EvolDir

February 1, 2016

Month in Review

Foreword

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

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

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

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Conferences

Ascona Switzerland EvolutionaryChange Jun5-9

In association with ETH Zurich's Center for Adaptation to a Changing Environment (ACE), we are writing to announce a conference on the 'Genomic basis of eco-evolutionary change.' The conference will take place this summer from June 5th - June 9th 2016 at the Monte Verità conference centre, located near Ascona in Switzerland.

The aim of this conference is to connect burgeoning information on the genomic basis of ecologically relevant traits to better understand and predict the dynamics of eco-evolutionary feedbacks.

The conference will bring together speakers from around the world to discuss recent developments in the genomics of ecologically relevant traits, the eco-evolutionary dynamics of species interactions and species responses to environmental change. Through talks, break-out sessions, and informal interactions, the participants will develop a research agenda for a genomics-based, predictive understanding of eco-evolutionary change.

Confirmed speakers: Frédéric Guillaume Andrew Hendry Nelson Hairston Hannah Kokko Tom Mitchell-Olds Patrik Nosil Ole Seehausen Daniel Wegmann Yvonne Willi

As the number of participants is limited to 73 scientists, we ask all applicants interested in the conference to send their curriculum vitae (max. 2 pages) and a motivation letter (max. one page) containing a description of their specific field of research, motivation to participate in the conference and an abstract of a poster to be presented at the meeting. We especially encourage early career scientists (PhDs and Postdocs) to apply.

Please send your application, all in one PDF, by the 21st of February to monte-verita@env.ethz.ch.

The costs, including the conference fee, accommodation and full board will be 1200 Swiss francs. In addition, participants must pay their travel costs.

For more information, please visit: http://www.adaptation.ethz.ch/education/monte-verita-conference2016.html Best wishes, The organising committee

James Buckley Katalin Csillery Robert Dunner Jonathan Levine Martin Turcotte Alex Widmer

"james.buckley@env.ethz.ch" <james.buckley@env.ethz.ch>

Austria InformationInSystemsBiology May18-20

Dear Colleagues,

We are now accepting applications for the IPISB 2016 conference on the use of probabilistic methods (stochastic modeling, inference, information theory, decision-making, control theory) in systems, synthetic, and evolutionary biology, to be held at the Institute of Science and Technology Austria (IST Austria), May 18-20, 2016.

Organizational details, registration and poster abstract submission form are available at the conference website:

http://ist.ac.at/ipisb/ Early registration deadline is March 31; late registration deadline April 30, 2016.

Invited speakers:

James Briscoe, Francis Crick Institute Frank Bruggeman, VU Amsterdam Johan Elf, Uppsala University Hana El-Samad, UC San Francisco Thomas Gregor, Princeton University Pascal Hersen, Univ. Paris Diderot Dagmar Iber, ETH Zurich Mustafa Khammash, ETH Zurich Edo Kussell, New York University Michael Lassig, University of Cologne Thierry Mora, ENS Paris Erik van Nimwegen, Biozentrum Basel Olivier Rivoire, University of Grenoble David Schwab, Northwestern University Udo Seifert, University of Stuttgart Guy-Bart Stan, Imperial College London Pieter Rein ten Wolde, AMOLF Amsterdam Aleksandra Walczak, ENS Paris Roy Wollman, UC San Diego

Please feel free to forward this information to anyone who you think might be interested in attending.

We hope to see you at the meeting at IST Austria and best regards,

Gasper Tkacik (IST Austria) gasper.tkacik@ist.ac.at Peter Swain (University of Edinburgh)

Nick BARTON <nick.barton@ist.ac.at>

Beijing PlantEvoDevo May15-19

15-19 May 2016

37th New Phytologist Symposium: Plant developmental evolution

https://newphytologist.org/symposia/37 Beijing, China

Travel grant submission deadline: Thursday 25th February 2016

Poster abstract submission deadline: Thursday 17th March 2016

The relatively new field of plant evolutionary-developmental biology ('evo-devo') seeks to understand how and why plant morphological characters have evolved to produce the tremendous diversity of form in living plants. This meeting will draw together researchers in plant evo-devo for exchange of ideas, current research, and discussion of future directions for the field.

Sessions: floral development; vegetative meristems, leaves, and inflorescences; plasticity and life history evo-devo; selected poster abstract talks.

Eighteen leading scientists will speak at the Symposium. We hope that this will stimulate focused discussion and the exchange of ideas at what will be a relatively small (around 120 delegates) and informal meeting. There will be a poster session, selected talks, discussion and a conference dinner.

Keynote speakers: Beverley Glover, University of Cambridge, UK; Mark Rausher Duke University, USA; Miltos Tsiantis, Max Planck Institute for Plant Breeding Research, Germany.

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Call for Symposia Got a great idea for your own symposium? The New Phytologist Trust is accepting proposals for symposia funding up to £43,000, for 2018 onwards. The deadline for proposals is 28th February 2016. Read more here: https://www.newphytologist.org/news/view/113 Dr Mike Whitfield Development Coordinator, New Phytologist

New Phytologist Central Office, Bailrigg House, Lancaster University, Lancaster, LA1 4YE, UK Tel: + 44 1524 592839; Fax: + 44 1524 594696 www.newphytologist.org Twitter: @NewPhyt Facebook: fb.com/NewPhytologist

The New Phytologist Trust, registered charity number 1154867

2014 Impact factor 7.672

Special and Feature Issues: Evolutionary plant radiations // Eucalyptus genome // Ecology and evolution of mycorrhizas

New Phytologist Symposia 2016 Plant developmental evolution (Beijing, China) // Colonisation of the terrestrial environment 2016 (Bristol, UK)

m.whitfield@lancaster.ac.uk

Cambridge PathogenHostShifts Apr12

Meeting: Pathogen Host Shifts, Cambridge UK, 12th April 2016

The meeting will cover the ecology, evolution, mechanisms, immunity and epidemiology underlying pathogen host shifts. The meeting aims to bring together a broad range of researchers working on this important topic, to discuss their work and develop collaborations. Full details can be found here http://www.infectiousdisease.cam.ac.uk/-events-and-training/pathogen-host-shifts-workshop The meeting is sponsored by Cambridge Infectious Diseases, the Genetics Society and the British Ecological Society Parasite and Pathogens special interest group.

Invited speakers include:

Kate Jones, Biodiversity Modelling Research Group, UCL

Marco Vignuzzi, Pasteur Institute, Paris

Wendy Barclay, Imperial College London

Santiago Elena, Instituto de Biología Molecular y Celular de Plantas

Lucy Weinert, University of Cambridge

Daniel Streicker, University of Glasgow

Ian Goodfellow, University of Cambridge

Registration fees: Â£8 students, Â£15 PIs and Postdocs- includes lunch and refreshments. We will also be accepting abstracts for talks and posters (submission deadline 6th March)- if you would like to submit an abstract please fill in the form on the event website. We particularly encourage submissions from female researchers to ensure a 50:50 sex ratio amongst speakers.

http://www.infectiousdisease.cam.ac.uk/events-and-training/pathogen-host-shifts-workshop – Ben Longdon Department of Genetics University of Cambridge +44 (0) 1223 333945 b.longdon@gen.cam.ac.uk http://-benlongdon.wordpress.com "bjl48@hermes.cam.ac.uk" <bjl48@hermes.cam.ac.uk>

Clearwater Florida DiseaseEvol Mar23-25

Dear colleagues,

We are very pleased to announce the launch of a new NIH/BBSRC funded Research Coordination Network on the role of Vector Behaviour in Transmission Ecology: VectorBiTE.

Over the next 5 years, this RCN will support annual meetings and workshops to promote collaborative research and training in order to improve our understanding of how the behavioural ecology of vectors impacts disease transmission. Additionally, a key component of this effort will be the creation of a global database on vector traits, population dynamics and transmission rates. For more information on our network goals please see: http://vectorbite.org/ Our first meeting will take place at in Clearwater, FL from March 23-25, 2016. During this first meeting we will organize participants into working groups and plan the online repository structure. Please register for the RCN on the website and apply for the meeting at http://vectorbite.org/. We plan to provide travel support for approximately 40 participants to attend. Applications received by February 1 will receive full consideration, although will continue to evaluate applications on a rolling basis until all spaces have been filled. We are pleased to begin this new adventure and look forward to providing a new platform for interaction in this important area.

Exciting times ahead!

Best wishes,

Leah Johnson, Lauren Cator, Erin Mordecai, Samraat Pawar, and Pete Hudson "l.cator@imperial.ac.uk" <l.cator@imperial.ac.uk>

Durham NorthCarolina EvolutionMedicine Jun22-25 2

The International Society for Evolution, Medicine & Public Health 2nd Annual Meeting will be held in Durham, North Carolina from June 22-25, 2016. ISEMPH 2016 brings together scientists, teachers, clinicians, and students in the evolution and medicine community to share ideas and create new connections that will advance the field. This open meeting is designed to bridge the many different disciplines where relevant research takes place, including infectious disease, public health, genetics, anthropology, psychology, oncology, ecology, and veterinary medicine.

Plenary speakers for the 2016 ISEMPH Meeting are Andrea Graham (Princeton University), Carl Zimmer (New York Times), Helen Ball (Durham University, UK), Joshua Schiffman (University of Utah), Marion Koopmans (Erasmus University, Rotterdam), and Martin Blaser (New York University).

Registration is currently open. Deadline for Abstract submission and early registration is January 30, 2016. For more information: http://evolutionarymedicine.org/isemph2016/ Travel awards are available for a limited number of students and junior faculty attending the meeting. The Travel Awards Committee will consider demonstrated interest, ability, need, and diversity. The Society would especially like to support participants from under-represented groups in the sciences and those from minority serving institutions, such as Historically Black Colleges and Universities. Travel Award application deadline is February 15, 2016.

For more info on travel awards, please see http://evolutionarymedicine.org/2016-isemph-travel-awards/ Jory P. Weintraub, Ph.D. Science Communication Director, Duke Initiative for Science & Society Senior Lecturing Fellow Duke University 304 Research Drive Box 90222 Durham, NC 27708-0222 (919) 668-0792 jory@duke.edu Skype: jory.weintraub [cid:55C7BCE5-D4C9-4381-92B7-F53A6AADF412]

Jory Weintraub <jory@duke.edu>

Madison Wisconsin ICQG5 QuantGenetics Jun12-17

ICQG5 - Madison, WI, USA - June 12-17, 2016 The 5th International Conference on Quantitative Genetics (ICQG5) will be held in Madison - Wisconsin, USA, during June 12-17, 2016 (www.icqg5.org) The registration page is now open so go ahead and secure your spot by registering as soon as possible! Early bid deadline is March 25, 2016 (midnight US Central Daylight Time). On the ICQG5 website you will find also links to hotels nearby the Conference venue. Hope to see you all in beautiful Madison in June! Sincerely, Guilherme (ICQG5 co-chair)

Guilherme J. M. Rosa University of Wisconsin - Madison 436 Animal Science Building 1675 Observatory Dr. Madison, WI 53706 USA Phone: + 1 (608) 265-8617 Fax: + 1 (608) 263-9412 E-mail: grosa@wisc.edu Webpage: http://www.ansci.wisc.edu/Facultypages/rosa.html GUILHERME J M ROSA <grosa@wisc.edu>

Marseilles EvolutionaryBiology Sep20-23 DeadlineJan31

Dear All The early dead line for the, 20th Evolutionary Biology Meeting at Marseilles (September 20-23 2016), is January 31 2016

The following subjects will be discussed:

Evolutionary biology concepts and modeling;

Biodiversity and Systematics;

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

Functional phylogeny;

Environment and biological evolution;

Origin of life and exobiology;

Non-adaptative versus adaptative evolution;

The "minor" phyla: their usefulness in evolutionary biology knowledge; Convergent evolution Evolution of complex traits (Evo-Devo) more info: http://sites.univ-provence.fr/evol-cgr/ or http://aeeb.fr/?page_id=3D333 best regards Pierre Pontarotti

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

MiamiU Ohio MidwestEcolEvolution MEEC Mar19-20

Dear colleagues,

We are excited to announce that the 2016 Midwest Ecology and Evolution Conference (MEEC) will be held March 19-20, 2016 at Miami University in Oxford, Ohio.

MEEC is a unique conference organized and operated by graduate students at a different Midwestern university each year. This conference is graduate and undergraduate student-focused, providing opportunities to interact with and learn from colleagues in a professional environment.

Along with oral and poster sessions, MEEC will include professional development panel sessions and tours of nearby natural areas and research facilities. We are also looking forward to plenary talks by Dr. Tia-Lynn Ashman (University of Pittsburgh) and Dr. Catherine Searle (Purdue University). Abstract submission and registration will be from February 1-29, 2016.

Additionally, the MEEC committee is working to compile a list of previous MEECs and their locations. If you have attended MEEC in the past, please contact the committee with the year and location of the conference (email address below). We are especially trying to fill in conferences in the 1980s and 1990s. Our website includes a list of the dates and locations we have found so far (https://meec2016.wordpress.com/general-information/).

We hope that you can join us for MEEC 2016! Please check our website (https://meec2016.wordpress.com/-) or Facebook page (https://www.facebook.com/-MEEC.conference/) for more information. Questions can be directed to the planning committee at meec2016@gmail.com.

Best,

MEEC 2016 Committee

Richard Moore <moorerc@miamioh.edu>

Montpellier MathCompEvolutionaryBiology Jun12-16

*** REGISTER AGAIN IF YOU DIDNT RECEIVE ANY CONFIRMATION EMAIL *** OUR WEBSITE HAD MALFUNCTIONS, SORRY ...

*** PLEASE DIFFUSE THIS ANNOUNCEMENT, THANKS!

MCEB - Mathematical and Computational Evolutionary Biology 12-16 June 2016 - Hameau de l'Etoile, Montpellier, South of France.

Webpage: http://www.lirmm.fr/mceb2016/ Pre-registration deadline: February 25th Notification to applicants: March 15th Final list of attendees: April 15th

Scope: Mathematical and computational tools and concepts form an essential basis for modern evolutionary studies. The goal of the MCEB conference (at its 8th edition) is to bring together scientists with diverse backgrounds to present recent advances and discuss open problems in the field of mathematical and computational evolutionary biology. The theme of this year's edition will be "forecasting evolution": while most analyses are designed to reconstruct the past in order to understand evolution, our modern society is in dire need of anticipating the future using sound scientific approaches. This is particularly true in the context of global warming and more generally global changes. New approaches that model future evolution are emerging, for example to predict epidemics, evolution of cancer, shifts in species/population distributions or species loss. Evolutionary biology is thus widening its focus, trying to predict future biological states and better define the range of applicability of these predictions. Making progress in this new research area will involve cross-disciplinary approaches, accurate statistical methods, and powerful computational techniques. Beyond this year's theme, general concepts, models, methods and algorithms will be presented and discussed, just as in the previous editions of MCEB. Keynote speakers will introduce a field of research and discuss their own work in this field. Afternoon will be for short presentations and posters, with plenty of time for discussions and outdoors.

Where and when: Hameau de l'Etoile, near Montpellier, in the South of France, 12-16 June 2016.

Cost: Conference fees including accommodation for four nights, meals, coffee breaks, buses, etc., will be between 300 and 550, all inclusive, and will vary depending on the room. PhD students and postdocs will benefit of the cheapest rooms.

Keynote speakers: Jeffrey Jensen - http://jensenlab.epfl.ch/ Ecole Polytechnique Fédérale de Lausanne, CH

Laura S. Kubatko - http://www.stat.osu.edu/~lkubatko/ Departments of Statistics and Evolution, Ecology, and Organismal Biology - The Ohio State University, USA

Amaury Lambert - http://www.proba.jussieu.fr/pageperso/amaury/index.htm Stochastics & Biology Group - Laboratoire de Probabilités & Modèles Aléatoires - UPMC - Université Paris 06, FR

Richard Neher - https://neherlab.wordpress.com/ Max Planck Institute for Developmental Biology - DE

Bruce Rannala - http://www.rannala.org/?page_id=111 UC Davis - University of California, USA

Isabel Sanmartín Bastida - http://www.rjb.csic.es/jardinbotanico/jardin/contenido.php?Pag=386&tipo=cientifico&cod=98&len=en

Real Jardín Botánico (RJB-CSIC), Madrid, SP

Yun S. Song - http://www.eecs.berkeley.edu/~yss/ Departments of Mathematics and Biology - Universty of Pennsylvania, USA

For more information and register: http://www.lirmm.fr/mceb2016/ Please forward this announcement

Olivier Gascuel <gascuel@lirmm.fr>

NorthCarolinaStateU EmergingPlantDisease Mar23-24

Event Title: A Symposium on Emerging Plant Disease and Global Food Security

Event Date & Time: Wednesday, March 23, 2016 at 9:00 AM to Thursday, March 24, 2016 at 4:00 PM

Event Description:

The Emerging Plant Disease and Global Food Security Chancellors Faculty Excellence Program cluster at NC State will host an international symposium March 23-24, 2016 in Raleigh, to bring together experts that study emerging plant diseases and their arthropod vectors. Managing the threats of emerging diseases that affect agricultural crop plants requires experts in genetics, biology, epidemiology, evolutionary biology, climate change, metadata analysis, geospatial analytics and global development policy.

We will synthesize new developments on emerging plant disease biology and discuss an expanding array of new technologies to gather, analyze, synthesize, and share knowledge about the evolution of emerging infectious diseases of plants that affect global food security. Four sessions with keynote speakers, a closing panel and posters are planned.

Location: Hunt Library

URL: https://www.ncsu.edu/mckimmon/cpe/opd/EPD/agenda.html *Contact:* Jean Ristaino Jean_Ristaino@ncsu.edu 919 515-3257

You may also view this event on the calendar < http://harvest.cals.ncsu.edu/dean/index.cfm?pageID=10569&eventid=16201&FromEmail=jbr@ncsu.edu >.

Jean <jbr@ncsu.edu>

OxfordUK InsectSymbionts Mar15

Royal Entomological Society Special Interest Group on Insect Symbionts

15th March 2016 in Oxford, UK

Invited speaker: Prof Christoph Vorburger, EAWAG, Switzerland

This meeting is open to researchers studying any aspect of insect endosymbiosis.

