fellow will interact with an international team involving mathematicians, behavioural ecologists and population geneticists. S/he will be responsible for the generation and analysis of genomic data (mainly RAD-seq) from species of the Noronhia genus, and is expected to be very fluent in English, scripting and population genetics theory. S/he will analyze spatial patterns and infer the demographic history of species within a framework of structured populations.

Candidates should have demonstrated their ability to publish their research in solid journals of the population genetics, evolution or molecular ecology fields. Publication in so-called high profile journals is not a plus, unless the number of co-authors is significantly lower than the impact factor.

The fellow will work at the University of Toulouse. The project will involve collaborations with EDB colleagues (G. Besnard, L. Chikhi), but also from outside (at IMT Toulouse, IGC Lisbon, Madagascar, Kew...).

Applicants should send their CV, a letter of intent describing candidate's motivation, qualifications, skills, and experience relevant to this position, and contact information for three references to guillaume.besnard@univ-tlse3.fr and chikhi@igc.gulbenkian.pt, before the end of September 2017. The position may start between October and December 2017."

besnard guillaume <guillaume.besnard@univ-tlse3.fr>

UWisconsin Madison EvolPopGenomics 2

Postdoctoral Position in Evolutionary/Population Genomics

A postdoctoral position is available to work on an NSF-funded project in the laboratory of Professor Carol Lee, in the Department of Integrative Biology and the Center of Rapid Evolution at the University of Wisconsin, Madison.

This project focuses on Rapid Evolutionary Responses to Global Change using the copepod Eurytemora affinis as a model system. With changes in global climate, the coastal oceans and estuaries at high latitudes are experiencing rising temperature along with rapid declines in salinity, due to increases in ice melt and precipitation. We have found evolutionary shifts in ion transport function, gene expression, and population genomic signatures of selection associated with changes in salinity. This postdoc project will entail conducting population genomic analyses along temperature and salinity gradients in the wild, and during selection experiments in the laboratory.

A key advantage of the E. affinis system is its short generation time (20d), ease of culturing large numbers (thousands per population), and ability to generate inbred lines. We have a full genome sequence of E. affinis and several reference transcriptome sequences. Additionally, the multiple independently-derived environmental clines enable the observation of parallel evolution.

The ideal candidate should hold a Ph.D. and have publications in peer-reviewed journals. A strong background in evolutionary biology is required, especially in population genetics/genomics. Relevant areas of expertise include computational and programming skills and statistics, with background in comparative physiology preferred.

Review of applications will begin immediately and will continue until the position is filled. The appointment could begin as early as October 2017 and can persist for up to three years. Interested candidates should email the application to Prof. Carol Lee (carollee@wisc.edu), including: (1) a CV, (2) a cover letter describing qualifications and relevant experience, (3) a list of references, and (4) samples of first authored publications. Enquiries regarding this position are most welcome.

The University of Wisconsin-Madison offers a large and intellectually vibrant community of evolutionary/population biologists, providing ample opportunities for interaction with excellent scientists (see http://www.evolution.wisc.edu/view_facultymembers). Madison is a culturally-rich community, in relatively close proximity to Chicago.

The University of Wisconsin is an Equal Opportunity/Affirmative Action Employer.

Carol Eunmi Lee, Ph.D. Professor Center of Rapid Evolution (CORE) and Department of Integrative Biology 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu http://carollee.labs.wisc.edu Carol Eunmi Lee <carollee@wisc.edu>

UWisconsin Madison EvolutionaryPopGenomics

Postdoctoral Position in Evolutionary/Population Genomics A postdoctoral position is available to work on an NSF-funded project in the laboratory of Professor Carol Lee, in the Department of Integrative Biology and the Center of Rapid Evolution at the University of Wisconsin, Madison.

This project focuses on Rapid Evolutionary Responses to Global Change using the copepod Eurytemora affinis as a model system. With changes in global climate, the coastal oceans and estuaries at high latitudes are experiencing rising temperature along with rapid declines in salinity, due to increases in ice melt and precipitation. We have found evolutionary shifts in ion transport function, gene expression, and population genomic signatures of selection associated with changes in salinity.

A key advantage of the E. affinis system is its short generation time (20d), ease of culturing large numbers (thousands per population), and ability to generate inbred lines. We have a full genome sequence of E. affinis and several reference transcriptome sequences. Additionally, the multiple independently-derived environmental clines enable the observation of parallel evolution.

The ideal candidate should hold a Ph.D. and have at least a few publications. A strong background in evolutionary biology is required, including a background in population genetics/genomics. Other relevant areas of expertise include some background in computational biology with programming skills, comparative physiology and/or statistics.

Review of applications will begin immediately and will continue until the position is filled. The appointment could begin as early as October 2017 and can persist for three years. Interested candidates should email the application to Prof. Carol Lee (carollee@wisc.edu), including: (1) a CV, (2) a cover letter describing qualifications and relevant experience, (3) a list of references, and (4) samples of first authored publications. Inquiries regarding this position are most welcome.

The University of Wisconsin-Madison offers a large and intellectually vibrant community of evolutionary/population biologists, providing ample opportunities for interaction with excellent scientists (see http://www.evolution.wisc.edu/view_facultymembers). Madison is a culturally-rich community, in relatively close proximity to Chicago.

The University of Wisconsin is an Equal Opportunity/Affirmative Action Employer.

Carol Eunmi Lee, Ph.D. Professor Center of Rapid Evolution (CORE) and Department of Integrative Biology

430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu

http://carollee.labs.wisc.edu carollee@wisc.edu

YaleU Biodiversity

We are seeking a postdoc (2-3y) addressing questions and research opportunities surrounding uncertainty-assessed models of species (co-) occurrences over time. Project work would benefit from range of carefully curated biodiversity data sources and novel remotely sensed layers from associated NASA projects. Contingent on funding, the position may address specific GEO BON use cases in support of Species Populations Essential Biodiversity Variables. We are open to a candidate's preferred taxa, regions, and questions and animal/plant and terrestrial/marine/freshwater expertise - qualifications and vision are more important than a specific system. We seek someone with as strong quantitative background and ability to traverse community- and single- species perspectives and spatial scales.

For more details see http://bgc.yale.edu/opportunities. This is one of several positions starting fall/winter 2017/18 are available associated with the Yale Center for Biodiversity and Global Change (http://bgc.yale.edu), Map of Life (https://mol.org) and the Jetz Lab (http://jetzlab.yale.edu). To apply please send, in one pdf, a short cover letter, CV and contact info for three referees to michelle.duong@yale.edu. For questions or associated PhD opportunities contact walter.jetz@yale.edu. The final selection process will begin on 18 Aug 2017, but applications before this date are welcome and will be reviewed as received.

Environment: The interdisciplinary BGC program (http://bgc.yale.edu) connects biodiversity scientists from across campus. Yale has a thriving and growing community of young scholars in ecology, evolution and global change science in the EEB Department, the Yale Institute for Biospheric Studies, the Peabody Museum, and the Yale School of Forestry and Environmental Studies. The town is renowned for its classic Ivy League setting, 75 miles north of New York City.

"walter.jetz@yale.edu" <walter.jetz@yale.edu>

YaleU MountainBiodiversity

A postdoc position (1-2y) is available to address questions surrounding spatial patterns and temporal changes in global mountain biodiversity. This position will build on the data and infrastructure collaboration of the Global Mountain Biodiversity Assessment and Map of Life (http://www.mountainbiodiversity.org). Targeted work aims to document the evidence base and causes behind geographical mountain biodiversity patterns and to integrate information about change and protection in support of Target 4 of Sustainable Development Goal 15. The successful candidate will have excellent spatial biodiversity modelling skills and statistical background, first-hand experience with observational field data collection, knowledge of global change scenarios and models, and a passion for mountain biodiversity.