Registration costs £10 (including lunch and refreshments). Further details and registration information are here: http://www.royensoc.co.uk/content/endosymbiont-special-interest-group-meeting-15th-march-2016 Offers for contributed talks (15 minutes) or posters are welcome (deadline 20th February). Please email abstracts (250 words) and meeting queries to ailsa.mclean@zoo.ox.ac.uk; registration to kirsty@royensoc.org.

ailsa.mclean@gmail.com

Roscoff France 50yrsMolecularHistory May9-13 Reminder

Thereis only one month left to apply to the Jacques Monod conference on molecularevolution in May 2016. We particularly encourage the application ofPhD students. Note that the inscription fees listed below include board andlodging. Selected applicants will be expected to present a poster.

Molecules as documents of evolutionary history: 50 years after - Roscoff, Brittany, France.

May 9-13 2016

Itis with the popularization of molecular tools and the disclosure ofgenome sequences that evolutionary models have become decisive in biology,in part because this information is simply so abundant and socomplex that only a comparative method could reveal its meaning. In2016, it will be 50 years that Emile Zuckerkandl and Linus Pauling havelaid the foundation of molecular phylogeny, and molecular evolution ingeneral, in their seminal article entitled “Molecules as documents ofevolutionary history”. The fundamental realization of this article wasthat DNA does not only encode the elementary functional elements of anorganisms, it also harbours abundant information on the evolutionary historyand life history traits of its ancestors.

Themodelling of the evolutionary processes that generated extent genomesshould reveal together the patterns of the diversification oflife, the processes by which evolution proceeds at the molecular level,and how both are affected by external conditions. Our challenge today,as evolutionary biologists, is to bridge the gap between species ecology,life history traits, population dynamics, species phylogeny, genephylogeny, genome structure, gene network and molecular mechanisms.

Therecent years have seen tremendous developments in this direction, whichwe will attempt to review in this conference.

Invitedspeakers (provisionaltitles)

ABBYSophie (Paris, France) Evolutionplaying a molecular building set: origins and distribution of bacterialsecretion systems

ACHTMANMark (Warwick, United Kingdom) Agesof bacterial pathogenes

ALMEric (Cambridge, USA) Drivingforces of microbiome evolution

DURETLaurent (Lyon, France) Biasedgene conversion as a 4rth evolutionary force

FARIANuno (Oxford, United Kingdom) Viralevolution

GALTIERNicolas (Montpellier, France) Populationgenomics of non model animals: genetic diversity, adaptive rateand effective population size

GILBERTThomas (Copenhaguen, Denmark) AncientDNA, ancient genomes, and the hype of de-extinction

GOGARTENPeter (Storrs, USA) Horizontalgene transfer: the pan-genome as shared genetic resource of alineage

GRAURDan (Houston, USA) Thevocabulary of molecular evolution and the transgressions of functional genomics:a rose by any other name would be misleading

GRIBALDOSimonetta (Paris, France) Phylogenomicsand the tree of life

HEATHTracy (Ames, USA) Molecular,morphological, and macroevolutionary models for dating species divergencetimes

KATZLaura (Northampton, USA) Theeukaryotic phylogeny

KOSIOLCarolin (Vienna, Austria) Polymorphism-awarephylogenetic models for species trees

LAGERGRENJens (Stockholm, Sweden) Generativemodels of gene family evolution

Lá≫PEZ-GARCIAPurificación (Orsay, France) Diversityof microbial life

McLYSAGHT Aoife (Dublin, Ireland) Wholegenome duplication

MORANNancy (Austin, USA) Symbiosisin evolution

PAGELMark (Reading, United Kingdom) Beyondmolecular data: information and evolution in the cultural realm

PHILIPPEHervé (Moulis, France) Modelsof sequence evolution

SANMARTINIsabel (Madrid, Spain) Spatiotemporalevolution of lineages and biotas using Bayesian approaches

SEMONMarie (Lyon, France) Insightsinto making different types of the same organ using developmental transcriptomesas molecular microscopes

STADLERTanja (Zürich, Switzerland) Modellingand inference of species diversification

SZÃLLÃSIGergely (Budapest, Hungary) Genomescale reconstruction of phylogenies

TELFORDMaximilian J. (London, United Kingdom) Thenew animal phylogeny

WARNOWTandy (Urbana, USA) Newcoalescent-based species tree estimation methods

Deadlinefor application: February 1rst, 2016

Registrationfee (including board and lodging)

430â¬*forPhDstudents*625â¬*forotherparticipants*

Applicationfor registration Thetotal number of participants is limited to 115 and all participants areexpected to attend for the whole duration of the conference. Selection ismade on the basis of the affinity of potential participants with the topicsof the conference. Scientists and PhD Students interested in the meetingshould send:

-their curriculum vitae -the list of their main publications for the 3 last years -the abstract of their presentation

tothe Chairperson of the conference (vincent.daubin@univ-lyon1.fr < http://dnamethylation.sciencesconf.org/ >)before the deadline. After it, theorganizers will select the participants. Except in some particular casesapproved by the Chairperson, it is recommended that all selected

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

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Roscoff France 50yrsMolecularHistory May9-13 Reminder2

Dear Colleagues,

Only a few days left (deadline is Feb. 1st). Hurry up!

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FARIA Nuno (Oxford, United Kingdom) Viral evolution

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to the Chairperson of the conference (vincent.daubin@univ-lyon1.fr < http://dnamethylation.sciencesconf.org/ >) before the deadline. After it,

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

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TexasAM EcolIntegration Mar31-Apr1

The 2016 Ecological Integration Symposium Committee invites you to attend the* 17th Annual Texas A&M University Ecological Integration Symposium *on *March 31-April 1 at Rudder Tower and Theater at Texas A&M University*. The Ecological Integration Symposium is an interdisciplinary, graduate student led and organized event that unites students with world renowned researchers in the themes of ecology, conservation, evolutionary biology, geography, and more.

During this free, two day event we will explore the ecological and social challenges we face towards achieving sustainability in a human dominated landscape through the theme of *Ecological Perspectives in Sustainability* *.* This year, we will be hosting a day of speaker presentations at Rudder Theater on March 31, and student presentations on the 4th floor of Rudder Hall on April 1, 2016.

The 2016 plenary speakers include *Dr.* *Jayne Belnap*, research ecologist with the USGS; *Dr. Ruth DeFries*, professor at Columbia University; *Dr. Lisa Naughton-Treves*, professor at University of Wisconsin-Madison; *Dr. Stuart Pimm*, professor at Duke University; and *Dr. Peter Vitousek*, professor at Stanford University.

We are now accepting *abstracts for student presentations in talk and poster formats*. Both graduate and undergraduate students are encouraged to present original research during the student research symposium on

Friday, April 1. Please visit our presentation registration page for more information on submission requirements and procedures:

http://eeb.tamu.edu/eis/2016-eis/2016-eis-student-presentation-registration/ *The deadline for abstract submissions is February 26, 2016*.

We are accepting *volunteer sign-ups* to help assist with the event on March 31 and April 1. Please visit http://eeb.tamu.edu/eis/2016-eis/2016-eis-volunteer-registration/ for more information and to register as a volunteer.

If you have any questions please feel free to contact the 2016 EIS Committee at theeis.tamu@gmail.com. Please visit our website http://eeb.tamu.edu/eis/2016-eis/ and Facebook page for more information and updates

We are looking forward to seeing you all this year during the 2016 Ecological Integration Symposium!

Regards,

2016 Ecological Integration Symposium Committee

Facebook: https://www.facebook.com/TAMUEIS/-?fref=3Dnf *Website:* http://eeb.tamu.edu/eis/2016-eis/ *Presentation Registration:* http://eeb.tamu.edu/-eis/2016-eis/2016-eis-student-presentation-registration/ *Judge Registration:* http://eeb.tamu.edu/eis/-2016-eis/2016-eis-judges-registration/ *Volunteer Registration:* http://eeb.tamu.edu/eis/2016-eis/-2016-eis-volunteer-registration/ *We thank all of our sponsors from Texas A&M University for making this event possible, including the Department of Ecology and Evolutionary Biology, the Association of Former Students, the Office of Graduate and Professional Studies, the College of Agriculture and Life Sciences, the Department of Geography, , the Department of Entomology, the Department of Wildlife and Fisheries Sciences, the Department of Ecosystem Science and Management, the Department of Animal Sciences, the Department of Agricultural Economics, the Department of Soil and Crop Sciences, and the Department of Oceanography.*

Danielle Macedo <dcdmacedo@gmail.com>

UCambridge EvolutionaryGeneticsGenomics Mar15

Dear all,

We are pleased to announce that the annual Evolutionary Genetics and Genomics Symposium (EGGS) will take place on Tuesday 15th March 2016 at the University of Cambridge.

This international one-day meeting is free to attend and no registration is required. Talks will cover all areas of evolutionary genetics from comparative genomics to evo-devo, and pathogen evolution to speciation.

Abstract submission is now open. If you would be interested in presenting a talk please send a title, abstract and your affiliation to: eggs.symp@gmail.com

We will also have talks by four invited speakers: - Mary J. OÂConnell, University of Leeds - Magnus Nordborg, Gregor Mendel Institute of Molecular Plant Biology, Vienna - Federica Di Palma, TGAC - Eric Miska, Wellcome Trust Sanger Institute, University of Cambridge

For more information, please visit http://-www.evolutionarygenetics.group.cam.ac.uk/eggs/ or email eggs.symp@gmail.com

Abstract can be submitted via this link: https://docs.google.com/forms/d/-1W2BMTt268_q4XEYv0IVwSiwnVmVlPs2KRYsXd_lJrNk/-viewform With best wishes,

The organising committee

– Dr Chuan Cao

Postdoctoral Researcher Francis Jiggins Group Department of Genetics University of Cambridge CB2 3EH Tel: +44(0)1223332584

Chuan Cao <cc625@cam.ac.uk>

UMichigan CommunityEvolution Mar12

CALL FOR NOMINATIONS: 12th ANNUAL EARLY CAREER SCIENTISTS SYMPOSIUM

The Department of Ecology and Evolutionary Biology at the University of Michigan invites nominations of outstanding scientists early in their careers to participate in an exciting international symposium entitled “Frontiers in Community Assembly.” The symposium events will take place on 12 March 2016, in Ann Arbor, Michigan. Dr. Tadashi Fukami and Dr. Rosemary Gillespie will be the keynote speakers.

Potential topics include phylogenetic and ecological models for inferring community structure, speciation and the evolution of secondary sympatry, genomic processes underlying colonization and local adaptation, the structuring of communities across environmental gradients, inferences from paleo-communities.

We welcome nominations of early career scientists who are studying ecological and evolutionary approaches to community assembly. Early career scientists are considered senior graduate students (who stand to receive their Ph.D. within one year) or postdoctoral researchers. A colleague or advisor may provide the nomination, however self nominations will be accepted. The selected nominees will be invited to present their work and to participate in panel discussions at the symposium.

The nomination consists of the nominees curriculum vitae, a brief abstract of the proposed presentation (< 200 words, written by the nominee), and an optional brief letter of recommendation addressing the nominees scientific promise and ability to give a compelling talk. Nominations should be sent electronically (in one file, please) to eeb-ecss-nomination2016@umich.edu using the nominees name as the subject line (last name first). More information is available at http://sites.lsa.umich.edu/-ecss/ . Review of nominations will begin on January 22nd, 2016. Selected participants will be contacted by February 1, 2016, and will have all expenses covered (registration, travel and accommodation). An official announcement of the list of speakers will be issued soon thereafter.

For more information, contact Carol Solomon at carollyn@umich.edu.

The 2016 Early Career Scientists Symposium scientific committee includes:

Lydia Beaudrot

James Pease

Marian Schmidt

Carol Solomon

Ben Winger

Senay Yitbarek

Marian Schmidt <marschmi@umich.edu>

UMichigan YoungScientist Mar12

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Senay Yitbarek

"marschmi@umich.edu" <marschmi@umich.edu>

UWashington EVO WIBO Apr15-17

Link: UWashington.EVO_WIBO.Apr15-17

Dear colleagues,

We are excited to announce the return of EVO-WIBO!

EVO-WIBO (Evolution in Washington, Idaho, British Columbia, and Oregon) is a gathering of evolutionary biologists of the Pacific Northwest. This meeting is held every second year and typically attracts 120-140 researchers for a fun weekend of presentations and discussions. The 2016 meeting will be held April 15th-17th.

As it has from its inception, the conference will be held at Fort Worden State Park in beautiful Port Townsend, WA. This Washington state park is right on Puget Sound on the Olympic Peninsula, with a small marine science center, a nice beach, and many recreation opportunities nearby.

A welcome reception will take place Friday evening April 15th. The meeting will run from Saturday morning the 16th through midday Sunday the 17th.

We are thrilled to report that Dr. Sarah Otto from UBC will be the plenary speaker for the 2016 meeting!

Please visit the conference website (http://evowibo.org/-) for more information and registration. The deadline for applications is March 1, 2016.

We hope to see you there!

Daniel Promislow, Ben Kerr, Katrina van Raay, Katie Dickinson, Robin Green, Devin Arbuthnott, & Leith Miller

Ben Kerr <kerrb@u.washington.edu>

Vairao Portugal Congenomics2016 May3-6

Congenomics2016 - Conference on Conservation Genomics http://congenomics2016.com Vairao, Portugal 3-6 May 2016

Early registration fees (deadline 31 March): 250 EUR (standard), 100 EUR (students) Submit your abstract online (deadline 21 February)

We are pleased to announce the Congenomics2016 - Conference on Conservation Genomics, the final meeting of the ConGenOmics ESF Research Networking Programme (*). This conference aims to gather the best research currently being performed on Genomics and its applications to Conservation.

The conference is organized by ConGen (Conservation genetics and wildlife management) research group and hosted in CIBIO/InBIO Associate Laboratory and the University of Porto facilities in Vairao, Portugal.

We aim to provide an inspiring atmosphere for discussing the aplication of genomics to conservation, namely for infering demography, population history, population viability, adaptative viability, taxonomy, as well as the use of metagenomics and environmental DNA.

The program includes six invited plenary lectures, submitted oral communications (regular and flash) and poster sessions, covering the state of art on conservation genomics. Travel grants are available for students and early career researchers (please see conference website for details).

Confirmed Invited Speakers:

Fred Allendorf (University of Montana) Mike Bruford (Cardiff University) Lisette Waits (University of Idaho) Natasha de Vere (National Botanic Garden of Wales)

Organizing & Scientific Committee:

Paulo Célio Alves (University of Porto) Ricardo Jorge Lopes (University of Porto) José Melo-Ferreira (University of Porto) Raquel Godinho (University of Porto)

Joop Ouborg (Radboud University) Philippine Vergeer (Wageningen University) Jacob Höglund (Uppsala University) Gernot Segelbacher (University of Freiburg) Craig Primmer (University of Turku)

(*) ConGenOmics is a ESF Research Networking Programme that aims to bring together European and pan' European specialists on conservation genomics, to develop and improve the knowledge transfer of the technical advances and challenges in conservation genomics, focusing specifically on the application of genomic techniques. ConGenOmics programme organizes workshops, summer schools, collaborative expert meetings and an exchange program at pan'European level, to further develop the field of conservation genomics and to aid in the knowledge transfer of the technological advances and challenges among European research groups focusing specifically on applications of genomic technologies in conservation biology. More details in http://www.ru.nl/congenomics Questions? Contact us by email (info@congenomics2016.com) or on Facebook/twitter

riclopes@me.com

Valencia RNAmodificationEvolution Mar1

SMBE Satellite Meeting. Valencia, Spain - Deadline: 1 March The deadline for the SMBE Satellite Meeting on RNA modification and its implication on adaptation and evolution has been extended to March 1, 2016. More information about the meeting can be found at: http://smbeed2016.cibiv.univie.ac.at/ Confirmed invited speakers: Jianzhi Zhang. University of Michigan, USA Jin Billy Li. Stanford University, USA Gideon Rechavi. Tel Aviv University, Israel Josh Rosenthal. Institute of Neurobiology, University of Puerto Rico Ann Ehrenhofer-Murray. Humboldt University, Berlin, Germany Ayelet Lamm. Technion - Israel Institute of Technology, Israel Yi Tao Yu. University of Rochester, USA Dee Scadden. University of Cambridge, UK Nina Papavasiliou. The Rockefeller University, USA Please, mark your calendars and do not miss this exciting event! Miguel Gallach <miguel.gallach@univie.ac.at> Arndt von Haeseler <arndt.von.haeseler@univie.ac.at > Michael Jantsch <Michael.Jantsch@univie.ac.at> Miguel Gallach Center for Integrative Bioinformatics Vienna (CIBIV) Max F. Perutz Laboratories(MFPL) Telf: +43 1 4277 74330 Postal Address: Ebene 1 Campus Vienna Biocenter 5 CIBIV, MFPL 1030 Vienna Austria e-mail: miguel.gallach@univie.ac.at migaca2001@gmail.com http://www.cibiv.at/-˜mgallach/ https://scholar.google.at/citations?user=-3DRNeDl2AAAAAJ&hl=3Den SMBE Satellite Meeting in VALENCIA http://smbeed2016.cibiv.univie.ac.at/ Miguel Gallach <miguel.gallach@univie.ac.at>

Volterra Italy SystemsBiol Jul8-14

* Our sincere apologies if you receive multiple copies of this announcement *

The 3rd International Synthetic & Systems Biology Summer School is a great opportunity to exchange ideas and information with colleagues and peers from around the world and discover the latest trends and new exciting results in Synthetic and Systems Biology.

International Synthetic and Systems Biology Summer School - SSBSS 2016, 8-14 July 2016, Volterra (Pisa) - Tuscany, Italy

* Application:ÂMarch 31, 2016Â * Oral Talk/Poster Submission:ÂMarch 31, 2016 http://www.taosciences.it/-ssbss/#application-form ssbss.school@gmail.com http://www.taosciences.it/ssbss/ Previous Editions: SSBSS 2015 http://www.taosciences.it/ssbss2015/ SSBSS 2014 http://www.taosciences.it/ssbss2014/ Other Events in Tuscany: 2nd International Workshop on Machine learning, Optimization & big Data - MOD 2016 August 26-29, 2016 - Volterra (Pisa), Tuscany, Italy http://www.taosciences.it/-mod/ Call for Papers:ÂFebruaryÂ28, 2016Â http://www.taosciences.it/mod/call-for-papers/ https://easychair.org/conferences/?conf=3Dmod2016 cfp.ssbss@dmi.unict.it

GradStudentPositions

ACAD Adelaide AncientDNA

Aboriginal Heritage Project: Phylogeography, Genetics and Ancient DNA

A PhD project is available at the Australian Centre for Ancient DNA (https://www.adelaide.edu.au/acad/) as part of several ongoing ARC-funded studies to reconstruct Aboriginal Heritage using ancient DNA and museum collections of hair samples from across Australia. The project is a close collaboration with Aboriginal families and communities across Australia and the South Australian Museum. It is aimed at reconstructing a continent-wide picture of Indigenous Australia prior to European colonisation, analysing migration and trade routes, and the distribution of genetic diversity and community relationships.