For more details see http://bgc.yale.edu/opportunities. This is one of several positions starting fall/winter 2017/18 are available associated with the Yale Center for Biodiversity and Global Change (http://bgc.yale.edu), Map of Life (https://mol.org) and the Jetz Lab (http://jetzlab.yale.edu). To apply please send, in one pdf, a short cover letter, CV and contact info for three referees to michelle.duong@yale.edu. For questions or associated PhD opportunities contact walter.jetz@yale.edu. The final selection process will begin on 18 Aug 2017, but applications before this date are welcome and will be reviewed as received.

Environment: The interdisciplinary BGC program (http://bgc.yale.edu) connects biodiversity scientists from across campus. Yale has a thriving and growing community of young scholars in ecology, evolution and global change science in the EEB Department, the Yale Institute for Biospheric Studies, the Peabody Museum, and the Yale School of Forestry and Environmental Studies. The town is renowned for its classic Ivy League setting, 75 miles north of New York City.

"walter.jetz@yale.edu" <walter.jetz@yale.edu>

YaleU SpeciesDiversification

We are seeking a postdoc (2-3y) to work on questions of species and trait diversification and the evolution of niche-relevant traits in geographic space and across spatial scales. Focal taxa include vertebrates, but we are open to work on invertebrate or plant taxa. The candidate should have a strong background in phylogenetic comparative methods and rate-based diversification analyses and ideally prior experience in the assembly of phylogenies, geospatial analyses, and a solid natural history background. Familiarity with R, python, and bash is desirable, as are strong writing and verbal communication skills, a successful track-record of publications, and strong team-working skills.

For more details see http://bgc.yale.edu/opportunities. This is one of several positions starting fall/winter 2017/18 are available associated with the Yale Center for Biodiversity and Global Change (http://bgc.yale.edu), Map of Life (https://mol.org) and the Jetz Lab (http://jetzlab.yale.edu). To apply please send, in one pdf, a short cover letter, CV and contact info for three referees to michelle.duong@yale.edu. For questions or associated PhD opportunities contact walter.jetz@yale.edu. The final selection process will begin on 18 Aug 2017, but applications before this date are welcome and will be reviewed as received.

Environment: The interdisciplinary BGC program (http://bgc.yale.edu) connects biodiversity scientists from across campus. Yale has a thriving and growing community of young scholars in ecology, evolution and global change science in the EEB Department, the Yale Institute for Biospheric Studies, the Peabody Museum, and the Yale School of Forestry and Environmental Studies. The town is renowned for its classic Ivy League setting, 75 miles north of New York City.

"walter.jetz@yale.edu" <walter.jetz@yale.edu>

WorkshopsCourses

Berlin BioinformaticsWithRBioconductor Jan22-26

Applied Statistics and Bioinformatics with R and Bioconductor

https://www.physalia-courses.org/courses-workshops/-course19/ 22-26 January 2018, Berlin (Germany)

Overview

This course will provide biologists and bioinformaticians with practical statistical and data analysis skills to perform rigorous analysis of high-throughput biological data. The course assumes some familiarity with genomics and with R programming, but does not assume prior statistical training. It covers the statistical concepts necessary to design experiments and analyze high-dimensional data generated by high-throughput sequencing, including: exploratory data analysis, principal components analysis, unsupervised clustering, batch effects, linear modeling for differential expression, gene set analysis.

Preparation

Come to the first class with the following installed:

* R and Bioconductor:http://www.bioconductor.org/-install * R Studio: https://www.rstudio.com/products/-rstudio/download3/ * Github desktop client (or any other Github client): https://desktop.github.com/- Additionally, please create an account athttp://-www.github.com/ , and use it to introduce yourself at https://github.com/waldronlab/AppStatTrento/issues . Instructors

Dr. Levi Waldron and Dr. Ludwig Geistlinger from the Waldron lab for computational biostatistics CUNY School of Public Health in New York City (http://-waldronlab.org/)

Labs

Each day will include a hands-on lab session, that students should attempt and hand in before the following day by committing to the course Github repository. A selection of labs will be reviewed the following day.

Course programme

https://www.physalia-courses.org/courses-workshops/-course19/curriculum-19/ Registration deadline

December 20th , 2017. Attendees are seated on a first-come, first-served basis.

Full list of our courses and Workshops

https://www.physalia-courses.org/courses-workshops/ Best regards,

Carlo

–

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator

info@physalia-courses.org

http://www.physalia-courses.org/ Twitter: @physacourses

mobile: +49 15771084054

https://groups.google.com/forum/#!forum/physalia-courses Carlo Pecoraro <info@physalia-courses.org>

Berlin GenomeAssemblyAnnotation Feb12-16

Course: Assembly and Annotation of genomes

https://www.physalia-courses.org/courses-workshops/-course20/ 12-16 February 2018, Berlin (Germany)

Instructor: Dr. Thomas D. Otto (University of Glasgow, UK; https://www.physalia-courses.org/-instructors/t28/) https://www.physalia-courses.org/-instructors/t28/ Overview

This course will introduce biologists and bioinformaticians to the concepts of de novo assembly and annotation. Different technologies, from Illumina, PacBio, Oxford Nanopoor and maybe 10X will be used mixed with different approaches like correction, HiC scaffolding to generate good draft assemblies. Particular attention will be given to the quality control of the assemblies and to the understanding how errors occur. Further, annotation tools using RNA-Seq data will be introduced. An outlook of potential analysis is given. In the end of the course the students should be able to understand what is needed to generate a good annotated genome.

Targeted Audience & Assumed Background

The course is aimed at researchers interested in learning more about genome assembly and annotation. It will include information useful for both the beginner and the more advanced user. We will start by introducing general concepts and then continue to step-by-step describe all major components of a genome assembly and annotation workflow, from raw data all the way to a final assembled and annotated genome. There will be a mix of lectures and hands-on practical exercises using command line Linux.

Attendees should have a background in biology. We will dedicate one session to some basic and advanced Linux concepts. Attendees should have also some familiarity with genomic data such as that arising from NGS sequencers.

Session content

Monday 12th - Classes from 09:30 to 17:30 - “get it starting”

Session 1: Introduction (morning)

In this session I will kick off with an introduction lecture about genome assembly and annotation - the past, the present and the future. I will use this introduction to motivate the five-day course. Next, I will explain the use of the virtual machine (VM), and the use of cloud computing. This is followed by short introduction to Linux (although I would prefer if student know a bit of Linux). Through the morning we will kick off our first assembly and put it through an annotation tool (Companion).

Session 2: Visualization (half afternoon)

During this afternoon, we are going to visualize the assembled and annotation genome from this morning in Artemis. The aim is to use the viewer to inspect the annotation, correct annotation and write out files. Next, we are going to perform a comparative exercise, (comparing the genome from the morning with a close reference) to understand the concept of syntheny, breakpoint or errors.

Session 3: Mapping

In this module, I will teach the basics of read mapping. We will map reads with bwa mem onto a reference and will examine duplications and errors through not proper mapped read pairs. This is important to exanimate the correctness of assemblies and will be used later the week.

Tuesday 13th - Classes from 09:30 to 17:30 - “learn it the old way”

Session 4: De Brujin graph and PAGIT

This module is dedicated to short read assembly. Although it might be superseded due to long reads, understanding the concept of short reads and De Brujin graph is crucial. After a seminar about this subject, we will assemble the same genome as before, but this time with Illumina: de novo assembly with velvet, contig ordering, error correction. Through comparative genomics we are going to look at errors in the assembly, and how they could be found with remapping short reads, and also split long reads. Last, we are going to compare the assembly to the assembly from Monday. This session will go into the afternoon of Tuesday.

Session 5: RNA-Seq

In this session, we will analysis the transcriptome of the sample we assembled so far, motivated through a little talk. In the exercise, we will map RNA-Seq reads, (short and long reads) understanding first the basics of RNA-Seq, but then will use the reads to correct gene models. We will discuss the concept of alternative splicing.

Finally, we will annotate our assembly with Augustus, using the mapped RNA-Seq data and some manually corrected genes.

Wednesday 14th - Classes from 09:30 to 17:30 - “do it yourself”

Session 6: Large genome assembly

First we are going to kick off an assembly of a larger genome, and let it run in the cloud over the day and the night. It will be important during the day to check if the assembly is still running.

Session 7: Group Taks I

Group task I: You will get a set of reads (from a random technology) and need to generate a draft genome assembly. Due to time restriction,

— / —

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

---

Berlin GenomicVisualizationsInR Sep11-15 deadline

Workshop title: Genomic Data Visualization and Interpretation

11th-15th September, Berlin (Germany)

https://www.physalia-courses.org/courses-workshops/course14/ Application deadline is the 10th of August 2017.

Topic: Advanced R and bioinformatics applications for visualization and interpretation of genomic data.

Instructors:

Dr. Obi Griffith (http://obigriffith.github.io/; Washington University School of Medicine, USA),

Dr. Malachi Griffith (http://malachig.github.io/; Washington University School of Medicine, USA)

Mr. Zachary Skidmore (Washington University School of Medicine, USA)

Course overview

The advent of rapid and relatively cheap massively parallel sequencing has dramatically increased the availability of genome, transcriptome, and epigenome profiling. Analysis workflows and published best practices are also now available to process raw sequence data into alignments, variant calls, expression estimates, etc., in relatively standardized file formats. Interpretation and visualization of these data, often consisting of thousands to billions of data points, and extracting biological meaning remains a serious challenge. In this workshop we will explore a number of best-in-class visualization tools, and provide working examples that demonstrate important principles of 'omic interpretation strategies.

Workshop format

The workshop will be delivered over the course of five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group. Computing will be done using a combination of tools installed on the attendees laptop computer and web resources accessed via web browser.

Who should attend

This workshop is aimed at researchers and technical workers who are analyzing some kind of omic data (e.g. WGS, exome, RNA-seq, variant files, etc.). Examples demonstrated in this course will involve primarily human genome/transcriptome data but many of the concepts learned will be applicable to model organisms, metagenomics, simulated data, etc.

Requirements

Attendees should have a background in biology and a basic knowledge of R. We will dedicate one session to a brief R/linux primer. Attendees should have also some familiarity with genomic data. The course will teach relatively advanced usage of R (especially ggplot2 and Bioconductor packages). Attendees should have a working installation of R and RStudio on their laptop.

Example data

Attendees will learn to visualize and interpret results from real human genome data sets generated at the McDonnell Genome Institute at Washington University School of Medicine. These data will be analyzed to determine previously known as well as potentially novel interpretations. Since the example data are not simulated or arbitrarily filtered, interpretation and visualization will be performed in the context of representative levels of sequence error, and other sources of technical and biological noise.

Session content

Monday 11th - Classes from 09:30 to 17:30 Lecture 1: Introduction to Genomic Data Visualization and Interpretation

* Central dogma * Omic technologies and data * Reference files: GTF, BAM, VCF, MAF, BED, etc * Genome annotation resources, browsers, etc. * Introduction to demonstration data sets

Lab 1: Genome Browsing and Visualization exercises

* IGV o Basics o Creating custom genomes o Sashimi plots * UCSC * Ensembl

Lab 2: Web resources for variant annotation and visualization

* VEP/SnpEff * ProteinPaint * CBioportal * Ensembl BioMart

Tuesday 12th - Classes from 09:30 to 17:30

Lecture 2. Introduction to R for Genomic Data Visualization and Interpretation

Lab 3: Intro to R

* Installation * CRAN and Bioconductor * Data types * Reading and writing Data * Data Frames, slicing, and manipulation * Basic control structures * apply() family of functions * Additional resources

Lab 4: Intro to ggplot

* wide vs long format * geom and aes * axis scaling and manipulation * faceting * themes and colours * ggvis * Additional resources

Lab 5: Real world examples using ggplot

* Heatmaps * Regression lines * Survival analysis * circos

Wednesday 13th - Classes from 09:30 to 17:30

Lab 6. Popular genomic visualizations with GenVisR

* Waterfall plots * TvTi plots * cnSpec plots * cnView

plots * lohSpec plots * genCov plots

Lecture 3: Differential gene expression and pathway analysis

Lab 7: Differential expression analysis

* DEseq2

Thursday 14th - Classes from 09:30 to 17:30

— / —

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

Berlin IntroAdvancedPython Oct-Nov

Dear all,

We are pleased to inform you that we will run two Python courses this year in Berlin:

1. Introduction to Python for biologists. 2-6 October 2017

Instructor: Dr. Martin Jones (founder, Python for biologists: https://www.physalia-courses.org/instructors/t1/)

This course is aimed at all researchers and technical workers with a background in biology who want to learn programming. Students should have enough biological background to appreciate the examples and exercise problems (i.e. they should know about DNA and protein sequences, what translation is, and what introns and exons are). No previous programming experience or computer skills (beyond the ability to use a text editor) are necessary, but you'll need to have a laptop with Python installed.

Syllabus: https://www.physalia-courses.org/courses-workshops/course11/curriculum-11/ For more information: https://www.physalia-courses.org/courses-workshops/course2/ 1. Advanced Python for biologists. 13-17 November 2017

Instructor: Dr. Martin Jones (founder, Python for biologists: https://www.physalia-courses.org/instructors/t1/)

The advanced course is aimed at people who want to develop bigger or more complicated programs in Python, or to learn more about the language, or to explore different approaches (object-oriented, functional) to programming. The material covered is very general purpose and can be applied to any kind of problem. Students should have enough biological/bioinformatics background to appreciate the examples and exercise problems (i.e. they should know what a protein accession number, BLAST report, and FASTA sequence is). They should also have basic Python experience (the Introduction to Python for Biologists course will fulfil these requirements). Students should be familiar with the use of lists, loops, functions and conditions in Python and have written at least a few small programs from scratch.

Syllabus: https://www.physalia-courses.org/courses-workshops/course12/curriculum-12/ For more information: https://www.physalia-courses.org/courses-workshops/course12/ Upcoming courses and workshops:

* Genomic Data Visualization and Interpretation (11-15 September 2017). Instructors: Dr. Malachi Griffith, Dr. Obi Griffith, Mr. Zachary Skidmore (Washington University School of Medicine. USA).

https://www.physalia-courses.org/courses-workshops/course14/ * Statistics for biologists using R (18-23 September 2017). Instructor: Dr. Ken Aho (Idaho State University, USA).

https://www.physalia-courses.org/courses-workshops/course13/ Full list of courses and Workshops: https://www.physalia-courses.org/courses-workshops/

–

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator

info@physalia-courses.org

http://www.physalia-courses.org/ Twitter: @physacourses

mobile: +49 15771084054

https://groups.google.com/forum/#!forum/physalia-courses Carlo Pecoraro <info@physalia-courses.org>

Berlin SingleCellRNAseq Feb5-8

Workshop: Analysis of single cell RNA-seq data

https://www.physalia-courses.org/courses-workshops/course18/ Dates: 5th-9th February 2018

Instructors:

Dr. Vladimir Kiselev (Wellcome Trust Sanger Institute, UK)

Dr. Tallulah Andrews (Wellcome Trust Sanger Institute, UK)

COURSE OVERVIEW

In recent years single cell RNA-seq (scRNA-seq) has become widely used for transcriptome analysis in many areas of biology. In contrast to bulk RNA-seq, scRNA-seq provides quantitative measurements of the expression of every gene in a single cell. However, to analyze scRNA-seq data, novel methods are required and some of the underlying assumptions for the methods developed for bulk RNA-seq experiments are no longer valid. In this course we will cover all steps of the scRNA-seq processing, starting from the raw reads coming off the sequencer. The course includes common analysis strategies, using state-of-the-art methods and we also discuss the central biological questions that can be addressed using scRNA-seq.