Relevant techniques include ancient DNA, phylogeography, archaeology, Aboriginal culture and history, and museum research. The project has strong potential to make major contributions to our understanding of Australian and Aboriginal history and assist with the Stolen Generation and reconciliation more broadly. The project is a close collaboration with the South Australian Museum, BioPlatforms Australia, the Australian

Genome Research Facility, and an international team of researchers. Fieldwork in remote communities will form a key part of the project.

A highly motivated candidate with strong initiative and organisational skills is required. The ideal applicant will have previous experience with molecular biology methods along with a background in areas such as genetics, archaeology, ancient DNA, phylogeography or anthropology and a strong interest in Aboriginal and Australian history. A publication record would be a distinct advantage. The position is open to both Australian and international candidates.

Contact Dr Ray Tobler, raymond.tobler@adelaide.edu.au, with a letter of interest and background information addressing the above criteria. The position will remain open until filled.

"raymond.tobler@adelaide.edu.au"
<raymond.tobler@adelaide.edu.au>

BrighamYoungU PlantGenomeEvolution

Multiple graduate student positions (MS and PhD) in the evolution of plant genomes are available beginning Fall 2016 in the Department of Plant and Wildlife Science, Brigham Young University. Research focus of these assistantships center on the genome evolution of polyploid plants (*e.g.* cotton; see http://udall-lab.byu.edu). During their thesis work, students will employ molecular, structural, and genetic approaches to address basic questions in the evolution of plant domestication and genetic diversity ofcotton. Specific technologies employed in the approaches include BioNano optical mapping, PacBio and Illumina DNA sequencing, and computational biology.

Successful applicants must be highly motivated, willing to work hard, and hopefully they are not too distracted by living in the most beautiful place in the world. Ideally, applicants should have a solid, but not necessarily deep, understanding of bioinformatics and an interest in genomics. Actual wet-lab experience with basic molecular biology techniques is a plus (PCR,cloning, sequence analysis, etc.).

Funding for this position is through a combination of Teaching and Research Assistantships from the National Science Foundation and Cotton Incorporated. This means students will be paid a stipend while they earn their graduate degree! In addition to the stipends, tuition and health insurance will also be provided for the accepted students. Interested students from other Universities than BYU could receive up to $30K per year through the HIDRA < https://-graduatestudies.byu.edu/content/hidra > program (for off-campus applicant to BYU) or through the University Graduate Research Award (after first year of studies).

Interested applicants should send a CV, transcripts, GRE scores (if available) and a statement of research interests to Joshua Udall (jaudall@byu.edu). Applications will be considered until to February 1st, 2016. International students with strong credentials are welcome and encouraged to apply.

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

Office: 801-422-9307

jaudall1@gmail.com

CharlesU Prague BirdAdaptation

PhD position available from October 2016 "Causes and consequences of ecological specialization in birds"

Project background: Populations of ecological specialists decline due to their sensitivity to global environmental changes. Although various studies confirmed this pattern, wider context of evolutionary causes and ecological consequences of species' specialization remains unclear. Proposed project focuses on elucidating these issues using birds as a study system. Birds are a taxon with detailed knowledge of ecological and life history traits, population and range sizes, phylogenetic relationships and extinction risk of all species. Within this project, we will use this information to learn more about evolutionary conservatism of ecological specialization (whereas avian species do not usually expand their niches after introduction outside native ranges, closely related species often show high variability in their niche breadth) and to focus on possible changes in specialization across species' geographic ranges, e.g. in relation to their local densities. The applicant will also collect own field data to examine relationships among habitat specialization at the individual, population and species level, respectively. Finally, knowledge from the above mentioned relationships will be applied in the analysis predicting global extinction risk of particular species by different facets of their specialization.

Eligibility: We expect a motivated student with good experience in ornithology, able (after some training) to work independently in the field in Eastern Europe. The ideal candidate for this PhD position is interested in ecology and evolutionary biology, and is willing to learn new methods. He/she must have finished the MSc. (or equivalent) by September 2016 at the latest.

Time and place: The student will work in a young team based at the Faculty of Science, Charles University in Prague, Czech Republic. Fieldwork will be conducted in the Czech Republic. The position is available for up to four years, starting in October 2016.

Salary: The PhD candidate's net monthly income will start at 16.500 CZK (ca 610 EUR) in the first year, and may increase with experience and achievements during the study. (Note that living expenses in the Czech Republic are generally lower than in Western European countries.)

Research team: JiÃí Reif (Institute for Environmental Studies, Charles University in Prague) - supervisor David HoÃák (Department of Ecology, Charles University in Prague) - co-supervisor

How to apply: If interested, send a motivation letter, CV, publication list, title or abstract of Master (Diploma) thesis, and contact details of 2 senior scientists that can provide references on you in a single PDF file to jirireif@natur.cuni.cz until February 10, 2016. Pre-selected candidates will be encouraged to submit an official application to the university.

–

JiÃí Reif <jirireif@natur.cuni.cz>

DurhamU EvolutionPlantGenetics

A competitive four year PhD studentship opportunity in evolutionary and ecological genetics is available at Durham University, UK.

Title:

The fitness consequences of inbreeding in wild flax.

Supervisory team:

Dr Adrian Brennan, Durham University, UK, with the co-supervision of Prof Rus Hoelzel, Durham University, UK, and Dr Kirsten Wolff, Newcastle University, UK.

Overview and application details

This project sits at the interface of evolutionary biology and applied plant breeding and will provide the student with valuable training and experience in next generation sequencing technologies and quantitative methods. These are highly sought skills for careers in academia or industry.

Full university fees and maintenance funding is limited to UK nationals and European Economic Area (EEA) nationals who have resided in the UK for the past three years. Other EEA nationals are eligible for a fees only grant. If interested in applying, please contact Dr Adrian Brennan, a.c.brennan@durham.ac.uk , with a CV and a covering letter. The deadline for applications is 12th February 2016.

Project description:

This project aims to improve our understanding of inbreeding and its relationship with fitness, a fundamental aspect of evolution. We will use wild flax as a model to study this important relationship, thereby raising the possibility of rapidly translating results into sustainably enhancing agricultural production via genetic improvement of crops. Our research in wild flax will allow for the comparison of natural populations exhibiting different levels of selfing, thereby revealing the extent to which natural selfing leads to purging and the development of a genome more resistant to inbreeding depression. We will use new genotyping by sequencing technologies to obtain an unprecedented genome-wide perspective on inbreeding and its evolution, allowing the identification of relevant genes, and therefore the consideration of molecular mechanisms.

Inbreeding is widely understood to reduce fitness through both the expression of recessive deleterious alleles in homozygotes, and through over-dominant allelic interactions. Even naturally highly inbreeding organisms cannot completely purge their genetic load by selection because of faster drift at reduced effective population size. For many crops, including flax, elite lines have been intensively inbred to optimize the stable expression of desirable traits. However, these same lines then suffer inbreeding depression. Studies of flax have found up to 91 % heterotic increases in F1 seed yield following controlled crosses. However, the agronomic potential of heterosis has only been fully realized in hybrid varieties of maize so far. Only recently have genotyping technologies advanced to a stage where it is possible to test the long-held hypothesis that heterozygosity positively correlates with fitness using genome-wide data for many individuals of non-model organisms. Initial results are encouraging but more research is needed in organisms showing a wider range of mating systems and population structures to better understand the fitness consequences and genetic basis of inbreeding.

“a.c.brennan@durham.ac.uk”
<a.c.brennan@durham.ac.uk>

EdinburghNapierU ModellingSocialEvolution

PhD Studentship in modelling the evolutionary origin of social groups

School of Computing, Edinburgh Napier University, Edinburgh, UK

Dr Simon T. Powers

Deadline: 14th January 2016

The School of Computing at Edinburgh Napier University is advertising fully-funded PhD studentships, open to both UK and international students, to start in the first or second quarter of 2016. One of the proposed studentships is to work with Dr Simon T. Powers on modelling the evolutionary origins of social groups. Specific projects include the evolution of protocells at the origin of life, the evolution of multicellularity, and the evolution of human social institutions during the Neolithic transition from hunter-gatherer groups to agricultural societies. Our main approach is to investigate the selective drivers towards social group formation by modelling the co-evolution of traits that affect group formation, such as dispersal or group size preferences, with social behaviours such as cooperation and punishment. For human evolution, we are interested in how cultural evolution can lead to the creation of social institutions that select for cooperation in large groups of unrelated individuals. Our main methodology is analytical and simulation modelling. However, we are also interested in projects proposing the use of evolutionary robotics as a modelling tool, and projects that propose applications to cooperation in agent-based computing.

Related reading can be found in Dr Powers' publications: https://scholar.google.co.uk/citations?user=-aBHiawoAAAAJ&hl=en http://www.unil.ch/dee/-en/home/menuinst/people/post-docs--associates/dr-simon-powers.html Candidates should have strong quantitative skills, demonstrated experience of computer programming, and an interest in the evolution of social behaviour.

The formal advert for the studentships can be found at: http://www.jobs.ac.uk/job/AMQ979/phd-studentships-x-4/ Students are encouraged to propose their own projects that broadly fit within the areas described above. Potential applicants are encouraged to informally discuss the position by email with Dr Powers: S.Powers@napier.ac.uk.

Dr Simon T. Powers Lecturer (Assistant Professor) School of Computing Edinburgh Napier University https://scholar.google.co.uk/citations?hl=3Den&user=-3DaBHiawoAAAAJ “S.Powers@napier.ac.uk” <S.Powers@napier.ac.uk>

ETHZurich EcologyEvolutionModeling

PhD position: Modeling ecology/evolution of a plant pathogen, ETH Zurich

The project

will explore population dynamics of Zymoseptoria tritici, an important fungal pathogen of wheat, using eco-evolutionary modeling and field/lab experimentation.

Plant diseases often cause serious yield losses in agriculture. Current chemical and genetic technologies used to manage plant diseases are highly vulnerable to pathogen evolution and are not sustainable. Pathogen evolution is facilitated by the genetic uniformity underlying modern agroecosystems. Thus, there is an urgent need to develop new, efficient and sustainable ways to control plant diseases.

This PhD project intends to make an important contribution towards achieving this goal. The first phase aims at comprehensive characterization of both epidemic and evolutionary factors of the pathogen by combining eco-evolutionary modeling, field/lab experiments and genome sequence analyses. In the second phase the models will be used to predict the rate of pathogen adaptation to disease control and propose optimal spatio-temporal patterns for applications of fungicides and resistant host varieties that can disrupt pathogen adaptation.

Working conditions

Plant Pathology group at the Institute of Integrative Biology, ETH Zurich offers a creative, collaborative research environment and excellent infrastructure (www.path.ethz.ch). Salary is approximately 48000 Swiss francs per year. Zurich is a vibrant, international and green city.

The PhD project is funded for three years by the Ambizione grant from the Swiss National Foundation with a possibility of extension for the fourth year.

Unique training in mathematical modeling, bioinformatics and field/lab experiments increases chances to find a job in academia, industry or governmental agencies.

Requirements

—Master's/diploma in a quantitative discipline (e.g. physics, mathematics or computer science), biology or agricultural/environmental sciences.

—Strong interest in mathematical/computational modeling in population biology

—Desire to link the models with real-world field experiments and spend about 40% of time doing experimental work

—Excellent communication skills in English

—Programming skills, experience in mathematical modeling or bioinformatics are important, but optional plus points

Application

For more details, please contact Dr. Alexey Mikaberidze by email. Please apply as early as possible, at latest February 15th, 2016. Project start: April 1st, 2016. To apply, please send Dr. Alexey Mikaberidze as a single pdf file

—a motivation letter that describes how your scientific interests and qualifications fit this project (1 page) —a CV —a copy of the MSc certificate —arrange 2-3 letters of recommendation to be sent by referees directly to Dr. Alexey Mikaberidze via email

Alexey Mikaberidze <alexey.mikaberidze@env.ethz.ch>

ETHzurich ParasiteGenomics

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

to study evolutionary ecology of host-parasite interactions, particularly parasite adaptation to host. The study system is the New Zealand freshwater snail Potamopyrgus antipodarum and its trematode parasite Microphallus sp. The goal of the project is to understand the genetic underpinnings of rapid parasite adaptation to new host types. The work includes field work in New Zealand and laboratory infection experiments followed by application of genomics and bioinformatics tools. General information about the research group can be found at http://www.ae.ethz.ch/. Co-PIs in the project are Dr. Hanna Hartikainen (ETH Zurich) and Prof. Roger Butlin (University of Sheffield).

Candidates must qualify for admission to the Ph.D. programme of ETH (https://www.ethz.ch/en/-doctorate.html). The duration of the position is three years, starting not earlier than May 2016. Salary is according to ETH-scale starting from 47 kchf/year.

Suitable qualified persons are invited to apply by email. Please attach a single PDF file including a letter of motivation, C.V. and names plus addresses of two references. Subject line should read “PHD-Position 2016”. Email address to use is jukka.jokela@env.ethz.ch.

Evaluation of applications starts January 2016, and continues until the position is filled.

jukka jokela professor of aquatic ecology ETH Zurich www.ae.ethz.ch “Jukka.Jokela@eawag.ch” <Jukka.Jokela@eawag.ch>

ExeterU EvolutionMicrobialResistance

Positions available at Exeter University, The Natural History Museum (London), and Cefas (Centre for Environment, Fisheries, and Aquaculture Science, UK)

PhD studentship in antimicrobial resistance in pond aquaculture systems: http://www.exeter.ac.uk/studying/funding/award/?id=3D2129 (Exeter University/Cefas; deadline 31 January 2016)

PDRA positions at The Natural History Museum (Hydroscape, NERC Freshwater Highlight Topic): 1. Disease distribution in the freshwater landscape 2. Gene flow and genetic diversity in fresh waters http://ow.ly/Xxbkk (scroll down to list of vacancies) Deadline 8 February 2016

Dr David Bass Research Leader Life Sciences Natural History Museum London SW7 5BD UK Tel: 0207 942 5387 Room DC1 406B

David Bass <d.bass@nhm.ac.uk>

GeorgiaSouthernU PlantSystematics

M.S. Position, Plant Evolution and Systematics, Georgia Southern University

The Schenk lab at Georgia Southern University invites applicants for a Masters Degree in plant systematics and evolution, starting Fall semester, 2016. Our lab group is interested in how botanical diversity has been shaped by the interactions among morphological, ecological, and species diversification. We apply statistical phylogenetic approaches that quantify and incorporate molecular, morphological, and ecological variation to plant systems in order to understand the evolutionary processes of how and why species diversify.

An ideal candidate will have interest in using plant systems to better understand the evolutionary processes of diversification by applying statistical phylogenetic approaches. Competitive students that meet all requirements will be supported with either a teaching or research assistantship.

Interested students should contact Dr. John Schenk (jschenk@georgiasouthern.edu) prior to submitting an application (the earlier the better).

For more information, visit the Schenk lab website (https://sites.google.com/a/georgiasouthern.edu/schenk) and the Department of Biology's website (http://cosm.georgiasouthern.edu/biology). More information about the Biology graduate program can be found at the departmental web page (http://cosm.georgiasouthern.edu/biology/graduate-program-2/).

Additional questions about the GSU graduate program can be directed to the Graduate Student Program Director: Dr. Checo Colon-Gaud (jccolon-gaud@georgiasouthern.edu). For full consideration, the application deadline is March 1st, 2016.

John J. Schenk, Ph.D.

Assistant Professor of Plant Biology Georgia Southern University Herbarium (GAS), Curator Department of Biology 4324 Old Register Road Georgia Southern University Statesboro, GA 30460-8042

Office: 2260 Biology Building Office phone: (912) 478-0848

Lab website: http://sites.google.com/a/georgiasouthern.edu/schenk Herbarium website: http://sites.google.com/a/georgiasouthern.edu/gasherbarium jschenk <jschenk@georgiasouthern.edu>

GuangxiU 2 PlantGenomicsBiodiversity

two MSc/PhD student positions available in Plant Genomics & Biodiversity at the Plant Ecophysiology & Evolution Group, Guangxi University, Nanning, China

The Plant Ecophysiology and Evolution Group at Guangxi University (Nanning, China) is seeking two highly motivated and productive International MSc or PhD students to engage in 3/4-year projects in Plant Genomics, Molecular Systematics, Biogeography and Plant Taxonomy. Multiple topics are available and can be further determined upon application, including one or a combination of the following themes:

(1) Plant Genomics - Understanding the geographic distribution and evolution of genetic diversity between species and within populations; understanding the role of isolation in the establishment of genetic divergence

and speciation.

(2) Plant Biogeography & Evolution - Temporal and spatial reconstruction of patterns of plant diversification in Asia and the Indian Ocean region in selected families and genera. Of particular interest to us are the roles of morphological/molecular change in adaptation and plant speciation on oceanic islands, where environments undergo substantial change over the course of an island's lifespan.

(3) Plant Taxonomy - There are several exciting opportunities for students to take part in the revision and reconstruction of a new regional Flora. Projects will involve training in taxonomy, nomenclature and fieldwork, but also include training in molecular systematics, phylogenetics and the most recent developments in the field.

Students will enroll in the International Graduate Program at the College of Forestry for 3-4-year projects, with complete waivers for tuition- and housing-fees. Housing will be provided in the International Student dormitories of the campus in Nanning. The first year consists of orientation and study of the Chinese language through courses. The following years will be filled with fieldwork, professional courses and the research project.

Applications are now invited for an intended starting date of projects in September 2016. The application deadline is March 31, 2016. Fellowships come with an ample monthly allowance for the full duration of the project. Applicants with a proven track record of successful publication in peer-reviewed journals will have an advantage in applying.

Opportunities for the development of individual research projects as well as collaborative work, exist within our lab and with external groups. Candidates will be integrated in a growing and multidisciplinary team of Chinese and foreign researchers, providing a creative and stimulating research environment, and will work as part of a team studying genomics, evolution and taxonomy of selected taxa in Asia and the Indian Ocean region. Prior knowledge of Chinese is not mandatory as courses form an integral part of the curriculum, and the working language in our research groups is English. Projects will be supervised by Associate Prof. Joeri S. Strijk (jsstrijk@gxu.edu.cn).