WORKSHOP FORMAT

The workshop will be delivered over the course of five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group. Computing will be done using a combination of tools installed on the attendees laptop computer and web resources accessed via web browser.

WHO SHOULD ATTEND

This workshop is aimed at researchers and technical workers who are analyzing scRNA-seq data. The material is suitable both for experimentalists who want to learn more about data-analysis as well as computational biologists who want to learn about scRNASeq methods. Examples demonstrated in this course can be applied to any experimental protocol or biological system.

REQUIREMENTS

The course is intended for those who have basic familiarity with Unix and bash and R scripting languages. We will also assume that you are familiar with mapping and analysing bulk RNA-seq data as well as with the commonly available computational tools.

EXAMPLE DATA

Attendees will learn to process, analyze, visualize and interpret results from one of the Gene Expression Omnibus (GEO) publicly available single cell datasets. These datasets were generated from different organisms and tissues. These data are representative of multiple scRNASeq protocols and various experimental designs. They will be analyzed to determine previously known as well as potentially novel interpretations.

CURRICULUM

Monday 5th - Classes from 09:30 to 17:30

Lecture 1 - scRNA-Seq experimental design and raw data processing

* General introduction Comparison of Bulk and single cell RNA-Seq * Overview of available technologies and experimental protocols * scRNA-Seq experimental design scRNA-Seq general computational workflow * Common single-cell analyses and interpretation

Lab 1 - Processing raw scRNA-Seq data

* File formats: FastQ, BAM, CRAM * Demultiplexing * Reads QC * Read Trimming

Lab 2 - Read alignment

* Alignment using STAR * Alignment using Kallisto

Tuesday 6th - Classes from 09:30 to 17:30

Lecture 2 - Read quantification

* Read & UMI counting * Gene length & coverage * Gene expression units

Lab 3 - Introduction to R/Bioconductor

* Installing packages: CRAN, Bioconductor, github * Data-types * Matrices, Data.frames, Bioconductor classes

Lab 4 - Introduction to scater, ggplot2 and pheatmap

* scater object * Intro to ggplot2 and pheatmap * Visualisation of scRNA-Seq

Wednesday 7th - Classes from 09:30 to 17:30

Interactive Lecture 3 - Expression QC, normalisation and batch correction

* Different normalisation methods * Batch correction methods * Evaluation methods for batch correction

Lab 5 - Analysis of GEO data

* Download data from GEO, create a scater object and perform the analysis above

Thursday 8th - Classes from 09:30 to 17:30

Lecture 4 - Identifying cell populations and Feature selection

* Dimensionality reduction * Clustering * Identifying marker genes * Differential expression *

Validation/follow-up

Lab 6 - Feature selection & Clustering analysis

* Comparison of clustering methods * Comparison of feature selection methods

Lecture 5 - Pseudotime cell trajectories

* Waddington Landscape * Pseudotime inference * Differential expression through pseudotime

Lab 7 - Pseudotime analysis

* Comparison of pseudotime methods

Friday 9th - Classes from 09:30 to 17:30

Lecture 6 - Combining scRNASeq datasets

* Projecting cells to existing reference

Lecture 7 - Review, Questions and Answers. Open discussion

Lab 8 - Analysis of GEO datasets

Lecture 8 - Presentation of results from GEO datasets

— / —

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

---

Berlin StatisticsForBiologistsUsingR Sep18-23 2

Dear all,

we have the last few spots available for the course “STATISTICS FOR BIOLOGISTS USING R” in Berlin (Germany): https://www.physalia-courses.org/courses-workshops/course13/ Dates: 18-23 September 2017

Instructor: Dr. Ken Aho. Dr. Aho is an associate professor at Idaho State University (USA) and author of the book “Foundational and Applied Statistics for Biologists Using R.”

Registration deadline: August 18th , 2017. Attendees are seated on a first-come, first-served basis.

Course overview: This course will demonstrate the extensive capabilities of the R environment, and seek to develop/broaden the competency of participants in the use of R statistical applications. The course will have two components presented in morning and afternoon sessions over five days. Component one (Monday Sept. 18, Tuesday Sept. 19) will emphasize R programming characteristics including data management, use of existing package functions, graphics, customized function writing, calling routines from compiled languages, and documentation. The second component (Wednesday Sept. 20 - Friday Sept. 22) will address implementation of statistical analyses with R, particularly linear models. The materials will be presented using biological examples, making frequent use of the library asbio (Applied Statistics and Statistical Pedagogy for Biologists).

Intended audience: This course is aimed at scientists, particularly biologists. While no previous experience with R is required, participants should have at least a basic familiarity with statistical terms and concepts.

Course programme: https://www.physalia-courses.org/courses-workshops/course13/curriculum-13/ Registration: https://www.physalia-courses.org/courses-workshops/course13/curriculum-13/ Full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ Best regards,

Carlo

–

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 15771084054 https://groups.google.com/forum/#!forum/physalia-courses Carlo Pecoraro <info@physalia-courses.org>

Ghent FunctionalPlantBioinformatics Sep14-15

Workshop FUNCTIONAL PLANT BIOINFORMATICS Organised by ELIXIR Belgium and the VIB Bioinformatics Core

Date: 14-15 September 2017 Location: Ghent, Belgium

Goals This workshop will introduce the basic concepts of comparative and functional -omics data analysis in plants through lectures and practical hands-on sessions. Both plant biologists and geneticists with an interest in bioinformatics, data analysis, and comparative & regulatory genomics should attend this training. After this workshop, you will have a good understanding of the organization and evolution of plant gene families and know how to extract relevant biological information from -omics gene sets.

Summary DAY 1 Introduction plant comparative genomics (genes, gene families, synteny analysis) + introduction PLAZA platform Functional characterization of plant genes (Families, GO, InterPro)

DAY 2 Gene set analysis for different plant -omics data sets: - functional interpretation of RNA-Seq and ChIP-Seq genes using the PLAZA Workbench - co-expression and Transcription Factor analysis

Prerequisites basic knowledge of genes, genomes, transcript profiling, BLAST, homology, Gene Ontology (no programming skills are required).

More info and registration: click here (http://www.vib.be/en/training/research-training/courses/Pages/Functional-Plant-Bioinformatics—PLAZA.aspx)

–

Prof. Dr. Klaas Vandepoele Tel. 32 (0)9 33 13822 VIB Department of Plant Systems Biology, Ghent University Technologiepark 927, 9052 Gent, Belgium

Lab website:http://bioinformatics.psb.ugent.be/cig/ BIG N2N:http://www.bign2n.ugent.be/ Twitter:http://twitter.com/plaza_genomics Klaas Vandepoele <klaas.vandepoele@psb.vib-ugent.be>

Lausanne Statistical Genetics Sep4-15

SWISS INSTITUTE IN STATISTICAL GENETICS

MODULE 1 - BAYESIAN STATISTICS FOR GENETICS

WHERE? University of Lausanne WHEN? 4-6 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Jonathan Wakefield (University of Washington - US) & Prof. Ken Rice (University of Washington - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p=1128&uid=3350 DESCRIPTION: The use of Bayesian methods in genetics has a long history. In this introductory module we will begin by discussing introductory probability. We will then describe Bayesian approaches to binomial proportions, multinomial proportions, two-sample comparisons (binomial, Poisson, normal), the linear model, and Monte Carlo methods of summarization. Advanced topics will be touched on, including hierarchical models, generalized linear models, and missing data. Illustrative applications will include: Hardy-Weinberg testing and estimation, detection of allele-specific expression, QTL mapping, testing in genome-wide association studies, mixture models, multiple testing in high throughput genomics.

MODULE 2 - POPULATION GENETIC DATA ANALYSIS

WHERE? University of Lausanne WHEN? 6-8 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p=1128&uid=3351 DESCRIPTION: A unified treatment for the analysis of discrete genetic data, starting with estimates and sample variances of allele frequencies to illustrate genetic vs statistical sampling and Bayesian approaches. A detailed look at Hardy-Weinberg and linkage disequilibrium, including the use of exact tests with mid-p-values and a new look at X-chromosome Hardy- Weinberg testing. A new characterization of population structure with F-statistics, based on allelic matching within and between populations with individual relationship estimation as a special case. Analyses illustrated with applications to forensic science and association mapping, with particular reference to rare variants.

MODULE 3 - QUANTITATIVE GENETICS

WHERE? University of Lausanne WHEN? 11-13 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Bruce Walsh (University of Arizona - US) & Prof. Guilherme J. M. Rosa (University of Wisconsin - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p=1128&uid=3744 DESCRIPTION: Quantitative Genetics is the analysis of complex characters where both genetic and environment factors contribute to trait variation. Since this includes most traits of interest, such as disease susceptibility, crop yield, growth and reproduction in animals, human and animal behavior, and all gene expression data (transcriptome and proteome), a working knowledge of quantitative genetics is critical in diverse fields from plant and animal breeding, human genetics, genomics, behavior, to ecology and evolutionary biology. The course will cover the basics of quantitative genetics including: genetic basis for complex traits, population genetic assumptions including detection of admixture, Fisher's variance decomposition, covariance between relatives, calculation of the numerator relationship matrix based on IBD alleles and an arbitrary pedigree, the genomic relationship matrix based on AIS alleles, heritability in the broad and narrow sense, inbreeding and crossbreeding, and response to selection. Also an introduction to advanced topics such as: Mixed Models, Best Linear Unbiased Prediction (BLUP), Genomic selection (GBLUP), Genome Wide Association Analysis (GWAS), QTL mapping, detection of selection from genomic data, correlated characters; and the multivariate response to selection.

MODULE 4 - MIXED MODELS IN QUANTITATIVE GENETICS

WHERE? University of Lausanne WHEN? 13-15 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Bruce Walsh (University of Arizona - US) & Prof. Guilherme J. M. Rosa (University of Wisconsin - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p=1128&uid=3745 DESCRIPTION: “Mixed models” refers to the analysis of linear models

— / —

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

---

Lausanne StatisticalGenetics Sep4-15

SWISS INSTITUTE IN STATISTICAL GENETICS

MODULE 1 - BAYESIAN STATISTICS FOR GENETICS

WHERE? University of Lausanne WHEN? 4-6 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Jonathan Wakefield (University of Washington - US) & Prof. Ken Rice (University of Washington - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p28&uid350 DESCRIPTION: The use of Bayesian methods in genetics has a long history. In this introductory module we will begin by discussing introductory probability. We will then describe Bayesian approaches to binomial proportions, multinomial proportions, two-sample comparisons (binomial, Poisson, normal), the linear model, and Monte Carlo methods of summarization. Advanced topics will be touched on, including hierarchical models, generalized linear models, and missing data. Illustrative applications will include: Hardy-Weinberg testing and estimation, detection of allele-specific expression, QTL mapping, testing in genome-wide association studies, mixture models, multiple testing in high throughput genomics.

MODULE 2 - POPULATION GENETIC DATA ANALYSIS

WHERE? University of Lausanne WHEN? 6-8 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p28&uid351 DESCRIPTION: A unified treatment for the analysis of discrete genetic data, starting with estimates and sample variances of allele frequencies to illustrate genetic vs statistical sampling and Bayesian approaches. A detailed look at Hardy-Weinberg and linkage disequilibrium, including the use of exact tests with mid-p-values and a new look at X-chromosome Hardy- Weinberg testing. A new characterization of population structure with F-statistics, based on allelic matching within and between populations with individual relationship estimation as a special case. Analyses illustrated with applications to forensic science and association mapping, with particular reference to rare variants.

MODULE 3 - QUANTITATIVE GENETICS

WHERE? University of Lausanne WHEN? 11-13

September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Bruce Walsh (University of Arizona - US) & Prof. Guilherme J. M. Rosa (University of Wisconsin - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p28&uid744 DESCRIPTION: Quantitative Genetics is the analysis of complex characters where both genetic and environment factors contribute to trait variation. Since this includes most traits of interest, such as disease susceptibility, crop yield, growth and reproduction in animals, human and animal behavior, and all gene expression data (transcriptome and proteome), a working knowledge of quantitative genetics is critical in diverse fields from plant and animal breeding, human genetics, genomics, behavior, to ecology and evolutionary biology. The course will cover the basics of quantitative genetics including: genetic basis for complex traits, population genetic assumptions including detection of admixture, Fisher's variance decomposition, covariance between relatives, calculation of the numerator relationship matrix based on IBD alleles and an arbitrary pedigree, the genomic relationship matrix based on AIS alleles, heritability in the broad and narrow sense, inbreeding and crossbreeding, and response to selection. Also an introduction to advanced topics such as: Mixed Models, Best Linear Unbiased Prediction (BLUP), Genomic selection (GBLUP), Genome Wide Association Analysis (GWAS), QTL mapping, detection of selection from genomic data, correlated characters; and the multivariate response to selection.

MODULE 4 - MIXED MODELS IN QUANTITATIVE GENETICS

WHERE? University of Lausanne WHEN? 13-15 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Bruce Walsh (University of Arizona - US) & Prof. Guilherme J. M. Rosa (University of Wisconsin - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p28&uid745 DESCRIPTION: "Mixed models" refers to the analysis of linear models with arbitrary (co)variance structures among and within random effects and may be due to such factors as relationships or shared environments, cytoplasm, maternal effects and history. Mixed models are utilized 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

MountainLake GrantWriting Jul24-29

Grant Writing Workshop at Mountain Lake Biological Station July 24-29 2017

Mountain Lake Biological Station (MLBS) will offer a 6-day hands-on grant writing workshop targeted at junior scientists who want to learn strategies, styles, and structures to improve their grant proposals. The experience is geared toward early career proposal writers including graduate students, postdocs, and early stage faculty, and will include direct discussions and writing sessions based on participants own proposal ideas. The workshop will be led by former PI and current NSF program officer Leslie Rissler.

The workshop will take place at MLBS, a residential field station atop Salt Pond Mountain in the southern Appalachians. Cost for the workshop is $250, plus room and board. Limited financial aid to defray room and board costs is available. Space in the workshop will be limited to enable close interaction. For more information, or to enroll, please email MLBS Station Manager Jaime Jones (jjones@virginia.edu) or visit MLBS.org.