Our research team is part of the College of Forestry, under the State Key Laboratory of Conservation and Utilization of Subtropical Agro-bioresources, which houses a wide range of laboratories and research groups. We are located in the heart of the large Nanning city campus, with easy access to on-campus housing and day-to-day facilities for life on campus. Guangxi University (>25,000 students) in subtropical Nanning is part of the National 211 University Scheme of China (http://en.wikipedia.org/wiki/Project_211) and aims to become a major research hub in Southern China. The city forms the natural gateway to South-East Asia, with Vietnam a mere 300kms away and direct international connecting flights available to most major cities in Asia from the new Nanning International Airport.

Please visit our website for more information on our group, it's members and their research:

http://www.plant-ecophysiology-evolution.com/ To apply for a position, please email a statement of research interests and goals, a curriculum vitae, and the email addresses of three references directly to:

Associate Prof. Joeri S. Strijk (jsstrijk@gxu.edu.cn).

Review of applications will commence immediately.

Dr. Joeri S. Strijk Associate Professor Plant Ecophysiology & Evolution Group State Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources College of Forestry, Guangxi University Nanning, Guangxi 530005 PR China

Joeri Sergej Strijk <jsstrijk@hotmail.com>

GuangxiU PlantEvolution

International Graduate Program with multiple MSc and PhD positions available at the College of Forestry of Guangxi University, Nanning, China

The Plant Ecophysiology and Evolution Group, Forest Ecology Group and Forest Dynamic Research Lab at Guangxi University (Nanning, China) are seeking highly motivated and productive International MSc and PhD students to engage in 4-year projects in:

(1) Plant Physiological Ecology including water relations, or Functional Plant Anatomy, or Photosynthesis and Photoprotection, supervised by Prof. Kun-Fang Cao (kunfang.cao@gxu.edu.cn or caokf@xtbg.ac.cn).

(2) Plant Genomics, Molecular Systematics, Biogeography or Taxonomy, supervised by Associate Prof. Joeri S. Strijk (jsstrijk@gxu.edu.cn).

(3) Ecological Genomics or Conservation Genetics, supervised by Associate Prof. Alison Wee (alisonwks@gmail.com).

(4) Seed Ecology and Physiology, supervised by Associate Prof. Uromi Goodale

(uromi.goodale@outlook.com).

The International Graduate Program at the College of Forestry offers MSc and PhD Fellowships for 4-year projects, with complete waivers for tuition fees and housing fees. Housing will be provided in the International Student dormitories of the campus in Nanning. The first year will consist of orientation and study of Chinese language through courses. The other three years will be filled with fieldwork, professional courses and the research project.

Project applications are now invited for an intended starting date of projects in September 2016. The application deadline is March 31, 2016. Fellowships come with an ample monthly allowance for the full duration of the project. Applicants with a proven track record of successful publication in peer-reviewed journals will have an advantage.

Opportunities for the development of individual research projects as well as collaborative work, exist within our lab and with external groups. Candidates will be integrated in growing and multidisciplinary teams of Chinese and foreign researchers, providing a creative and stimulating research environment, and will work as part of a team studying the evolution, ecology, distribution and/or ecophysiology of selected taxa in Asia. Prior knowledge of Chinese is not mandatory as courses form an integral part of the curriculum, and the working language in our research groups is English.

All research groups are part of the College of Forestry, under the State Key Laboratory of Conservation and Utilization of Subtropical Agro-bioresources, which houses a wide range of laboratories and research teams. We are centrally located on the large Nanning city campus, with easy access to on-campus housing and day-to-day facilities for life on campus. Guangxi University (>25,000 students) in subtropical Nanning is part of the National 211 University Scheme of China (http://en.wikipedia.org/wiki/Project_211) and aims to become a major research hub in Southern China. The city forms the natural gateway to South-East Asia, with Vietnam a mere 300kms away and direct international connecting flights available to most major cities in Asia from the new Nanning International Airport.

Please visit our website for more information on our group and research:

http://www.plant-ecophysiology-evolution.com/ To apply for any of these positions, please email a statement of research interests and goals, a curriculum vitae, and the email addresses of three references directly to the individual project leaders:

(1) Plant Physiological Ecology. Functional Plant Anatomy. Photosynthesis and Photoprotection.

Prof. Kun-Fang Cao (kunfang.cao@gxu.edu.cn or caokf@xtbg.ac.cn).

(2) Plant Genomics. Molecular Systematics. Biogeography. Taxonomy.

Associate Prof. Joeri S. Strijk (jsstrijk@gxu.edu.cn).

(3) Ecological Genomics. Conservation Genetics.

Associate Prof. Alison Wee (alisonwks@gmail.com).

(4) Seed Ecology and Physiology.

Associate Prof. Uromi Goodale (uromi.goodale@outlook.com).

Review of applications will begin immediately.

Dr. Joeri S. Strijk Associate Professor Plant Ecophysiology & Evolution Group State Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources College of Forestry, Guangxi University Nanning, Guangxi 530005 PR China

Joeri Sergej Strijk <jsstrijk@hotmail.com>

Halle Germany HoneybeeResistance

Halle_Germany.HoneybeeResistance

PhD project in the Molecular Ecology group at Martin-Luther-University, Halle-Wittenberg, Germany.

The aim of the project is to find genetic basis of the honey bee Apis mellifera resistance to Varroa destructor. This will be done by using the latest methods in genomics, transcriptomics and proteomics. Thus representing a unique opportunity to gain experience in an area which is of high demand in the research field. The group has excellent laboratory facilities with all state of the art equipments including a next generation sequencing platform.

The PhD position is funded for three years in which time the PhD student is expected to finish her/his degree.

The chosen PhD student is expected to work independently within the project framework. The skills should reflect the project description. The candidate will be familiar with standard molecular methods in the lab as well as bioinformatics and running scripts. Willingness to learn new methods is a must as well as ability to adapt to ever-changing circumstances. Some travelling to France or India might be included. Excellent command of English in both writing and speaking is essential. Knowledge of German is beneficial but not must.

Information of the research group can be obtained from Dr. Jarkko Routtu, tel: 0049 (0) 345 55 26382, email: jarkko.routtu(at)zoologie.uni-halle.de

http://www.mol-ecol.uni-halle.de/staff/routtu-j/ http://www.mol-ecol.uni-halle.de/research/genomics/-varroa_resistance/ Extended application deadline before 8th of February 2016, subject line referring to Ãâ¬$\mathring{A}PhDresistance\tilde{A}\hat{a}$¬ï?‘1$_{\overline{2}}$, together with your letter of motivation, CV, publication list, names of two referees in a single pdf file.

Jarkko Routtu <jarkko.routtu@zoologie.uni-halle.de>

Halle Germany HoneybeeResistance 2

Halle_Germany.HoneybeeResistance

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The chosen PhD student is expected to work independently within the project framework. The skills should reflect the project description. The candidate will be familiar with standard molecular methods in the lab as well as bioinformatics and running scripts. Willingness to learn new methods is a must as well as ability to adapt to ever-changing circumstances. Some travelling to France or India might be included. Excellent command of English in both writing and speaking is essential. Knowledge of German is beneficial but not must.

Information of the research group can be obtained from Dr. Jarkko Routtu, tel: 0049 (0) 345 55 26382, email: jarkko.routtu(at)zoologie.uni-halle.de

http://www.mol-ecol.uni-halle.de/staff/routtu-j/ http://www.mol-ecol.uni-halle.de/research/genomics/-varroa_resistance/ Extended application deadline before 8th of February 2016, subject line referring to "PhD resistance", together with your letter of motivation, CV, publication list, names of two referees in a single pdf file.

Jarkko Routtu <jarkko.routtu@zoologie.uni-halle.de>

ImperialCollege London BeeFitness

PhD position advertised to research how bee foraging performance and colony fitness are affected by stressors in fragmented rural landscapes'

Supervisors: Dr Richard Gill (r.gill@imperial.ac.uk), Dr Samraat Pawar (Life Sciences)

Location: Department of Life Sciences, Imperial College London, Silwood Park campus

Deadline: 18ˆth January 2016

Increased agricultural practices have resulted in the clearance and fragmentation of many natural habitats posing potential challenges to wildlife such as insect pollinators. For eusocial bees (e.g. honeybees & bumblebees), who provide a crucial pollination service, increased floral habitat patchiness may increase foraging demands making it significantly more difficult to sustain the colony's energetic requirements. It is thus important we consider how environmental stressors set limits on bee foraging performance and how bees are able to cope with such pressures.

For further details, how to apply and eligibility please go to: https://workspace.imperial.ac.uk/grantham/-Public/SSCP%20DTP/DTP%20projects%202016/-LS_Gill_2016.pdf But in brief, the studentship will investigate what specific behavioural mechanisms are being affected by stress factors associated with agricultural practices and the knock-on effects thus has to colony functioning and fitness. The research project will provide the PhD student with a number of benefits: i) it will integrate a number of critical interdisciplinary skills including controlled experiments and modelling; ii) it crosses a number of scientific fields such as behavioural ecology, evolutionary and theoretical biology; iii) the research is of high impact and will result in quality publications as well as results that can inform end users and policy makers; and iv) the student will join a productive, diverse and social research group.

Imperial College is a world leading university; Life Science dept. was placed top of the UK universities for research intensity in the Research Excellence Framework, and placed 6th best dept. in the world in the Times Higher Education 2015. The student will be based at Silwood Park which has an internationally renowned community of researchers, excellent facilities for the project, and the GCEE initiative has invested significantly into ensuring world leading research addressing important global issues.

Selected references:

Raine & Gill 2015 Nature N&V

Gill & Raine 2014 Functional Ecology (doi:10.1111/1365-2435.12292)

Bryden, Gill et al. 2013 Ecology Letters (doi:10.1111/ele.12188)

Gill et al. 2012 Nature (doi:10.1038/nature11585)

Pawar et al. 2012 Nature (doi:10.1038/nature11131)

Gill & Hammond 2011 Proc. Roy. Soc. B

Gill et al. 2009 Proc. Roy. Soc. B

"Gill, Richard J" <r.gill@imperial.ac.uk>

ImperialCollege London PlantFungiInteractions

ImperialCollege_London.PlantFungiInteractions

Plant-fungal interactions in alpine ecosystems

A Ph.D. studentship is available to investigate plant-fungal interactions in alpine ecosystems focusing on environmental drivers and the influence of plant host genetic variation on mycorrhizas across elevation and latitudinal gradients. Alpine plant and fungal communities are models for understanding pioneer communities, the primary components of resilient ecosystems. Climate change is one of the biggest threats to organismal and functional diversity and this project aims to understand its impacts on widespread symbiotic interactions. A strong interest in fungal and/or plant molecular ecology and evolution is essential. A first class degree in biological sciences is required and a Masters degree in a relevant area is desirable. The student will be affiliated with the Department of Life Sciences at Imperial College London (http://www.imperial.ac.uk) and based at the Royal Botanic Gardens (http://www.kew.org). A stipend, tuition fees and research funds are provided. The student can join the Grand Challenges in Ecosystems and Environment Doctoral Training Programme. The starting date is in the Spring of 2016.

Informal enquiries should be made to Dr Martin Bidartondo (m.bidartondo@imperial.ac.uk). Applications should contain a full CV and the names and contact details of two academic referees and should be sent to Dr Bidartondo. Only UK or EU applicants are eligible. Deadline for receipt of applications is 15 February 2016.

"Martin I. Bidartondo" <m.bidartondo@imperial.ac.uk>

ImperialCollege London StressFitnessConsequences

PhDStudentship advertised at Imperial College London, Silwood Park campus, UK

On:Trans-generational fitness consequences of chronic stress induced by global change

Supervisors:Dr Julia Schroeder (Imperial College London) and Prof Terry Burke (University of Sheffield)

Applicationdeadline: 10 January 2016 < http://-airmail.calendar/2016-01-10%2012:00:00%20GMT >.

Projectdescription: Human-inducedglobal changes impose chronic environmental stress on ever more natural populations. The physiological symptoms of chronic stress are changes in hormone levels that can lead to stunted growth and increased risk of infection. Furthermore, the physiological mechanisms invoked by stressed are similar to those in ageing individuals. Recent studies suggest that chronic stress can lead to faster senescence (measured in telomere shortening rates), not only in affected individuals but also in their offspring. What are the trans-generational fitness consequences of a chronic stress response, and how is it adaptive? Stress could "prime" offspring to enable them to endure stressful conditions in the future, by a "life-fast die-young" trade-off. This projects tests the hypothesis that chronic stress primes the next generation. To test this, we make opportunistic use of an exceptionally well suited long-term "natural experiment" in wild passerines and supplement statistical analyses on existing long-term data with focused experiments on captive birds.

Theaim of this study is to quantify the fitness consequences of chronic stress to gain a better understanding of the long-term fitness costs and benefits of chronic stress in a wild population the consequences for population viability. The student will utilise a unique long-term study of a wild passerine population. The precise direction and emphasis of the project will be determined by collaboration between the student and the supervisors. Nextto the traditional academic skills, the student will also learn and improve key skills such as state-of-the-art statistical modelling, data management, experimental design and field work. The student can expect to receive exceptional training in state-of-the-art analytical methodology, as well as benefitting from a well established and rewarding field project.

ImperialCollege London is a world leading university; it has been Ranked 3rd in Europe and 8th in the world by the Time Higher Education Rankings 2015-16. The student will be based at the Silwood Park campus < http://www.imperial.ac.uk/visit/campuses/silwood-park/ > which has a large graduate student community, with internationally renowned researchers.

Thefunding for this post is covered by an SSCP DTP-NERC studentship, and covers home fees and a stipend for 3.5 years. Applicants, who must be residents of the EU OR have been ordinarily resident in the UK for 3 years prior to the start of the studentship, must have an outstanding honours degree, a masters degree, or equivalent, in a relevant subject, should complete an online application, upload a supporting statement explaining why they want to pursue this PhD (maximum 1 page), their CV, and 2 references, at: http://www.imperial.ac.uk/grantham/education/science-and-solutions-for-a-changing-planet-dtp/ Anyenquiries about the project should be directed to:

DrJulia Schroeder julia.schroeder@imperial.ac.uk

julia.schroeder@imperial.ac.uk

IndianaStateU SparrowGenomics

PhD opportunities in Ecological Genomics

We are looking for motivated students interested in behavioral, evolutionary, and ecological genomics to join our laboratory at Indiana State University (ISU). These graduate positions are part of an exciting new interdisciplinary initiative at ISU, The Center for Genomic Advocacy (TCGA), which is focused on the application of genomic technology to the betterment of society. TCGA is developing a state-of-the-art next generation sequencing facility, which will be used to provide hands-on experiences for students as well as strong infrastructure for modern genomic studies.

Graduate research will be expected to combine traditional behavioral ecology studies with next-generation sequencing technology to examine the evolution of polymorphism in the white-throated sparrow. Students will conduct extensive laboratory work as well as participate in field based data collection during the breeding season. This species exhibits a clear link between phenotype and genotype, making it an ideal system in which to pinpoint the determinants of complex sexual and parental behavior. We have amassed 27 years of detailed data on this species making it possible to identify the genetic, epigenetic, and environmental bases of behavior. Morphs of the white-throated sparrow provide a unique opportunity to study intraspecific genomic differences, which have resulted from two separate, yet linked evolutionary trajectories - such results can transform our understanding of the evolution of genomes.

To apply, please send a letter of intent, curriculum vitae, and the names and email addresses of 3 references. Applications will be accepted until January 30, 2015.

For more information about the positions, please feel free to contact Dr. Elaina M. Tuttle (Elaina.Tuttle@indstate.edu) or Dr. Rusty A. Gonser (Rusty.Gonser@indstate.edu), at The Center for Genomic Advocacy (TCGA), Indiana State University, Terre Haute, IN 47809.

For more information about the lab, TCGA, the department, and the university, see:

www.whitethroatedsparrow.org http://www.indstate.edu/biology/ http://www.indstate.edu/home.php http://www.indstate.edu/sogs/ Dr. Elaina M. Tuttle Interim Associate Dean of Graduate Programs, College of Graduate & Professional Studies (CGPS) Chairperson, Institutional Animal Care & Use Committee (IACUC) Professor, Department of Biology & The Center for Genomic Advocacy (TCGA) Indiana State University Terre Haute, IN 47809

Phone: 812-237-4363 (CGPS) 812-237-2838 (Biology) Fax: 812-237-8060 (CGPS) 812-237-3378 (Biology) Email: Elaina.Tuttle@indstate.edu Elaina.Tuttle@gmail.com Web: http://www.whitethroatedsparrow.org http://www.unboundedpossibilities.com/the-center-for-genomic-advocacy.aspx http://biology.indstate.edu http://www.indstate.edu/graduate/ “Nothing in biology makes sense except in the light of evolution.” Theodosius Dobzhansky

Elaina.Tuttle@indstate.edu

Liverpool JMU MolecularEvolutionEcology

PhD Studentship in Molecular Evolution and Ecology

Liverpool John Moores University - School of Natural Sciences and Psychology

Duration of Studentship: 36 months.

There is an opportunity to apply for a fully funded PhD studentship at the interface between Molecular Evolution and Ecology. Please note that due to funding regulations the position is available to UK or EU nationals only.

Project title: Using biogeographic and phylogenetic patterns of Conophytum to inform the conservation of this endemic genus of the Succulent Karoo

Project description:

The aim of this project is to understand the key drivers of the current distribution and evolutionary divergence of one of the most diverse plant genera of the Succulent Karoo (SK). In doing so we will be better able to project the potential responses of the Conophytum to global environmental change, towards the development of conservation measures that reduce the extinction risk of these vulnerable taxa.

Lying within south-western corner of Africa, the SK biome is recognised as one of the World's most important regions of floral biodiversity. Here members of the Aizoaceae are especially well adapted to the arid desert environment, occupying niche habitats. This is most evident in the speciose dwarf succulent genus Conophytum, a SK specialist that shows a remarkable degree of range-restricted endemism and 20%+ of taxa can be considered as such [1]. The SK has also been identified as being at high risk from the effects of climate change, with preliminary data suggesting that dwarf succulents may be especially vulnerable [2-4]. However, neither the underlying mechanisms that influence the distribution and associated speciation of these succulents nor how they might respond to specific environmental conditions is understood. We now have an opportunity to address this by bringing together a range of complimentary techniques using the genus Conophytum as a model.

The project will take a unique, multidisciplinary approach, combining the expertise of the three supervisors (spatial modelling, molecular phylogeny and evolution, biochemistry and succulent plant biology). In addition, this study is only now possible because of the availability of two unique resources at LJMU: (1) the student will have full access to the most comprehensive database of ~3000 locality records covering all taxa in the genus and (2) a genetic resource arising from a complete in situ collection of all Conophytum taxa in the genus.