"Brodie, Edmund Darrell (Butch) (edb9j)" <edb9j@eservices.virginia.edu>

PuertoIguazu Argentina GenomicsBioinformatics Aug6-8

GENOMICS AND BIOINFORMATICS WORKSHOP ORNITHOLOGICAL CONGRESS OF THE AMERICAS - PUERTO IGUAZU, ARGENTINA, AUGUST 6-8 2017 http://www.afonet.org/2017iguazu/site/scientific-program/ Organizers: Scott V. Edwards, Timothy Sackton, Allison Shultz and Gustavo Bravo, (Museum of Comparative Zoology, Harvard University, US), Cecilia Kopuchian, (CECOAL-CONICET, Argentina)

Dates: 6-8 August (3 days)

Registration fee: Free. This workshop is supported by the “Sistema Nacional de Datos Genomicos” from Argentina (MINCYT). There are some travel grants (for flights within Argentina) for attendees of this workshop. To register, send an email before 12 of July to ckopuchian@gmail.com with your name, DNI/Passport number and your position. Travel grant applicants should also send a reduced CV and a short letter of interest in this workshop and why is important for your research or work.

Summary of objectives: Each student should bring his own laptop for practical classes. The objective of this workshop is for students to learn about the different genomic tools available to apply to their own research projects. The course will be taught in English and Spanish.

Requirements: Participants are strongly recommended to bring a laptop, as large sections of the workshop will be hands on. Linux and macs strongly preferred. Some previous experience with R or the linux command line would be helpful, but not required. We will provide software and example datasets; participants should download and install everything prior to the workshop. Links will be provided two weeks prior to the workshop.

Syllabus of topics to be covered: Introduction to genomic methods and marker types. Marker types and what can be done with them: RAD-seq, ultraconserved elements (UCEs), and whole-genome methods. Overview of tools for genomic analysis. Introduction to the UNIX command line. RAD-seq. Overview of RAD techniques. Analysis approaches: Reference genome based, Non-reference based, Quality checks on SNP data. Using command line tools to understand variant call files:Quality checks, Filtering. Population genetics in R. Introduction to R. Tools for analysis of SNP data (adagenet). Principal component analysis and related methods in R. Sequence-capture. Introduction to sequence capture methods and marker types. Using the PHYLUCE pipeline for UCE data. Preprocessing and quality checks. Building alignments. Building phylogenies with species tree methods. Whole-genome approaches. Introduction to whole genome methods: Genome assembly, Transcriptome assembly. Population resequencing: Mapping, filtering and SNP calling. Using genomic data. Population genomics with ANGSD and NGSTools. Argentinean genomic research and resources

Valentina Ferretti, PhD IEGEBA-CONICET Departamento de EcologÃa, Genetica y Evolucion Facultad de Ciencias Exactas y Naturales Universidad de Buenos Aires Pabellon 2 - Ciudad Universitaria Av. Int. Guiraldes 2160, C1428EGA CABA “Ever tried. Ever failed. No matter. Try again. Fail again. Fail better.” ˜Samuel Beckett

Valentina Ferretti <ferrettivale@gmail.com>

Scotland PhylogenticDataAnalysis Paradis Jan28-Feb2

“Phylogenetic data analysis using R”

Delivered by Dr. Emmanuel Paradis

www.prstatistics.com/course/introduction-to-phylogenetic-analysis-with-r-phyg-phyl02/ This course will run from 28th January - 2nd February 2018 at SCENE field station, Loch Lomond, Glasgow.

The main objectives of the course are to teach the theoretical bases of phylogenetic analysis, and to give the ability to initiate a phylogenetic analysis starting from the files of molecular sequences until the interpretation of the results and the graphics. The introduction will cover a brief historical background and an overview of the different methods of phylogenetic inference. Different kinds of data will be considered, but with a special emphasis on DNA sequences. The software used will be based on R and several specialized packages (particularly ape and phangorn). Other software will be used (e.g., MUSCLE or Clustal) called from R. Overall, the course will cover almost all aspects of phylogenetic inference from reading/downloading the data to plotting the results. This course is intended for PhD and postgraduate students, researchers and engineers in evolutionary biology, systematics, population genetics, ecology, conservation.

Course content is as follows Day 1 - Refresher on R: data structures, data manipulation with the indexing system, scripts, using the help system. - Introduction to phylogenetic inference. - Basics on phylogenetic data (sequences, alignments, trees, networks, “splits”) and other data in R. - Reading / writing data from files or from internet. - Matching data. Manipulating labels. Subsetting data. - Main package: ape. Day 2 - Plotting and annotating trees. - Theory of sequence alignment. Comparing alignments. Graphical analyses of alignments. - Main packages: ape (with MUSCLE and Clustal). Day 3 - Theory and methods of phylogeny reconstruction. - Parsimony methods. - Evolutionary distances. - Distance-based methods: General principles and the main methods (NJ, BIONJ, FastME, MVR). - Methods for incomplete distances matrices (NJ*, BIONJ*, MVR*). Methods for combining several matrices (SDM). - Main packages: ape, phangorn. Day 4 - Theory of maximum likelihood estimation. - Application to phylogeny reconstruction. - Substitution models. - Tree space and topology estimation. - Main packages: ape, phangorn. Day 5 - Tree comparison, consensus methods. - Topological space and distances. - Bootstrap. - Bayesian methods.

Please email any inquiries to oliverhooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

PRstatistics upcoming courses - email for details oliverhooker@prstatistics.com for details

1. META-ANALYSIS IN ECOLOGY, EVOLUTION AND ENVIRONMENTAL SCIENCES #METR01 24th - 28th July, Scotland, Prof. Julia Koricheva, Prof. Elena Kulinskaya http://www.prstatistics.com/course/meta-analysis-in-ecology-evolution-and-environmental-sciences-metr01/ 2. SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R #SPAE 7th - 12th August 2017, Scotland, Prof. Jason Matthiopoulos, Dr. James Grecian http://www.prstatistics.com/course/spatial-analysis-ecological-data-using-r-spae05/ 3. ECOLOGICAL NICHE MODELLING USING R #ENMR 16th - 20th October 2017, Scotland, Dr. Neftali Sillero http://www.prstatistics.com/course/ecological-niche-modelling-using-r-enmr01/ 4. GENETIC DATA ANALYSIS AND EXPLORATION USING R #GDAR 23rd - 27th October, Wales, Dr. Thibaut Jombart, Zhian Kavar http://www.prstatistics.com/course/genetic-data-analysis-exploration-using-r-gdar03/ 5. STRUCTURAL EQUATION MODELLING FOR ECOLOGISTS AND EVOLUTIONARY BIOLOGISTS USING R #SEMR 23rd - 27th October, Wales, Prof Jarrett Byrnes, Dr. Jon Lefcheck http://www.prstatistics.com/course/structural-equation-modelling-for-ecologists-and-evolutionary-biologists-semr01/ 6. LANDSCAPE (POPULATION) GENETIC DATA ANALYSIS USING R #LNDG 6th - 10th November, Wales, Prof. Rodney Dyer http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg02/ 7. APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS #ABME

— / —

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

---

Trento Italy MachineLearningForBiologists Sep4-7

Please circulate this email to those who might be interested.

ELIXIR-IIB, in collaboration with Fondazione Bruno Kessler and Fondazione E. Mach, Trento, Italy, is pleased to announce the upcoming training course on “Machine Learning for Biologists”.

IMPORTANT DATES: *Deadline for applications*: 21 July 2017 *Course date*: 4-7 September 2017

Selected participants will be notified by 25 July 2017. A maximum of 24 candidates will be accepted in the course. Priority will be given to candidates from ELIXIR-IIB member institutions and ELIXIR nodes.

VENUE: Fondazione Edmund Mach, Palazzo della Ricerca e della Conoscenza, Via E. Mach 1, San Michele all’Adige (TN), Italy, (zip code 38010).

Full details at: https://elixir-iib-training.github.io/website/2017/09/04/ MachineLearning-Trento.html

COURSE DESCRIPTION: The aim of the course is to provide a practical introduction to the analysis of “omics” data. Topics will range from data visualization/exploration to univariate/multivariate analysis and machine learning. Practical exemples and applications will be illustrated by using R and Python.

COURSE MILESTONES: - Data exploration and visualization - Univariate/Multivariate analysis - Introduction to machine learning: classifiers, performance measures, diagnostics - Machine learning tools for the analysis of Gene Expression data - The Data Analysis Plan (DAP) - intro to unbiased pipelines for (binary) classification - Performance measures and diagnostic plots - Accuracy, MCC, Stability: theory and graphics - Differential network analysis - co-expression networks, graph comparison, community detection: theory and examples in R/Python, visualization by the igraph library and use of the ReNette web interface - Basic application of ML to gene prediction

Should you have any question, do not hesitate to contact the ELIXIR-IIB Training Team (elixir.ita.training@gmail.com) and/or the local organiser Dr. Alessandro Cestaro (alessandro.cestaro@fmach.it).

Thank you for your interest,

The Organisers and the ELIXIR-IIB Training Team
Alessandro Cestaro (Fondazione E. Mach, Trento, Italy)
Vincenza Colonna (ELIXIR-IIB Training Team)

* * * Vincenza Colonna, PhD http://www.igb.cnr.it/-popgenlab Consiglio Nazionale delle Ricerche Istituto di Genetica e Biofisica "Adriano Buzzati-Traverso" piano 1, stanza 20 -via Pietro Castellino 111 - 80131 Napoli - IT

tel +39 081 6132 254 - fax +39 081 6132 706 - skype enza.colonna email vincenza.colonna@igb.cnr.it google scholar < http://goo.gl/SzimG0 >

—-

would you like to know about the most amazing project ever? http://www.igb.cnr.it/obilab ——- interested in Life Science and/or Mathematics? visit http://www.bmtl.it/ vincenza colonna <vincenza.colonna@igb.cnr.it>

UCollege London GWAS DataAnalysis Sep5

Understanding the genetic architecture of complex traits through SNP-based heritability analysis

Date: Tuesday 5th September, University College London, 10-4pm

Tutors: Prof David Balding (Melbourne and UGI) and Dr Doug Speed (UGI)

Cost: 40 (or 30 for UCL Members)

Advance Registration is REQUIRED

https://www.eventbrite.com/e/ucl-genetics-short-course-methods-for-analysing-complex-trait-gwas-data-tickets-36314483598 *—- *

*Background: *In recent years there has been great progress in developing genome-wide statistical analyses for detecting causal variants, constructing prediction models and better understanding the genetic architecture of complex traits. However the underlying regression model involves very large numbers of predictors, and strong modelling assumptions are required to tackle the consequent problem of over-fitting. The results can be sensitive to these assumptions, and also to the effects of population structure, genotyping errors and the extent to which rare SNPs are included.

*Course outline: *We will cover mixed-model association analysis (e.g., Fast-LMM, GEMMA), risk prediction (e.g., polygenic risk scores, BLUP and MultiBLUP) and heritability analyses (GCTA, LDAK, LDSC), both using individual-level genetic data and summary statistics. We will emphasise the common elements of these methods, highlighting a standard framework that has emerged for genome-wide SNP analysis, while also contrasting the differences in underlying modelling assumptions.

The practicals will provide step-by-step details for analysing genetic data, starting either with indvidual-level data (e.g., PLINK files or the output from IMPUTE2) or summary statistics (p-values from a GWAS). There will be a selection of worked examples; to take part in the practicals, participants should bring a laptop with either MAC or LINUX OS

Prerequisites: Participants should be proficient in statistics including some familiarity with random-effects regression models. In genetics, knowledge of SNP genotypes and Hardy-Weinberg and linkage equilibrium will be assumed. Computer scripts and output will be discussed that assume some familiarity with scientific computing using linux. Some familiarity with PLINK would be helpful but is not essential.

**

*—-

Provisional Timetable

10:00 - 12:40: Lecture 1 followed by Practical 1

Introduction to analysing GWAS data, including QC, single-SNP analysis,polygenic risk scores, mixed-model analysis and gene-based analysis

12:40 - 13:20: Lunch

13.20-16:00: Lecture 2 followed by Practical 2

Estimating heritability, bivariate correlations and enrichment of functional categories

Room details will be provided closer to the time; any questions, email doug.speed@ucl.ac.uk

Doug Speed <doug.speed@ucl.ac.uk>

UEdinburgh IntroductionPython Sep11-15

INTRODUCTION TO PYTHON FOR BIOLOGISTS

DATE: Monday 11 - Friday 15 September 2017

VENUE: The King's Buildings, The University of Edinburgh, Edinburgh, Scotland, UK

REGISTRATION DEADLINE: Monday 28 August 2017 noon

CANCELLATION DEADLINE: Monday 4 September 2017 noon

PLACES: 20 (first come, first served)

REGISTRATION FEE: ????525 (includes coffee/tea, but no lunch)

INFORMATION: Bert Overduin (bert.overduin@ed.ac.uk), Martin Jones (martin@pythonforbiologists.com)

TO REGISTER: http://genomics.ed.ac.uk/services/-introduction-pyt hon-biologists

Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at complete beginners and assumes no prior programming experience. It gives an overview of the language with an emphasis on practical problem-solving, using examples and exercises drawn from various aspects of bioinformatics work. The workshop is structured so that the parts of the language most useful for bioinformatics are introduced as early as possible, and that students can start writing plausibly-useful programs after the first few sessions. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackling problems in their own research and (2) continue their Python education in a self-directed way.

"Great learning from someone with a biology background rather than computer science - meant we were on the same wavelength." (February 2016) "Brilliantly well-run. From the book; to the USB stick with all the files we need; to the topics covered; to the system of helping us one-on-one, I cannot fault this course." (February 2016)

INSTRUCTORS Dr. Martin Jones (Founder, Python for Biologists) Dr. Bert Overduin (Training and Outreach Bioinformatician, Edinburgh Genomics)

WORKSHOP FORMAT The workshop is delivered over ten half-day sessions. Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organiser's discretion. Each session uses examples and exercises that build on material from the previous one, so it's important that students attend all sessions. A description of the sessions can be found at the bottom of this page.

WHO SHOULD ATTEND This workshop is aimed at researchers and technical workers with a background in biology who want to learn programming. The syllabus has been planned with complete beginners in mind; people with previous programming experience are welcome to attend as a refresher but may find the pace a bit slow. If in doubt, take a look at the detailed session content below or drop Martin Jones or Bert Overduin an email.

REQUIREMENTS Students should have enough biological/bioinformatics background to appreciate the examples and exercise problems (i.e. they should know what a protein accession number, BLAST report, and FASTA sequence is).

No previous programming experience or computer skills (beyond the ability to use a text editor) are necessary. During the workshop students will use their own laptops. Instructions for any software to be installed will be sent out prior to the course.