A three step approach to the work will be employed: (1) The existing spatial database and an ensemble of Species Distribution Modelling (SDMs) techniques (regression and machine learning models) available in the BIOMOD2 library [5,6], run and calibrated within the R statistical programming environment [7], will be used to quantify the role of climate and other environmental variables on the current distribution of the 166 taxa in the Conophytum genus. Of particular interest will be a comparison of the climatic niches of (a) 16 defined closely-related groups of taxa of varying vulnerability to extinction within the genus [8,1] and (b) point endemics (small vulnerable populations) versus those taxa with a ubiquitous distribution. (Months 1-12) (2) The Conophytum phylogeny will be reconstructed using suitable genetic markers developed based on Next Generation Sequencing from isolated DNA available from the in situ collection at LJMU. This combined with the biogeographic and spatial data will allow an assessment of the phylogeny in the context of the climatic and environmental drivers. In addition, a methodology typically applied to island endemic plants (see previous study by Kapralov et al., 2013 in Hawaii [9]), will be applied to the island-like populations of Conophytum on isolated inselbergs to understand the role of adaptation during radiation. The Conophytum phylogeny will therefore act as the foundation for further studies and will be used to map on it species ecology, morphology, distribution, pigment composition, physiology, and anatomy. This would allow us to better understand mechanisms behind the evolution of the genus and to compare roles of adaptation versus stochastic isolation for its prolific speciation. (Months 10-30) (3) Future threats from climate change will be assessed using the SDMs outlined in Step 1 incorporating a range of climate change scenarios to project the impacts on the future distribution of the Conophytum taxa [10-12]. Two time slices (2021 to 2050 and 2050 to 2080) will be used with a range of Regional Climate Models (RCM) (CCSM3, HadCM3, ECHAM5) and Special Report on Emissions Scenarios (SRES) (B1, A2, A1b) to provide 12 different climate change datasets to account for the RCM and SRES uncertainty in the modelling. Gap analysis will be used to assess the effectiveness of the current protected area network under future climates [10]. (Months 24-36 - thesis submission)

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LMU Munich PopGeneticsCancer

The Statistical Genetics group of Prof. Dr. D. Metzler at the Ludwig Maximilians- Universität (LMU) München (Munich, Germany) offers a

PhD Position for 3 years (65% TVL-E13)

for a researcher with a master's degree in

Bioinformatics, Statistics, Mathematics, or a related field.

(Exceptional candidates with a bachelor of honors (advanced degree) may be considered.)

The successful candidate will work in the project

Population genetics of hematopoietic neoplasms

within the collaborative reseach centre "Genetic and Epigenetic Evolution of Hematopoietic Neoplasms" (DFG Sonderforschungsbereich SFB 1243, http://www.sfb1243.biologie.uni-muenchen.de/index.html) and will have the chance to earn the Dr. rer. nat. degree.

In this project we will combine stochastic modelling, computational statistics, efficient algorithms, theoretical population genetics and, to some extent, also programming. Applicants with experience in one or more of these fields will be given priority. For more information about the project please see http://www.sfb1243.biologie.uni-muenchen.de/forschung/a16-metzler/index.html .

The LMU Munich is an equal opportunity employer and encourages women to apply. Handicapped candidates with equal qualifications will be given preference. If you are interested, please apply via http://portal.graduatecenter-lmu.de/ocgc/sfb1243 for the doctoral position in project A16. We will accept applications until 20. February 2016.

Prof. Dr. Dirk Metzler http:// evol.bio.lmu.de/_statgen pdf-version: http://evol.bio.lmu.de/_statgen/PhD_Position_SFB1243_A16.pdf Dirk Metzler <metzler@biologie.uni-muenchen.de>

MaxPlanckInst Berlin EvolutionHumanBehaviour

PhD position on Human Collective Behaviour. Max Planck Institute for Human Development, Berlin.

Starting data: The position is available from May 2016 onwards, but later start dates are possible.

Description: The PhD project will investigate the role of individual differences in human and animal collective behaviours, including group formation, group coordination and conflict resolution. It will involve experiments with human crowds using GPS tracking devices & video tracking, virtual interactive platforms and simulations. Limited work on animal groups (e.g., fish) is also possible. We seek a PhD student with a strong empirical background and excellent skills in (spatial) data analysis. Programming skills are a bonus.

The Center for Adaptive Rationality at the Max Planck Institute for Human Development (www.mpib-berlin.mpg.de) is a highly interdisciplinary and international research group where English is the working language. We offer an excellent infrastructure including support staff and equipment for conducting experiments (e.g., behavioural laboratory, GPS tracking and supercomputers).

The predoctoral contract is for three years. Applications (consisting of a cover letter describing your research interests, a CV, up to two publications, and two letters of recommendation) should be sent as a single PDF file, with your name as the file name, to Monika Oppong (oppong@mpib-berlin.mpg.de; Max Planck Institute for Human Development, Lentzeallee 94, 14195 Berlin).

Applications will be considered until the position is filled. Application review will begin on February 1, 2016 but applications after this date will be considered equally. For further inquiries about the position, please contact Ralf Kurvers (kurvers@mpib-berlin.mpg.de).

More information:

https://www.mpib-berlin.mpg.de/sites/default/files/download/jobs/stelle nanzeige_predoctoral_contract-arc_39-2015_10.12.2015_intern.pdf

"Kurvers, Ralf" <kurvers@mpib-berlin.mpg.de>

MississippiStateU EvolutionaryBiol

Opportunities for graduate studies in Ecology & Evolutionary Biology are available in the Department of Biological Sciences at Mississippi State University. The Department maintains active research programs in all areas of the Biological Sciences, with recent grant funding from all major federal agencies.

Current efforts in Ervin's lab include investigations of interplay between land use change and plant species distributions and studies of wetland restoration efforts on agricultural lands of the Mississippi Alluvial Valley.

Current research projects in Wallace's lab include systematics of Acmispon (Fabaceae) and evolutionary ecology of legume-rhizobium relationships. Additionally, GRA funding is available to support students interested in herbarium curation and use of the collection for studies of Southeastern flora.

The Welch lab is currently studying adaptive evolution at the level of gene expression in sunflowers. Several students are studying population genetic dynamics of Caribbean iguanas. Also needed is help identifying native estuarine grasses for Gulf Coast restoration using a molecular approach.

Funding for students may be provided through a combination of research and teaching assistantships within the department, and a limited number of competitive stipend enhancement awards are available.

Please contact Gary Ervin (gervinATbiologyDOTmsstateDOTedu), Lisa Wallace (lisawallaceATbiologyDOTmsstateDOTedu), or Mark Welch (welchATbiologyDOTmsstateDOTedu) for more information. Also, a CV that includes information regarding prior education, and research experience would be appreciated. For more information about the Ervin, Wallace, and Welch Labs, please visit our websites. http://lw404.biology.msstate.edu/, http://www.garyervin.net/, http://markwelch.net/Welcome.html

Mark E. Welch, Ph.D.

Associate Professor Graduate Coordinator Dept. of Biological Sciences Mississippi State University P.O. Box GY Mississippi State, MS 39762

E-mail: welch@biology.msstate.edu Webpage: http://markwelch.net Phone: 662.325.7564 Fax: 662.325.7939

"welch@biology.msstate.edu" <welch@biology.msstate.edu>

NorthernMichiganU WildebeestPopGenetics

We are seeking an MS student in Biology at Northern Michigan University (http://www.nmu.edu/biology/node/1) to start in August 2016. The student will work on analyses of population genetic (RADseq) data from blue wildebeest (Connochaetes taurinus) in southern Africa. This work is a collaboration between the laboratories of Kate Teeter, Alec Lindsay, and Jeff Horn at NMU, and the Zambian Carnivore Programme. The majority of the work for this project will be in bioinformatics and population genetic analyses, although there is a possibility for some additional molecular biology bench work. Support for this position includes two years of support during the academic year as a teaching assistant (tuition wavier and stipend).

Required minimum qualifications: - Familiarity with topics in genetics and evolutionary biology - Bachelor's degree in Biology or related field - Undergraduate GPA of 3.0 and GRE scores available - Other requirements for admission to MS program - see http://www.nmu.edu/biology/graduate-studies-admission

Desired qualifications: - Previous experience in bioinformatics and/or population genetics - Experience writing scripts in Python - GPA of 3.5 or above

To apply, please submit the following to Kate Teeter at kteeter@nmu.edu by February 1st, 2016: - A statement of interest (500 words or less; describe why you are interested in the position and any relevant research or course experience) - Current CV, with a focus on research and academic experience - Transcripts and GRE scores (unofficial reports are ok) - Contact info for three references.

The successful candidate will then need to apply to NMU for formal admission to the graduate program by March 1st. Informal email inquiries for more info about NMU Biology and the project are welcome (to kteeter@nmu.edu). NMU is an equal opportunity, affirmative action employer.

Katherine C. Teeter, Ph.D. Associate Professor, Biology Northern Michigan University

"kteeter@nmu.edu" <kteeter@nmu.edu>

NTNU MuseumTrondheim EvolutionaryGenomics

The NTNU University Museum, Department of Natural History

PhD-position in Evolutionary Genomics

The NTNU University Museum, Department of Natural History has a vacant PhD-position in Evolutionary Genomics from June 1, 2016.

The PhD-candidate will be part of the Systematics and Evolution research group (SEG) at the Department of Natural History. The position is financed by the Research Council of Norway (project number 250541: "Speciation genomics of peat mosses (Sphagnum) - testing speciation-with-gene-flow hypotheses in a highly diverse genus").

The position is for 3 years with the possibility of until 1 year extension with 25% duties in agreement with the department, and available for highly qualified candidates that wish to pursue a research career in biodiversity science using high-throughput sequencing.

Information about the department and the open position can be obtained from Professor Hans K. Stenøien, phone: +47 73 59 22 84, e-mail: stenoien@ntnu.no. Further information about NTNU: http://www.ntnu.edu/ The application should be submitted electronically through:

https://www.jobbnorge.no/en/available-jobs/job/121290/phd-position-in-evolutionary-genomics Deadline: February 15, 2016.

hans.stenoien@ntnu.no

NTNU Norway 2 Biodiversity

Dear all,

excellent candidates for a PhD position on "Biodiversity in heterogeneous environments" are wanted at NTNU. Department of Biology at NTNU in Trondheim (Norway) can fund two PhD positions among 14 different topics: https://www.ntnu.edu/biology/phd. We would like to find an excellent and highly motivated candidate for going into the competition of the projects funded by the Department of Biology. Our project aims to test theories on how landscape topography with all its microclimatic variation affects species capacity to adapt or disperse in response to climate change. The approaches to study this topic will involve fieldwork, theoretical and/or macroecological methods. If this sounds interesting to you, please read more about the project here: https://www.ntnu.edu/documents/140096/1267160052/Graae-Ratikainen.pdf/ and take contact with one of us before 22nd of January using the below email addresses:

Irja Ida Ratikainen: irja.i.ratikainen@ntnu.no Jonathan Lenoir: jonathan.lenoir@u-picardie.fr Bente Jessen Graae: bente.j.graae@ntnu.no

The official announcement can be found here: https://www.jobbnorge.no/en/available-jobs/job/120545/phd-positions-in-biology Best regards, Jonathan, Bente and Irja

Irja Ida Ratikainen Researcher, CBD (Centre for Biodiversity Dynamics) Department of Biology Norwegian University of Science and Technology http://www.nt.ntnu.no/users/irja/ irja.i.ratikainen@ntnu.no

NTNU Taipei InsectIslandSpeciaiton

The Systematics & Evolutionary Biology Lab at the Department of Life Sciences, National Taiwan Normal University (NTNU) in Taipei, Taiwan is seeking a self-motivated and enthuasiastic PhD student to work on comparative phylogeography of ecological speciation on Asian continental and oceanic islands.

The Project:

This research project will analyze the speciation mechanism of endemic freshwater insects between Taiwan and Yaeyama Islands of Japan (oceanic island), and between mainland Asia and Hainan Island (continental island). Several insect species are endemic to these islands and show adaptation to novel environments (ecological speciation) between islands. (See a damselfly example, Lee & Lin 2012: http://web.ntnu.edu.tw/~treehopper/lib/publications_lib_pdf/lee_lin_2012_mol_ecol.pdf)

The project will generate sequence/genomic data from multiple individuals of selected endemic species of the islands. First, phylogenetic and population genetic analyses will be used to infer the process of speciation between species pairs on the islands. Second, the level of intrinsic reproductive isolation between species pairs will be measured through crossing experiments. Third, the strength of natural selection between species pairs will be accessed through field studies of fitness components. Lastly, through the analysis of genome-wide DNA polymorphism of target species, the genomic regions and candidate genes underlying ecological speciation will be uncovered. International students with an interest in studying tropical island biology are encouraged to apply.

Funding:

Funding includes a competitive monthly stipend of NT$34,000 (US$ 1,133) for up to 3 years for both domestic and international students through the TIGP Biodiversity (Taiwan International Graduate Program - Biodiversity) (http://biodiv.sinica.edu.tw/TIGP-BP/), a jointed graduate program between NTNU and Academia Sinica. Students are also eligible for on-campus housing during the years of their studies.

Eligibility:

The position is open to all applicants that meet TIGP admission criteria, but preference will be given to students with a master degree or prior experiences in phylogenetics, population genetics and insect biology. Criteria/material used to evaluate the applicantÂÂs qualifications for the admission: (http://biodiv.sinica.edu.tw/-TIGP-BP/index.php?page=admission)

How to apply:

Interested candidates should email (1) a CV, (2) a list of prior experience and publication, (3) three references (contact info & e-mails), and (4) a one-page statement of research interests in one PDF file to Chung-Ping Lin (treehopper@ntnu.edu.tw) with the subject line “TIGP application ÂV Island Speciation”.

Additionally, candidates should submit a formal online application for admission in TIGP Biodiversity (http:/-/db1x.sinica.edu.tw/tigp/index.php). Deadline for applications through the online portal is March 31st for a September 2016 start.

Web pages:

The Systematics & Evolutionary Biology Lab

(http://web.ntnu.edu.tw/~treehopper/index.php?page=home&lang=en)

The Department of Life Sciences

(http://www.biol.ntnu.edu.tw)

National Taiwan Normal University

(http://en.ntnu.edu.tw)

TIGP Biodiversity Program Website

(http://biodiv.sinica.edu.tw/TIGP-BP/)

Biodiversity Research Center, Academia Sinica

(http://biodiv.sinica.edu.tw/en/)

Treehopper <treehopper@ntnu.edu.tw>

NTNU Trondheim TelomereLifeHistoryDynamics

A PhD position is available at the Department of Biology at the Norwegian University of Science and Technology (NTNU) in Trondheim on the functional relationships between telomere dynamics, physiology and life history traits in a small passerine bird, the House Sparrow (Passer domesticus). We are seeking a highly qualified candidate with a background in either evolutionary, behavioral or population ecology or eco-physiology. It is an advantage if the candidate has laboratory experience in genetic analyses. The aim of the PhD project will be to investigate central questions related to the functional associations between telomere dynamics, physiological parameters and individual behavior (“personality”), and how these are associated with trade-offs between life history traits such as growth rate, body size, reproduction and lifespan. Read more about the project here: https:/-/www.ntnu.edu/documents/140096/1266919530/-Ringsby+Functional+relationships-.pdf/888f0380-a998-43be-ae93-0c8660261963 Here is the link to the formal announcement: https://www.jobbnorge.no/ledige-stillinger/stilling/120545/phd-positions-in-biology Application deadline is 1st February. For further information contact: thor.h.ringsby@ntnu.no.

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

OklahomaStateU GrassEvolution

Graduate position: Oklahoma State University, Evolutionary and quantitative genetics of branching in grasses

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

Essential qualifications include masters degree in genetics and/or molecular biology, experience in molecular lab techniques, experience in growing plants and analyzing them using microscopic and other methods, and excellent writing skills. Desirable qualifications include experience with quantitative and phylogenetic analysis software, and programming in R and/or Python.

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

Application deadline: February 29th, 2016; but applications will be reviewed as they arrive.

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

Andrew Doust Department of Plant Biology, Ecology, and Evolution Oklahoma State University Physical Sciences 301 Stillwater, OK 74078

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

Websites: http://botany.okstate.edu/people_research/-Doust/index.html http://tillering.okstate.edu/ http://osubioret.okstate.edu/ "Doust, Andrew" <andrew.doust@okstate.edu>

Oslo Bioinformatics

http://uio.easycruit.com/vacancy/1567523/64290?iso=-no Description follows below:

position as PhD Research fellow (postition code 1017) is available at Department of Informatics.

The fellowship will be for a period of 3 years, with no compulsory work or for a period of 4 years, with 25 % compulsory work (teaching responsibilities at the department) contingent on the qualifications of the candidate and the teaching needs of the department. Starting date no later than 1 October 2016. No one can be appointed for more than one fixed-term period at the same institution.

The research fellow will take part in the Centre for Computational Inference in Evolutionary Life Sciences (CELS). CELS is a multidisciplinary centre within life sciences comprising strong research environments in biology and statistical and computational methods for data analysis. CELS addresses fundamental biological questions related to the genotype-phenotype paradigm, how the environment affects genome evolution and development of methods for integrated analysis of genomic and other biotic and abiotic data. A main goal is to develop interdisciplinary research activities generating science of true interest for computer scientists, statisticians and biologists.

Project description:

Metagenomics is the study of the genetic material in a sample containing a mix of different microbial organisms. These samples may have be obtained from such diverse locations as the vertebrate gut (e.g. human or fish), from the depths of the oceans, from the soil somewhere on earth and so forth. Recent advances in DNA sequencing technologies have enabled very large amounts of such data to be obtained for analysis. Extracting biological meaningful information from these huge datasets involve hard computational challenges that can only be solved by good algorithms and efficient parallelization. Interpreting the data correctly can advance science by a better understanding of, for example, the diversity of ecosystems or how the immune system responds to exposure to microorganisms.

We are seeking a highly motivated candidate to develop new or improved algorithms or

tools for metagenomics with improved functionality, accuracy or speed that will be valuable for the scientific community. This is an opportunity to develop open source software in areas like error detection and removal, clustering, searching, classification, genome assembly as well as other areas of metagenomics. We have already contributed with tools like Swarm (http://dx.doi.org/-10.7717/peerj.593) and VSEARCH. The successful candidate will be embedded in a vibrant bioinformatics environment connected to two Norwegian Centres of Excellence, and have access to first-rate computational infrastructure. The position is associated with the Centre for Computational Inference in Evolutionary Life

Science (CELS) at UiO. The CELS research environment offers extensive experience with high-throughput sequencing and assembly of large genomes such as that of Atlantic cod (http://dx.doi.org/10.1038/nature10342). The candidate will be supervised by an interdisciplinary team of scientists and will collaborate with other PhD research fellows within CELS.