SESSION CONTENT 1. Introduction In this session I introduce the students to Python and explain what we expect them to get out of it and how learning to program can benefit their research. I explain the format of the course and take care of any housekeeping details (like coffee breaks and catering arrangements). I outline the edit-run-fix cycle of software development and talk about how to avoid common text editing errors. In this session, we also check that the computing infrastructure for the rest of the course is in place (e.g. making sure that everybody has an appropriate version of Python installed). Core concepts introduced: source code, text editors, whitespace, syntax and syntax errors, Python versions 2. Manipulating text In this session students learn to write very simple programs that produce output to the terminal, and in doing so become comfortable with editing and running Python code. This session also introduces many of the technical terms that we'll rely on in future sessions. I run through some examples of tools for working with text and show how they work in the context of biological sequence manipulation. We also cover different types of errors and error messages, and learn how to go about fixing them methodically. Core concepts introduced: terminals, standard output, variables and naming, strings and characters, special characters, output formatting, statements, functions, methods, arguments, comments.

3. Working with files I introduce this session by talking about the importance of files in bioinformatics pipelines and workflows, and we then explore the Python interfaces for reading from and writing to files. This involves

— / —

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

UK ModellingForEvolutionaryBiol Oct23-27

"Structural Equation Modelling for Ecologists and Evolutionary Biologists"

Delivered by Dr. Jarret Byrnes and Dr. Jon Lefcheck

www.prstatistics.com/course/structural-equation-modelling-for-ecologists-and-evolutionary-biologists-semr01/ This course will run from 23rd - 27th October 2017 at Margam Park Discovery Centre, Wales, UK

Course only and all inclusive packages are available.

The course is a primer on structural equation modelling (SEM) and confirmatory path analysis, with an emphasis on practical skills and applications to real-world data.

Structural Equation Modelling (SEM) is a rapidly growing technique in ecology and evolution that unites multiple hypotheses in a single causal network. It provides an intuitive graphical representation of relationships among variables, underpinned by well-described mathematical estimation procedures. Several advances in SEM over the past few years have expanded its utility for typical ecological datasets, which include count data, missing observations, and nested or hierarchical designs. We will cover the basic philosophy behind SEM, provide approachable mathematical explanations of the techniques, and cover recent extensions to mixed effects models and non-normal distributions. Along the way, we will work through many examples from the primary literature using the open- source statistical software R (www.r-project.org). We will draw on two popular R packages for conducting SEM, including lavaan and piecewiseSEM. Participants are encouraged to bring their own data, as there will be opportunities throughout the course to plan, analyse, and receive feedback on structural equation models.

Course content is as follows

Day 1 Introduction to SEM Module 1: What is Structural Equation Modeling? Why would I use it? Module 2: Creating multivariate causal models Module 3: Fitting piecewise models Readings: Grace 2010 (overview), Whalen et al. 2013 (example)

Day 2 SEM Using Likelihood Module 4: Fitting Observed Variable models with covariance structures Module 5: What does it mean to evaluate a multivariate hypothesis? Module 6: Latent Variable models Module 7: ANCOVA revisited & Nonlinearities Readings: Grace & Bollen 2005, Shipley 2004 Optional Reading: Pearl 2012, Pearl 2009 (causality)

Day 3 Piecewise SEM Module 8: Introduction to piecewise approach Module 9: Incorporation of random effects models Model 10: Autocorrelation Reading: Shipley 2009; Lefcheck 2016

Day 4 Advanced Topics with Likelihood and Piecewise SEM Module 11: Multigroup models and nonlinearities Module 12: Composite Variables Module 13: Phylogenetically-correlated data Module 14: Prediction using SEM Module 15: How To Reject A Paper That Uses SEM Readings: Grace & Julia 1999, von Hardenberg & Gonzalezâ2013

Day 5 Open Lab and Final Presentations

Please email any inquiries to oliverhooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

---

PR stats other courses

1. META-ANALYSIS IN ECOLOGY, EVOLUTION AND ENVIRONMENTAL SCIENCES #METR01 24th - 28th July, Scotland, Prof. Julia Koricheva, Prof. Elena Kulinskaya http://www.prstatistics.com/course/meta-analysis-in-ecology-evolution-and-environmental-sciences-metr01/ 2. SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R #SPAE 7th - 12th August 2017, Scotland, Prof. Jason Matthiopoulos, Dr. James Grecian http://www.prstatistics.com/course/spatial-analysis-ecological-data-using-r-spae05/ 3. ECOLOGICAL NICHE MODELLING USING R #ENMR 16th - 20th October 2017, Scotland, Dr. Neftali Sillero http://www.prstatistics.com/course/ecological-niche-modelling-using-r-enmr01/ 4. GENETIC DATA ANALYSIS AND EXPLORATION USING R #GDAR 23rd - 27th October,

Wales, Dr. Thibaut Jombart, Zhian Kavar http://www.prstatistics.com/course/genetic-data-analysis-exploration-using-r-gdar03/ 5. STRUCTURAL EQUATION MODELLING FOR ECOLOGISTS AND EVOLUTIONARY BIOLOGISTS USING R #SEMR 23rd - 27th October, Wales, Prof Jarrett Byrnes, Dr. Jon Lefcheck http://www.prstatistics.com/course/structural-equation-modelling-for-ecologists-and-evolutionary-biologists-semr01/

— / —

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

---

Vienna ExperimentalEvolution Nov6-10 2

Dear colleagues,

a reminder about the upcoming Experimental Evolution course in Vienna, Austria:

The Vienna Graduate School of Population Genetics is now accepting applications for the course "Experimental evolution: From theory to practice" at the University of Veterinary Medicine in Vienna, November 6-10, 2017.

Experimental evolution is extensively used to address questions of evolutionary biology by exposing evolving populations to different environmental conditions. It offers the opportunity to replicate experiments and test for convergent outcomes. With the recent drop in DNA sequencing cost and the advance of sequencing technologies, the combination of experimental evolution with next generation sequencing of pools of individuals (Evolve & Resequence) has become a state-of-the-art method to link phenotypic responses to genetic changes. Although the availability of replicated time series data is one key advantage of E&R, the analysis of such data sets is still in its infancy. This course will introduce the participants to several new approaches for the analysis of genomic time series data covering the latest software tools as well as required statistical and computational skills. The course is targeted towards researchers interested in experimental evolution combined with NGS and will cover the design of experimental evolution studies as well as the analysis of Pool-Seq time series data.

The course aims to introduce participants to:

State-of-the-art software packages Modeling of neutral data Identifying selected regions Comparison of n-point analysis with time series data Inferring linkage structure of Pool-Seq data Estimating selection coefficients Calling transposable elements in time series data Inferring selection in transcriptomics data

Morning lectures by internationally renowned faculty will be followed by computer practicals on the analysis of experimental evolution data in the afternoon.

Faculty:

Jeffrey E. Barrick (The University of Texas at Austin, US) Anthony M. Dean (University of Minnesota, US) Tadeusz J. Kawecki (University of Lausanne, CH) Christian Schlötterer (Vetmeduni Vienna, A) Marina Telonis-Scott (Monash University, AUS) Olivier Tenaillon (French Institute for Medical Research, FR) Henrique Teotonio (IBENS, FR)

The course is free but will be restricted to a maximum of 15 participants for the practical sessions (hands on computer lab). Additional seats will be available for attending the lectures, only. Students and researchers are invited to apply by submitting a single .pdf file containing 1) a short CV, 2) a motivation letter and a statement of computer skills to popgen.vienna@gmail.com by August 15, 2017. Confidence in working with Unix command line as well as in R, is strongly recommended for the practicals. Participants are expected to arrange their own accommodation.

Further information and updates available at http://www.popgen-vienna.at/training/experimental-evolution-2017.html – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at https://twitter.com/PopGenViennaPhD c/o Institut für Populationsgenetik Veterinärmedizinische Universität Wien (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@vetmeduni.ac.at

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.