Requirements:

The Faculty of Mathematics and Natural Sciences has a strategic ambition of being a leading research faculty. Candidates for these fellowships will be selected in accordance with this, and expected to be in the upper segment of their class with respect to academic credentials.

Applicants must hold a Master's degree or equivalent in bioinformatics or computer science, and need to document good software development skills.

The candidate would need to learn genomics/metagenomics during the project, but no formal prior knowledge of biology is required.

The purpose of the fellowship is research training leading to the successful completion of a PhD degree.

The fellowship requires admission to the PhD programme at the Faculty of Mathematics and Natural Sciences. The application to the PhD programme must be submitted to the department no later than two months after taking up the position. For more information see:

http://www.uio.no/english/research/doctoral-degree-and-career/phd/application/ http://www.mn.uio.no/-english/research/doctoral-degree-and-career/phd-programme/index.html A good command of English is required.

http://www.mn.uio.no/english/research/doctoral-degree-and-career/regulations/proficiency-requirements.html

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OxfordBrookesU GeneDuplication

A PhD position is available in the lab of Professor Alistair McGregor at Oxford Brookes University.

Project title: Investigating the role of gene duplication and divergence during the evolution of spiders, scorpions and other arachnids

Project description: Gene duplication is an important mechanism underlying the evolution of organismal diversity. The duplication of genes in arachnids represents an excellent opportunity to systematically study the role of gene duplication in the evolution of gene regulatory networks, development and phenotypic variation. This project will study the expression of paralogous genes and characterize their function using CRIPSPR/Cas9 and RNAi to evaluate the subfunctionalisation, neofunctionalisation and co-evolution of duplicated coding and noncoding genes during the development of spiders, scorpions, harvestmen and other arachnids.

This project will be carried out in collaboration with Dr. Prashant Sharma (University of Wisconsin-Madison). The successful applicant will join a dynamic international team and training will be provided in all molecular biology, developmental biology, molecular evolution and bioinformatics approaches. During the project the student will also have the opportunity to travel to the collaborating lab and attend national and international conferences.

As part of your training you will be required to assist in demonstrating on undergraduate practicals during semesters.

Main supervisor Professor Alistair McGregor

Details of the position: Eligibility: Only open to UK/EU applicants (who must be permanently resident in UK/EU)

Start date: 19th September 2016

Bursary: Â£14057 pa for academic year 2016/17 & fees

Closing date: 21st February 2016

Applicants should be of the highest quality and capable of submitting a PhD thesis within 3 years. Requirement a good Honours degree (2.1 or equivalent).

EU applicants must have a valid IELTS Academic test certificate minimum score level 6 in each of the four areas of reading, writing, listening and speaking with overall minimum score 7.0 issued since the 23rd April 2015 by an approved test centre please see web site below. Or an undergraduate degree awarded by a recognised UK university within the last two years.

For further information on the project please contact Professor Alistair McGregor: amcgregor@brookes.ac.uk + 44 (0)1865 484191

How to apply:

Please complete the Application Form, which you can download from

http://www.hls.brookes.ac.uk/images/research/phd-studentship-application-form-jan-14.doc Additionally with your application you should enclose a CV plus scanned copy of your degree certificates and transcripts and letter from awarding body. Additionally if appropriate a valid IELTS Academic test score and passport number.

Applications only accepted by e-mail to the following address: hlsapplications@brookes.ac.uk

– Professor Alistair P. McGregor Department of Biological and Medical Sciences Oxford Brookes University Gipsy Lane Oxford OX3 0BP United Kingdom

Tel: +44 (0)1865484191 Fax: +44 (0)1865483242 amcgregor@brookes.ac.uk www.mcgregor-evo-devo-lab.net twitter: @McGregorLab

"p0076379@brookes.ac.uk" <p0076379@brookes.ac.uk>

RoslinInstitute UEdinburgh CanineGenomics

Ph.D. Studentship at The Roslin Institute (University of Edinburgh) DEADLINE: 01 FEBRUARY 2016.

We are currently recruiting a 3-year Ph.D. student to investigate genetic diversity and evolutionary changes in dogs using genomic techniques.

Domesticated animals provide an ideal study system for addressing a variety of questions in biology due to their substantial phenotypic variation, the rapid rate of phenotypic change and the broad diversification between breeds within a species. Dogs are particularly extreme in this regard, showing wide variation in both physical and behavioural characteristics, and thus are an excellent model species for questions in evolutionary biology, genetics and behavioural biology.

The student will apply population genetic and genomics techniques to investigate diversity within and between dog breeds, to identify genomic regions that show evidence of selection and to address whether signals of selection are enriched in regions of the genome associated with behavioural traits, as has been hypothesized more generally for domesticated animals. Bioinformatics analyses will be applied to investigate functional classes of genes that are enriched in genomic regions associated with these behavioural traits and in regions showing evidence of selection.

The studentship will provide training in transferable skills and techniques in quantitative and population genetics, statistics, bioinformatics and genomic analysis. The student will also be expected to regularly attend seminars, journal clubs and local meetings including the Edinburgh Alliance for Complex Traits. There will be opportunities for attendance at national and international conferences.

We are seeking an enthusiastic individual with an interest in population and evolutionary biology and animal genetics as well as aptitude with computer-based statistical analyses. The candidate should possess a good quality first degree in a relevant subject. Enthusiasm, dedication and aptitude are the most important characteristics; additional training in genetics, genome analysis and animal behaviour are available through MSc courses at the University of Edinburgh.

For further information about the project, contact Pam Wiener (pam.wiener@roslin.ed.ac.uk). For information about the application process and to apply, go to http://www.roslin.ed.ac.uk/postgraduate/studentships/genetics-of-dogs-breed-structure-and-the-impact-of-human-mediated-selection/ .APPLICATIONS MUST BE SUBMITTED ONLINE.

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

"pam.wiener@roslin.ed.ac.uk"
<pam.wiener@roslin.ed.ac.uk>

StockholmU EvolutionaryGenomics

PhD student position in Evolutionary Genomics at Stockholm University/SciLifeLab

The complete ad for this position is available on the Stockholm University webpage at http://www.su.se/english/about/vacancies/vacancies-new-list?rmpage=3Djob&rmjob=958 Background and Project The position is associated with the project 'Adaptive significance of cis-regulatory changes in plants'. In this project, we aim to elucidate the impact of natural selection on regulatory variation in crucifers with well-characterized genomes. The PhD student will use a combination of gene expression analyses and population genomics to identify cis-regulatory variation and quantify selection on regulatory regions. A particular focus will be on testing for parallel cis-regulatory changes associated with the selfing syndrome, a suite of floral changes that have evolved repeatedly following transitions from outcrossing to self-fertilization. The project will greatly benefit from established bioinformatics pipelines for analyses of allele-specific gene expression (e.g. Steige et al 2015 MBE 32:2501-2514) and population genetic analyses of selection (e.g. Slotte et al 2013, Nature Genetics 45:831-835, Steige et al 2015 BioRxiv doi:10.1101/034025).

Infrastructure and Environment The student will be based in the Slotte lab (http://www.tanjaslottelab.se), a part of the Dept. of Ecology, Environment and Plant Science, Stockholm University (http://www.su.se/emb/english/). We are located at the Science for Life Laboratory in Stockholm (http://www.scilifelab.se), which holds considerable expertise in high-throughput sequencing technology and bioinformatics. The working atmosphere is international with English as the working language, and the position offers plenty of opportunities for scientific exchange with both geneticists, evolutionary biologists and ecologists at SciLifeLab and Stockholm University. The city of Stockholm is known for its beauty, its buildings and architecture and its abundant clean and open water.

Qualifications Applicants must have a Masters degree, including at least 15 credits from a course in Ecology or a related subject, as well as 30 credits from a relevant master project.

Selection For this position, a strong interest and documented training in evolutionary genetics is required. An aptitude for computational genomics and documented experience in programming or scripting using e.g. Python, Perl, or another scripting language is desirable. Experience of basic molecular genetics lab work or experimental work with plants is beneficial.

Selection among eligible candidates will be based on their capacity to benefit from the training. The following criteria will be used to assess this capacity: the candidates' documented knowledge in a relevant field of research, written and oral proficiency, the capacity for analytical thinking, the ability to collaborate, as well as creativity, initiative, and independence. The assessment will be based on previous experience and grades, the quality of the degree project, references, relevant experience, interviews, and the candidate's written motivation for seeking the position.

Admission Regulations for Doctoral Studies at Stockholm University are available at: www.regelboken.su.se . Terms of employment PhD studies involve four years of full-time study. Doctoral students should primarily devote themselves to their own education, but may engage in teaching, research, and administration corresponding to a maximum of 20 % of a full-time position.

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

Contact For more information, please contact Dr. Tanja Slotte, tanja.slotte@su.se

Union representatives Anqi Lindblom-Ahlm (Saco-S) and Lisbeth Häggberg (Fackförbundet ST), telephone: +46 8 16 20 00 (operator), Gunnar Stenberg (SEKO), telephone: +46 70 316 43 41, and PhD student representative, fredrik.c.l@sus.su.se.

Application Apply for the position no later than February 20th, 2016, at Stockholm University's recruitment system by clicking the "Apply" button (see http://www.su.se/english/about/vacancies/vacancies-new-list?rmpage=3Djob&rmjob=958). We recommend that you hand in your application, including all required documents, in English.

Please include the following information with your application * Your contact details and personal data * Your highest degree * Your language skills * Contact details for 2ï¿½"3 references and, in addition, please include the following documents * Cover letter

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StockholmU HostParasitoidEvolution

PhD student in Ecology with a focus on Ecological Genomics

at the Department of Ecology, Environment and Plant Sciences, Stockholm university.

Project description The position will be associated with the project 'The ecology and evolution of indirect interactions in host-parasitoid systems', that is a multidisciplinary project involving a research group with experience in Ecology, Population Genomics and Molecular Biology of insect immune system. The overall aim of the project is to understand the evolutionary mechanisms underlying geographic variation in host immune responses and parasitoid virulence in a well studied model system, and potentially also the speciation process. The specific aim of the PhD-position is to explore the genomic basis and the evolutionary mechanisms underlying the geographic variation in parasitoid virulence. The main task includes laboratory studies, but the work may also involve field collecting trips and experiments. Previous experience in molecular genetics or ecological genomics is meriting.

Contact For more information, please contact Professor Peter Hambäck, peter.hamback@su.se. See also http://www.su.se/english/about/vacancies/vacancies-new-list Application Apply for the position at Stockholm University's recruitment system by clicking the "Apply" button. The instructions for applicants are available at: http://www.su.se/english/about/vacancies/instructions-applicants. Closing date: 20 February 2016.

"peter.hamback@su.se" <peter.hamback@su.se>

SwanseaU CampylobacterEvolution

PhD studentship in Campylobacter Genomics and Evolution (2016-2019)

Research will be conducted under the direct supervision of Prof Samuel K. Sheppard, and based in the Department of Medical Microbiology and Infectious Diseases at the Swansea University Medical School (Wales, United Kingdom).

Project description:

The successful applicant will join a multidisciplinary group focusing on population biology and evolution of bacterial pathogens of public health importance. They will investigate the genetic basis and ecology of Campylobacter by explaining the factors involved in generating and maintaining genotypic and phenotypic diversity in among isolates in the primary reservoir of human disease, poultry. Comparative genomics and functional characterisation approaches will examine the genetic structuring and answer fundamental questions about how genetic variation and genome plasticity influence adaptation and the evolution of pathogenicity. Bioinformatics will be exploited for the design of vaccines for the control of Campylobacter in broiler chickens on farm. They will be responsible for culturing isolates, extracting DNA for genetic characterisation, analysing genomic data and carrying molecular and functional characterisation in the lab. The student will also spend a three month placement at Ridgeway Biologicals Ltd where he/she will be directly involved in the manufacture of autogenous vaccines prior to testing on farm.

Requirements:

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

Details:

- The duration of a studentship is 3 years (2016-2019). - The position is open until filled, but a preferred deadline for application is 1st March 2016, to allow for registration and the project to start ASAP. - Salary will be commensurate with regular UK postgraduate stipends, i.e. ??16,450 (circa 21,000) per annum tax-free. - Please contact Samuel Sheppard (s.k.sheppard@swansea.ac.uk) for informal inquiries or applications (please attach CV and describe motivation).

Application:

To apply by e-mail, please describe motivation and attach a CV to sheppardlab@gmail.com.More details about the laboratory: http://www.sheppardlab.com/ Dr. Guillaume M????ric NISCHR Research Fellow

Swansea University Medical School Medical Microbiology and Infectious Disease

ILS1 Room 140 (MRC CLIMB Centre) Singleton Campus, Swansea SA2 8PP United Kingdom ~ Sheppard Laboratory: http://www.sheppardlab.com/ MRC CLIMB: http://www.climb.ac.uk/ "MERIC G." <g.meric@swansea.ac.uk>

Switzerland WhitefishSpeciationGenomics

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is a Swiss-based and internationally networked aquatic research institute within the ETH Domain (Swiss Federal Institute of Science and Technology). It is committed to the ecologically, economically and socially responsible management of water resources and aquatic ecosystems.

The Department of Fish Ecology and Evolution (FishEc) located in Kastanienbaum (Lucerne, Switzerland) has a vacancy for a 1 PhD-student in Whitefish Speciation Genomics.

Speciation research has started to address long-standing questions on the genomic basis underlying and the genome evolution accompanying the speciation process. However, the accurate interpretation of genomic patterns is challenging due to a variety of different processes, such as drift, selection, gene flow, and recombination, all acting simultaneously in shaping the genome and contributing to the heterogeneity of divergence observed along the genome. A system like the Swiss whitefish radiation (Coregonus lavaretus complex) permits us to assess genomic divergence along a continuum of geographic, genetic, and ecological differentiation, in order to understand which evolutionary processes drive adaptation and divergence and to gain insights on the genomic basis of ecological speciation.

The PhD project advertised here is aiming to build a reference genome backbone and assess the variation in genome structure across whitefish species in Swiss lakes. Another goal will be to investigate the genetic architecture of ecological and reproductive traits differing across whitefish species and to compare patterns of genomic divergence across different sympatric and allopatric species. This will require the development of innovative analysis methods, which make full use of the fantastic study system to enhance our knowledge on the genomic basis of adaptation and speciation.

The successful candidate will have substantial opportunities to develop his or her own research skills and to assist in the supervision of Bachelors, and Master students. The work will consist of the analysis of next generation whole genome data, the development of bioinformatics pipelines and tools, and the interpretation and publication of the results. This study will be carried out in a close collaboration between the Fish Genomics group of Philine Feulner (http://www.eawag.ch/en/-department/fishec/main-focus/fish-genomics/) and the Evolutionary Biodiversity Dynamics group of Ole Seehausen (http://www.eawag.ch/en/department/fishec/-main-focus/biodiversity-dynamics/) at Eawag Kastanienbaum.

Applications are sought from individuals with a profound interest in Bioinformatics and Evolutionary Genomics. Applicants should have earned an MSc-degree (or equivalent) in a relevant field of evolutionary biology, or bioinformatics. Excellent communication skills in English and skills in team work are essential. The duration of the position will be three years, financed by the Swiss National Science Foundation.

We are a research department of Eawag (Department of Fish Ecology and Evolution; http://www.eawag.ch/en/-department/fishec/) and a division (Aquatic Ecology) of the Institute of Ecology and Evolution of the University of Bern, and the successful candidate will greatly benefit from the possibility to take advantage of both these excellent academic environments. The work place is at Eawag's Center for Ecology, Evolution and Biogeochemistry in Kastanienbaum, Lucerne, which besides the Fish Ecology and Evolution Department hosts research group from the Departments "Aquatic Ecology" and "Surface Waters - Research & Management" and offers a beautiful workplace at the shores of Lake Lucerne, a friendly international working climate and a strong cross-disciplinary research environment. The successful candidate will be enrolled in the University of Bern PhD-student program.

Eawag is an equal opportunity employer. Women are explicitly encouraged to apply to increase their share in science and research. Applications should include a concise statement describing your motivation to work on this research project, curriculum vitae, copies of your academic qualifications and names for two references.

The deadline for applications is 29 February 2016 but we consider applications until the position is filled. The starting date for the position is anticipated as soon as possible. For further information, please contact Philine Feulner(philine.feulner@eawag.ch ; +41 58 765 21 06).

We look forward to receiving your application through this webpage, any other way of applying will not be considered. Please click on the link below, this will take you directly to the application form.

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TexasChristianU EvolutionaryGenomics

MS position* A graduate research assistantship position (TA funded) is available in the lab of Dr. Matt Hale in the Biology Department at Texas Christian University starting in August 2016. The student will develop a MS project on the genetic basis of complex phenotypic traits. Some possible research projects include questions relating to the genetic basis of migration in salmonid fishes, and the presence and identity of genes showing patterns of sex-bias in expression, also in the salmonid fishes. The applicant should have some previous lab experience, including DNA extraction, PCR amplification, and DNA sequencing. Ideally, the candidate will also have experience with RNA extraction, cDNA synthesis and bioinformatics, although training in these areas will be provided. Interested applicants should send a CV, a cover letter describing their research interests and reasons for applying, and the names and contact details of two potential referees. Review of applications will begin on January 20th 2016. Please send inquires and applications to Matt Hale (m.c.hale@tcu.edu) Interested students are encouraged to view the Biology Department website (http://www.bio.tcu.edu) for more information on the graduate program.

"Hale, Matthew" <m.c.hale@tcu.edu>

TexasTechU EvolutionaryMetagenomics

Graduate position: PhD Studentship

Topic: Evolution of the extended host phenotype: metagenomes in mammalian systems

Synopsis: Continuing the long history of excellence in mammalian evolutionary and ecological research at Texas Tech University and the Natural Science Research Laboratory, the laboratory of Caleb Phillips is accepting applications for a PhD position in mammalian evolutionary metagenomics. The successful applicant will receive a well-rounded training on the laboratory, bioinformatic, and biostatistical methods for metagenomic research. The focus of the successful applicant?s dissertation research will be on improving our understanding about how metagenome gene and community composition evolve in response to selection pressure from host phenotype. This project is positioned at the interface between evolutionary genomics and ecological research and will integrate principles towards a systems-level synthesis of how genomic content, community assembly processes, and selection pressure shape metagenomes and promote host success. The applicant?s project will utilize bats as a study system. The order Chiroptera displays remarkable dietary diversity, lineages that hibernate and undergo torpor, and experience extreme energetic demands associated with volant flight, migration, and reproduction. An integral role of the metagenome in supporting these processes provides a system to develop a mechanistic understanding of the metagenome as an extended host phenotype. Temperate and tropical field work will be a component of the applicant?s experience.

How to apply: Complete application packages should include a 1) full CV, 2) names and contact information for two academic referees, 3) a personal statement describing research experience, interests and career goals (1000 words maximum), and 4) a cover letter.

Completed applications should be submitted to Dr. Caleb Phillips (caleb.phillips@ttu.edu) with subject line ?EXTENDED HOST PHENOTYPE?.

Graduate student financial support will derive from a flexible combination of research and teaching assistantships providing the advantage of developing both teaching and research portfolios.

Resources: https://www.depts.ttu.edu/biology/ http://www.nsrl.ttu.edu/ Caleb D. Phillips, Ph.D. Curator or Genetic Resources Natural Science Research Laboratory Assistant Professor Biological Sciences Texas Tech University Lubbock, Texas, 79409 caleb.phillips@ttu.edu 806-834-8181

"Phillips, Caleb" <caleb.phillips@ttu.edu>

UAmsterdam MothSexualSelection

PhD position available at the University of Amsterdam, Institute for Biodiversity and Ecosystem Dynamics, Dept. Evolutionary Biology

Project: Understanding sexual selection: which sex leads the dance when both are signallers?

Supervisor: Dr. Astrid T. Groot

http://home.medewerker.uva.nl/a.t.groot/ Sexual selection generally assumes that one sex is the signaller and the other sex the responder. The forces of sexual selection are likely more complex when both sexes are signallers and responders. In moths, the species-specific female sex pheromones to which males are attracted from a distance have been studied in detail, because these pheromones can be used for pest management. However, at close-range males produce and emit a biosynthetically related but different pheromone, which is likely important for close-range female choice and/or male competition. This project aims to determine the role of close-range courtship in generating variation in the sexual communication channel to assess the strength of mutual mate choice in a species where we have found a within-population polymorphism in the female sex pheromone. This project will combine behavioral and chemical analyses with genetic (quantitative trait locus) analyses to answer the questions whether the female and male sex pheromone genetically linked, what are the genes underlying the male pheromone variation, what is the importance of male sex pheromone variation in female choice and what is its role in male-male competition.

Requirements

-MSc in Biology, with focus on evolution, and interest in chemical ecology and entomology;

-Experience with molecular biological techniques, preferably also with genetic analyses

-Interest to combine laboratory and field studies with genetic and chemical analyses

-Skills in experimental design and statistical analysis

-Proficiency in scientific writing and communication

Applications should include a detailed CV, a motivation letter, and the names and contact addresses of two references from which information about the candidate can be obtained. Applications should be sent before 5 February to application-science@uva.nl. Please quote vacancy number 16-005 in the subject field. Interviews will be held in the week of 15 February.

Appointment The position will start preferably March or April 2016. The full-time appointment will be on a temporary basis for a maximum period of four years. Initial appointment will be for a period of 18 months and after satisfactory evaluation it will be extended for a total duration of four years. The full-time gross monthly salary will range from 2,173 in the first year to 2,778 in the final year, according to the Dutch salary scales for PhD candidates. The Collective Labour Agreement for Dutch Universities is applicable. The annual salary will be increased by 8 % holiday allowance and 8.3 % end-of-year bonus.

Astrid Groot <A.T.Groot@uva.nl>

UAuckland HarvestmenEvolution

PhD Scholarship: Evolution of exaggerated male weaponry in harvestmen

$27,000 NZD per year for 3 years.

School of Biological Sciences, University of Auckland, New Zealand

Supervisor: Dr Greg Holwell

I invite suitably motivated and dedicated applicants to apply for a fully funded PhD scholarship to work on the evolution of extreme male weaponry in New Zealand harvestmen (Opiliones). Males from the genera Pantopsalis and Forsteropsalis possess among the most exaggerated weapons in the animal kingdom. Their chelicerae can comprise 50% of their body weight and in some species are polymorphic with males displaying either elongated or short broad forms within the same population. The specific details of the student's project is up to negotiation but would combine some of the following: field observations throughout New Zealand, behavioural experiments, microCT imaging, geometric morphometrics, molecular phylogenetics and/or comparative methods. The scholarship is available for application now. The successful candidate will have research experience, a strong academic record and possess a MSc or Honours research degree in behavioural ecology, evolutionary biology and/or morphology. The successful candidate will work under the supervision of Dr Greg Holwell (The University of Auckland, NZ), and will have access to a range of world-class facilities at the University of Auckland with the opportunity to travel for both fieldwork and collaboration. This position is funded through the Marsden Fund of the Royal Society of New Zealand, and the successful applicant is expected to begin in early 2016.

Please submit applications directly to Dr Greg Holwell at g.holwell@auckland.ac.nz and provide a CV, academic transcript and a letter detailing your research interests and motivation for considering the project

Best wishes Greg Dr Greg Holwell - Senior Lecturer School of Biological Sciences, University of Auckland Private Bag 92019, Auckland 1142, New Zealand Phone: +64 (0)9 373-7599 extn 83652 http://www.bioscienceresearch.co.nz/staff/-1021/dr-greg-holwell/ Our new book, Austral Ark, published by Cambridge University Press at www.cambridge.org/9781107033542 Gregory Holwell <g.holwell@auckland.ac.nz>

UCLouvain Belgium PlantHybridFitness

I am looking for good candidates to pursue a PhD in my group on the subject of fitness of natural hybrids between two Rhinanthus species (see Natalis & Wesselingh Oecologia 2012, Am J Bot 2012, Evolution 2013). The aim of the project is to study fitness in hybrids of known descent and link their performance to the composition of their genome. The work will involve field observations (plant size, pollinator behaviour, seed production) and genetic analyses using NGS techniques. UCLouvain is located in Louvain-la-Neuve, a small campus town in the French- speaking part of Belgium, at 30 km from Brussels, Namur and Leuven.

I need a good candidate before 15 February 2016 to include in an application for a 15-month university grant: the results will be known in June 2016. Obtaining this starting grant is not guaranteed (competition is quite strong), and if it is granted, it will be necessary to apply for another type of grant to have funding for the full 4-year PhD period, for which the first opportunity will present itself in September 2016. The net monthly salary is 1831 in the first year.

A good candidate has: - a university degree in Biology that gives access to a PhD programme (so a 2-year MSc degree in Europe), or will obtain a degree of this kind before the end of September 2016 - very good study results - a passion for evolutionary ecology - good communication skills in English or French: the second grant application process involves giving an oral presentation and answering questions on the project in front of a selection committee - some knowledge of bio-informatics, especially on how to work with NGS data, would be very useful, but is not mandatory.

If you are interested, please send me your CV and motivation by email. I will select the best candidate and submit the first grant proposal on 15 February 2016, so I need to receive your declaration of interest before Friday 12 February 2016.

For the first grant, I will only need the CV of the applicant, a detailed listing of the study results (year by year) and the subject of the master thesis. You will not have to have to write anything for this grant application, but you will be involved in the subsequent grant proposal. I have to stress that the starting grant is nominative: if your name is on the application and you decide not to do it, I will not be able to hire someone else. So a certain level of commitment is desirable: if you are not sure you really want to do this, please do not apply.

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

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

Renate Wesselingh <renate.wesselingh@uclouvain.be>

UCollege Dublin eDNA

A 3-year PhD scholarships are available in University College Dublin on an EPA-funded, multidisciplinary project (ReConnect) to harness the existing knowledge base and develop a validated methodology for prioritising selection of barriers on rivers for modification or removal to improve hydromorphology and connectivity in Irish freshwater systems.

The students will be involved in fieldwork mapping barriers on selected Irish rivers but each student will work on a different component of the project. All will benefit from interaction with a multi-disciplinary team of researchers and with each other. Start date: April 1st 2016 (or as soon after that as possible) Scholarship: euro 22,550 in year 1 to euro 23,902 in year 3 (Note: annual registration fees are deducted from these figures)

PhD Position Location: UCD School of Biology & Environmental Science; Supervisor: Dr Jens Carlsson The research will investigate the feasibility of using environmental eDNA (species specific qPCR and next generation sequencing based metabarcoding) to examine the catchment-wide impact of various types of barriers, singularly or in combination, on key fish and macroinvertebrate species. Applicants should have a good honours Bachelor or Masters degree in Zoology, Genetics or related discipline. Experience in lab-based genetics is a requirement while familiarity with qPCR and/or eDNA would be an advantage.

A letter of application and CV should be forwarded by email to jens.carlsson@ucd.ie (PhD Position 3) by Friday February 5th, 2016

jens.carlsson@ucd.ie

UCologne ArabidopsisAdaptation

PhD position on "Regional adaptation in Arabidopsis thaliana " in the Lab. of J. de Meaux, University of Cologne, Germany. In this project, the PhD candidate will decipher the molecular basis of plastic responses in the model species A. thaliana, that have provided regional adaptation in plant growth in the presence of distinct light cues. The candidate will grow A. thaliana plants originating from various European regions side-by-side next to plants originating from China, which form an outgroup. Plants will be exposed to various light and temperature regimes and both their growth and their transcriptome will be compared. the importance of several plastic responses for regional adaptation. With this project, the PhD candidate will acquire skills ranging from genomics to molecular genetics and ecology.

The applicant must hold a Master degree in Evolutionary Biology, Genetics, Genomics or Bioinformatics and prove interest in plant molecular, population or ecological genetics. Experience in statistical analysis of quantitative data is required. This position is open to applicants of all nationalities but the language in the lab is English. Applications or questions regarding the position should be sent by mail to jdemeaux@uni-koeln.de, with the following subject line - PhD application Regional adaptation thaliana - de Meaux lab. A letter of motivation, a CV and the contact to 2 independent referees should be provided, all in a single pdf file. Revision of applications will begin on Feb. 15th, 2016 and continue until the position is filled. Funding is for 3-4 years with starting date in between May and July. For more information on our lab and research visit our website http://www.botanik.uni-koeln.de/1146.html. Interested students currently completing their Master thesis are encouraged to informally contact the PI if they have questions concerning the position.

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

"jdemeaux@uni-koeln.de" <jdemeaux@uni-koeln.de>

UConnecticut PlantComputationalGenomics

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The Plant Computational Genomics lab in the Department of Ecology and Evolutionary Biology at the University of Connecticut seeks motivated PhD and MS students to join the lab in the Summer/Fall of 2016. Our research focuses on the computational analysis of genomic and transcriptomic data generated by next-generation sequencing platforms from non-model forest tree species. We implement this through analysis related to gene finding, gene expression, transcriptome assembly, and conserved element identification, through machine learning and computational statistics. We use these methods to address questions related to genome biology and population genomics. In addition, we develop web-based applications that integrate BIG data across domains to facilitate the forest geneticist or ecologists ability to analyze, share, and visualize their data (http://treegenesdb.org). Such integration requires the implementation of semantic technologies and ontologies to connect genotype, phen otype, and environmental resources.

Research Topics: Potential research topics in our group include 1) development of visualization tools to support genome-wide association studies in forest trees; 2) application of genomic and transcriptomic techniques to evaluate the impact of climate change on tree populations; 3) development of software solutions to improve assembly and characterization of non-model plant transcriptomes; 4) interrogation of natural genetic variation across populations in large, complex conifer genomes; 5) and your ideas here!

To Apply: Financial support for M.S. and Ph.D.

students is available through research assistantships, teaching assistantships, and university fellowships. To learn more about our research, please visit: http://-compgenomics.lab.uconn.edu/. Excellent written and oral communication, as well as strong quantitative skills, are required. Backgrounds in genetics/genomics, evolutionary biology, bioinformatics, and computer science are desired. Interested candidates should send an email describing their research interests along with a CV, unofficial undergraduate/graduate transcripts, and GRE scores to Jill Wegrzyn (jill.wegrzyn@uconn.edu). Qualified candidates will be contacted directly for Skype interviews following review.

About UConn: The University of Connecticut (UConn) has been one of the nations leading public institutions since its founding in 1881. Located in Storrs, UConns main campus is situated in the picturesque rolling forests and fields quintessential of New England, yet is only 30 minutes from Hartford, and has close connections to Providence, Boston and New York. The Department of Ecology and Evolutionary Biology consists of over 30 faculty and 60 graduate students with research spanning nearly all major groups of organisms. The Department maintains close ties with the Departments of Physiology and Neurobiology, Molecular and Cell Biology, Marine Sciences, and Natural Resources Management and Engineering, as well as the Center for Environmental Sciences and Engineering and the Institute for Systems Genomics, which together comprise one of the largest groups of biologists in the Northeast.

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UEdinburgh PlantBiodiversity

MSc/Dipl. Course in the Biodiversity and Taxonomy of Plants

A one year course organized by the Royal Botanic Garden Edinburgh and the University of Edinburgh

Running since 1992, this highly acclaimed course benefits from a close connection between the Royal Botanic Garden Edinburgh, one of the leading institutions for the study and conservation of plants, and the University of Edinburgh, one of the top universities in the world.

* Students are based at RBGE, with major collections of living and preserved plants, an extensive library, and modern research facilities; * World experts deliver and design the course and students benefit from a supportive and inspiring environment; * Edinburgh is one of four Scottish gardens run by RBGE, encompassing many habitats and an incredible plant collection; * In addition, Edinburgh is a great city to be a student with a thrilling cultural and social life.

Taught part of the course The course covers following modules:

* Evolution and biodiversity of angiosperms * Evolution and biodiversity of cryptogamic plants and fungi * Phylogenetics and Population genetics * Conservation science, statistical analysis and fieldwork techniques * Herbarium taxonomy, collections, and conservation * A tropical field course in Central or South America

Research project The course includes a three-month scientific research project enabling the student to become part of a research team, benefiting from extensive experience. The course places great emphasis on fundamental knowledge (identifying plants and their evolution), as well as acquiring practical field- and herbarium techniques, giving a strong basis for botanists, ecologists and other natural scientists embarking on a career in biodiversity. There are excellent prospects for graduates in academia, industry, and conservation.

The course aims to be more than just a degree V it unlocks a better understanding of the world of plants and their importance to humanitys future. This aspiration becomes increasingly important in our present world, where demographic pressures push the natural world to its limits despite huge areas remaining unexplored. The course can be spread over two years on request. To find out more and download the course handbook go to: www.rbge.org.uk/msctaxonomy Contact For more information contact: Vicky Mactaggart (Programme Administrator) -Phone: +44 (0)131 651 7052 - Email: btpmsc@ed.ac.uk or the Course Directors: Dr. Louis Ronse De Craene (l.ronsedecraene@rbge.ac.uk) and Prof. Andrew Hudson (andrew.hudson@ed.ac.uk)

To apply: go to http://www.ed.ac.uk/studying/-postgraduate/degrees/index.php?r=site/view&i=d=1

< http://www.ed.ac.uk/studying/postgraduate/-degrees?id=1&cw_xml=de=tails.php >

and search under Biological, Biomedical and Life Sciences, where you will find a link to the program.

– The Royal Botanic Garden Edinburgh is a charity registered in Scotland (No SC007983)

Louis Ronse de Craene <L.RonsedeCraene@rbge.ac.uk>

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-University Göttingen invites applications for a

PhD Position in Plant Systematics and Biogeography (German salary class: EG 13 TV-L (65%))

for three years, starting presumably in May 2016 (plus/minus one month). The position will be financed by the DFG (German Science Foundation) Project: "Biogeography and evolution of the largest adaptive radiation of woody plants (Melicope, Rutaceae) on the Hawaiian Islands". In the course of the project, we will study the adaptive radiation of a group of plants from the Citrus family on the Hawaiian Islands using the Next-Generation Sequencing method RADseq (restriction site associated DNA sequencing).

The applicant should have a Master's degree (or equivalent) in Biology and proficient skills in scientific English (oral and written). We expect a deep interest in plant systematics, tropical (island) biogeography and evolutionary processes including polyploidy and hybridization. Theoretical and practical background knowledge in DNA sequencing techniques as well as phylogenetic methods is essential. Plant samples will be collected in the course of this study, so that the willingness to carry out field work under (sub)tropical conditions and to identify species of a taxonomically difficult genus is required. Knowledge regarding Next-Generation Sequencing and especially bioinformatic analyses of Next-Generation sequence data are advantageous. We expect high motivation, creativity, a cooperative personality and integration into the research team.

We offer a PhD position for three years, scientific research with a highly motivated international team, fully equipped laboratories, flow cytometry and other research facilities in the department. The research material will be collected during a field trip to the Hawaiian Islands at the beginning of the project. Our PhD program offers a comprehensive mentoring program, specific courses for plant evolution and systematics including courses in Next-generation Sequencing, opportunities for conference presentations, gaining teaching experience, and further support for career development.

The University of Göttingen is an equal opportunities employer and places particular emphasis on fostering career opportunities for women. Qualified women are therefore strongly encouraged to apply. Disabled persons with equivalent aptitude will be favored.

Please send your application with the usual documents (motivation letter, CV, publication list, a copy of the MSc (or equivalent) certificate and a letter of reference) until January 31st 2016 by email to:

Dr. Marc Appelhans, Georg-August-Universität Göttingen, Department of Systematics, Biodiversity and Evolution of Plants, Untere Karspüle 2, 37073 Göttingen, Germany; Email: marc.appelhans@biologie.uniâgoettingen.de.

The application files will be destroyed after a holding period of three months.

"Appelhans, Marc" <marc.appelhans@biologie.uni-goettingen.de>

UHaifa Evolution

Biology, mathematics, computer science and bioinformatics students/researchers are needed

Dr. Livnat's new lab for the study of evolution at the University of Haifa in Israel is seeking applications for Ph.D, postdoc, lab manager and other positions from individuals with a background in biology, mathematics, computer science or bioinformatics and a record of past excellence.

We study the deep principles of how evolution works both theoretically and experimentally. 1) Students with a background in theoretical computer science or other branches of mathematics may participate in work at the interface of evolutionary biology and theoretical computer science whose goal is to form a new mathematical framework for evolution. Our lab works in collaboration with leading computer scientists abroad and in Israel. 2) Students with a background in bioinformatics and students with molecular biology lab skills may participate in evolutionary research involving cutting-edge sequencing methods. 3) Students interested in the evolution of behavior are also encouraged to apply.

Applicants should send a cover letter and a CV to alivnat@univ.haifa.ac.il, including the names of 2-3 references. More info at http://sci3.haifa.ac.il/˜alivnat/ adi.livnat@gmail.com

UJohannesburg SharkPopulationGenetics

Graduate position: PhD or MSc Studentship

Topic: Genetic investigation of female philopatry in the raggedtooth shark (Carcharias taurus).

The Molecular Zoology Laboratory at the University of Johannesburg (Auckland Park, South Africa) invites applications for a full-time PhD or MSc position (with the option to upgrade to PhD) to investigate genetic structure in the raggedtooth shark (Carcharias taurus) along the South African coast.

The position is funded by the National Research Foundation (NRF) for a maximum of 2 years and is available immediately. Although the NRF gives preference to local applicants, students from outside of South Africa are encouraged to apply and will be selected if they are clearly more qualified, particularly if one or more of the following criteria apply: a) a distinction in their previous degree (e.g. BSc honours); b) good genetic laboratory skills, and preferably experience working with microsatellites; c) at least one publication in a reputable journal.

This project is part of a multidisciplinary collaboration including Prof. Peter Teske (University of Johannesburg), Dr Kolobe Mmonwa and Dr Matt Dicken (both KwaZulu-Natal Sharks Board). The student will be based at the University of Johannesburg (http://bit.ly/1mnAZHo) for the duration of the project, with occasional visits to the KwaZulu-Natal Shark Board (www.shark.co.za). There will be no sampling trips, as all genetic samples have already been collected.

Remuneration is R (ZAR) 40 000 per year for an MSc position and R 60 000 for a PhD position + top-up funding from the University of Johannesburg. A short summary of the project is included below.

Interested students should please contact Prof. Peter Teske: pteske101@gmail.com. Please include a) a full CV; b) contact information of 3 academic referees, and c) a personal statement describing research experience, interests and career goals (500 words maximum).

Summary:

The raggedtooth shark (Carcharias taurus) is listed by the IUCN as globally vulnerable. Off South Africa, it is commonly found along the East and South coasts, from Cape Town to northern KwaZulu-Natal. Tag-recapture studies suggest that this species exhibits philopatry to specific pupping, mating and gestating areas. This project aims to use genetic samples from mature female and juvenile sharks to investigate the extent of site fidelity, and test for genetic differentiation among sharks from different nursery areas.

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Prof. Peter Teske *Molecular Zoology LabDepartment of ZoologyUniversity of Johannesburg, Kingsway CampusAuckland Park 2006South AfricaTel +27 (0)11 559 3373*

pteske101@gmail.com

ULeicester GenomicsSocialOrganization

A competition funded PhD studentship at the Department of Genetics, University of Leicester, UK

PhD title: Genomics of social organisation

Supervisors: Dr Rob Hammond & Dr Sandra Beleza (Genetics, University of Leicester) Collaborator: Dr Y.Wurm, (Queen Mary University of London)

The evolution of highly integrated social groups with a reproductive division of labour, exemplified by the eusocial Hymenoptera (ants, bees and wasps), is a major evolutionary transition offering unparalleled opportunities to understand how organisation at a higher level evolves and diversifies. Furthermore, changes in social organisation are of great economic importance as they are linked to the invasiveness and pest status of social insects. However, to date, little is known about genetic influences on social organisation in social insects. This is changing. Next generation sequencing (NGS) is now able to reveal the genomic architecture underpinning variation in social organisation, and, in turn, the genomic effects of social living [1, 2].

We propose an ambitious PhD investigating the population genetics and genomic architecture underlying a polymorphism in social organisation in the ant, Leptothorax acervorum [3, 4].

Aims and objectives:

(1) Assess geographical variation in colony social organisation among isolated populations in southern Europe (central and north west Spain, Spanish/French Pyre-

nees, France & Italy). (2) Assemble a draft genome of L.acervorum from a haploid male using PCR- free libraries and MiSeq data. (3) Investigate signatures of selection across the genome of L. acervorum using a combination of genome re-sequencing and Restriction site Associated DNA sequencing (RADseq). (4) Compare the genetic architecture underlying the polymorphism in social organisation in L.acervorum with the 'social chromosomes' found in other ant species [1,2].

Refs: [1] Wang et al. Nature, 2013. 493:664-668 [2] Purcell et al. Cur. Biol. 24:2728-2732 [3] Gill et al. Proc. Roy. Soc. B. 2009 276: 4423-4431 [4] Gill & Hammond Proc. Roy. Soc. B. 2011. 278: 1524-1531.

Studentship Funding: The successful student will be funded by one of two Doctoral Training Partnerships (DTP). Applicants are encouraged to apply to both schemes to maximise their funding success. UK and EU citizens are eligible for funding through these two DTPs (please contact rh225@le.ac.uk if you are unsure about eligibility).

DTP1: Midlands Integrative Biosciences Training Partnership (MIBTP) funded by the BBSRC

Deadline: 10/01/2016

Further details: https://www2.le.ac.uk/colleges/medbiopsych/research/Postgraduate%20Opportunities/mitbp-at-the-university-of-leicester/additional-information/rob-hammond-proposal How to apply: http://www2.warwick.ac.uk/fac/cross_fac/mibtp/pgstudy/phd_opportunities/application DTP 2: Central England NERC Training Alliance (CENTA) funded by NERC

Deadline: 25/01/2016

Further details: http://www.centa.org.uk/themes/evolution/l32/ How to apply: http://www2.le.ac.uk/research/degrees/funding/centa/how-to-apply-for-a-centa-project Successful applicant: This studentship would suit a highly motivated person with a deep interest in evolutionary biology, genetics and bioinformatics. The PhD will involve collecting ants in the field, molecular biology and bioinformatics.

For any further information please contact Dr Rob Hammond (rh225@le.ac.uk).

Dr Rob Hammond Lecturer in Evolutionary Biology

Department of Genetics University of Leicester, University Road, Leicester, LE1 7RH, UK

t: +44 (0)116 252 5302 e:Â rh225@le.ac.uk w: http://www2.le.ac.uk/departments/genetics/people/hammond
"rh225@leicester.ac.uk" <rh225@leicester.ac.uk>

ULeicester TwycrossZoo GibbonEvolution

PhD in Gibbon Evolutionary Genomics at the Department of Genetics, University of Leicester, UK , with placements at Twycross Zoo, UK Funded for UK and other EU nationals only.

PhD project title: Developing mobile element based genetic markers for individual identification, captive breeding, and conservation genetics of gibbons

Principal Supervisor: Dr Richard Badge Co-supervisor: Dr Ed Hollox Non-academic partner: Dr Charlotte Macdonald Application Deadline: 31st March 2016 Start Date: October 2016

Context: Gibbons are the smallest of the apes and comprise a group of highly endangered species, key to the ecology of Asian tropical forests. Gibbons are threatened by habitat loss and have been identified as priority species for conservation by the IUCN. International conservation efforts have focused on habitat preservation, but degradation of tropical forests through palm oil planting is inexorable. As a result, maintenance, genetic management, and expansion of zoo populations are essential to gibbon conservation. Twycross Zoo is a world leader in primate welfare, research and conservation and plays a key role in the preservation of captive gibbon populations. Also the Zoo's Director of Life Sciences, Dr Charlotte Macdonald, is Chair of the Gibbon Taxon Advisory Group for the European Association of Zoos and Aquaria (EAZA).

Background: In addition to their critical role in tropical ecosystems, gibbons are of intense interest to evolutionary biologists, having exceptionally fluid genome structure, highlighted in the publication of the gibbon genome in 2014. Not only are gibbon genomes evolving rapidly, but this evolution is hypothesised to be driven by mobile genetic elements, or transposons. This observation presents an excellent opportunity for fundamental research into genome evolution and dynamics (a research focus of the Genetics Department) to synergise with modern genomic analysis for the advancement of animal husbandry, welfare and conservation. In particular, transposon insertions are fundamental to understanding the pace of gibbon genome evolution, but additionally enable robust and cost-effective molecular analysis of relatedness. This analysis is essential for maintaining genetic health, the identification of species and hybrids, and potentially, genetic tagging of individuals for mol ecular ecology studies.

Research: A pilot study has demonstrated that we can identify novel (i.e. absent from the reference genome) gibbon transposon insertions. Having established feasibility, this PhD project involves expansion of this marker panel to gain insights into genome evolution, and conservation genetics. The pivotal role that Twycross Zoo plays in captive gibbon population management means the project will have unprecedented access to samples. Successful development of individual specific genetic markers will directly impact on animal welfare and health, improving the long-term viability of captive populations. In addition the potential to resolve taxonomic ambiguities will be an important contribution to gibbon systematics, and fundamental research on rapid genome evolution in these species will lead to new knowledge of primate genome dynamics.

Techniques: The experimental aspects of the project involve primate biosample handling, nucleic acid extraction, construction of genomic libraries, PCR, nucleic acid electrophoresis, DNA sequencing (Sanger and NGS) and bioinformatic analysis of gibbon and related ape genomes. During placements at Twycross Zoo the student will be trained in the practical and legislative technicalities of collecting, managing and utilising samples from endangered animals (including CITES). The student will also be trained in interpreting the Zoo's research activity to the visiting public.

Contact Richard Badge rmb19@le.ac.uk or Ed Hollox ejh33@le.ac.uk for more details.

Apply: Go to http://www2.le.ac.uk/research/degrees/-phd/genetics Prepare a brief personal statement (1000 words max) and complete the online application form, indicating the project and supervisors above. Please Note: This studentship is project-based (i.e. candidates apply to carry out the research project described above, at the University of Leicester) but is hosted within the Midlands Integrative Biosciences Training Partnership (MIBTP). The studentship is subject to the benefits and requirements of this programme.

MIBTP Benefits: A full student stipend for 4 years, including registration fees (UK nationals, and EU nationals who have been resident in the UK for three years or more are eligible for the full stipend. EU nationals who have not been resident in the UK for 3 years of more are eligible, but will only have their registration fees paid, and receive no stipend). Every student will receive a Macbook Pro laptop to support their studies and will have full access to the MIBTP

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UMississippi AquaticEvolution

Graduate Student Research Assistantships in Aquatic Ecology/Evolution

The Resetarits Lab (http://www.olemiss.edu/-resetaritslab/index.html) at The University of Mississippi currently has openings for highly qualified PhD. students as Doherty Research Assistants in Freshwater Biology. These are newly established, competitive, 12 month Research Assistantships in the Department of Biology, providing 5 years of support. Current stipend is 25k/year, with health insurance, and full tuition remission. Recipients are expected to design and implement independent dissertation projects (empirical and/or theoretical) at the interface between community, behavioral, and evolutionary ecology in freshwater systems, or at the freshwater/terrestrial interface, as well as participate in ongoing projects. Current studies in the Lab address a variety of questions, including the role of habitat selection in the assembly of communities and the dynamics of metacommunities, the role of diversity and species interactions in community assembly/ecosystem function, life history evolution in amphibians and insects, and biochemical, behavioral, evolution and community dynamics of chemical camouflage. Study organisms include amphibians, aquatic insects, other aquatic invertebrates, and fish, while focal habitats range from small ephemeral, coastal plain ponds to headwater mountain streams. Funding for past and ongoing research has come primarily from the National Science Foundation, along with EPA/NASA.

Recent/representative papers:

Resetarits, W. J. Jr. & A. Silberbush. 2015. Local contagion and regional compression: habitat selection drives spatially explicit, multi-scale dynamics of colonization in experimental metacommunities. Ecology Letters in press doi: 10.1111/ele.12553

Resetarits, W. J. Jr. and C. A. Binckley. 2013. Patch quality and context, but not patch number, drive multiscale colonization dynamics in experimental aquatic landscapes. Oecologia 173:933-946. pdf

*Resetarits, W. J. Jr. and C. A. Binckley. 2013. Is the

Pirate really a Ghost? Evidence for generalized chemical camouflage in an aquatic predator, Pirate Perch (Aphredoderus sayanus). American Naturalist 181:690-699. *Featured in a variety of media, including: New Scientist, Nature Research Briefs, Inside Science, Scientific American, and Wikinews. pdf

Resetarits, W. J., Jr. and C. A. Binckley. 2009. Spatial contagion of predation risk affects colonization rate and community structure in experimental landscapes. Ecology 90:869-876. pdf

Resetarits, W. J., Jr. and D. R. Chalcraft. 2007. Functional diversity within a morphologically conservative genus of predators: implications for functional equivalence and redundancy in ecological communities. Functional Ecology 21:793-804.*Selected for 100 Influential Papers Published in 100 Years of British Ecological Society Journals. pdf

Resetarits, W. J., Jr. 2005. Habitat selection links local and regional scales in aquatic systems. Ecology Letters 8:480-486. pdf

The Resetarits Lab is based in the Department of Biology and housed primarily at the University of Mississippi Field Station (UMFS), approximately 11 miles from the main campus in Oxford. The Lab has outstanding space and facilities and access to over 200 experimental ponds and wetlands at the UMFS (check us out on Google maps

https://www.google.com/maps/@34.425776,-89.3935815,15.02z), hundreds of mesocosms of various sizes for experimental work, and dedicated field vehicles. The Department of Biology at The University of Mississippi has an organismal focus, including a dynamic and growing group of ecologists and evolutionary biologists (http://biology.olemiss.edu/). The University of Mississippi is dedicated to fostering diversity at all levels within the University community (http://50years.olemiss.edu/). Oxford is a small, dynamic, progressive community with excellent cultural amenities, great food, a fun atmosphere, and a reasonable cost of living. The University of Mississippi campus is one of the most beautiful in the country.

For more information contact me at the address below. To begin the application procedure, please attach a letter of interest, unofficial transcripts and GRE scores, and resume (including contact information for 3 references) to Dr. William Resetarits (wresetar@olemiss.edu).

William J. Resetarits, Jr.

Professor of Biology and Henry L. and Grace Doherty Chair in Freshwater Research Department of Biology The University of Mississippi P.O. Box 1848 University, MS 38677-1848 Phone: (662) 915-5804 Fax: (662) 915-6554 http://www.olemiss.edu/resetaritslab Experiments are only experience carefully planned in advance. R. A. Fisher

— / —

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

UNorthDakota BisonGeneticsEvolution

U. North Dakota. AncientModernBisonGenetics. The Laboratory of Human and Forensic Genetics at the University of North Dakota (www.und.edu) is inviting applications from potential graduate students who pursue the MS degree. PhD candidates will be also considered.

A student will be engaged to a project on the historic, current and future status of bison herds from biological, archaeological, and cultural perspectives. It is a collaborative effort with Theodore Roosevelt National Park (THRO). This cross-disciplinary project represents an opportunity to get intensive training in the methods of ancient and modern DNA analyses including DNA isolation from a variety of tissues, next-generation and traditional sequencing, quality control of DNA templates, and bioinformatics. Genetic, phylogenetic, and demographic studies of extirpated and extant bison specimens will be used to generate important insights for management of bison at THRO and other locations throughout the Midwest.

Candidates should demonstrate motivation for hard laboratory work and strong interest in molecular genetics and evolution. Preference will be given to students with a proven record of molecular biology skills. Additional experience in bioinformatics is a plus. If you are interested you need to apply to the University of North Dakota Biology Graduate Program using the regular procedure that can be found in the UND Graduate School website:

http://graduateschool.und.edu/programs/degrees.cfm The additional information can be also found in the Biology Department website:

http://arts-sciences.und.edu/biology/graduate/programs.cfm The position starts in August /September 2016. To receive full consideration, applications and required materials should be received by the Biology Graduate Program not later than February 15, 2016.

Potential graduate students are strongly encouraged to make contact with Dr. Igor Ovchinnikov. Contact information:

Dr. Igor Ovchinnikov Associate Professor Lab. Of Human and Forensic Genetics Department of Biology University of North Dakota Email: igor.ovtchinnikov@email.und.edu

"Ovtchinnikov, Igor" <igor.ovtchinnikov@email.und.edu>

UppsalaU DeepSeaSpongeGenomics

Ph.D. position on Metabolomics/Genomics of Deep Sea Sponges,

Dept. of Medicinal Chemistry, Uppsala University, SWEDEN.

I am seeking a highly motivated PhD candidate to work within the frame of the newly EU funded SponGES consortium. This consortium will investigate deep-sea north Atlantic sponge grounds. The candidate will develop a suite of genomic and metabolomic resources to investigate the population diversity of key sponge species and assess connectivity between sponge grounds. These resources will also unlock the potential of sponge grounds for drug discovery, in which the candidate will also play a part.

For more info and to apply, use the link below (in Swedish, for the English version click on "English", upper-right corner). https://mp.uu.se/web/info/vart-uu/lediga-jobb/-/jobb/86997 duration of position: possibly 5 years

application deadline: 18th of January 2016

For specific information about the announced Ph.D. position and details of the project, please contact me (paco.cardenas@fkog.uu.se).

Dr. Paco Cardenas Div. of Pharmacognosy, Dept. of Medicinal Chemistry, Uppsala University BMC Box 574, SE 75123 Uppsala, Sweden paco.cardenas@fkog.uu.se

Paco Cardenas <paco.cardenas@ebc.uu.se>

UppsalaU EvolutionSexualDimorphism

PhD position on the evolution of sexual dimorphism in life-histories, at Uppsala University

A PhD position is available at Animal Ecology, the Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, Sweden, starting spring 2016.

Research focus Males and females often have different optimal life histories (for example regarding rate of reproduction and lifespan), but they largely share the same genome. This leads to conflicts over trait expression. We expect stronger conflict when individuals mate with multiple partners over life and weaker conflict under monogamy, because then the evolutionary interests of the sexes align. The conflict can be resolved by decoupling the genetic basis of the trait, allowing evolution of sexual dimorphism, but the evolutionary processes leading to such sexual dimorphism remain poorly understood. This project will use quantitative genetic methods combined with experimental evolution in the nematode worm, C. remanei, to investigate how different mating systems lead to changes in the genetic basis of sexual conflict over evolutionary time.

Qualifications The ideal candidate will have a keen interest and documented knowledge in evolutionary ecology. You are motivated, highly reliable, driven and well-organised, with the ability to work both independently and in a group. The position requires an MSc degree (or equivalent) in evolution, ecology or a related field and fluency in spoken and written English. Strong statistical skills are a plus.

Position The candidate will receive her/his postgraduate training within the postgraduate school at the Evolutionary Biology Centre (http://www.ebc.uu.se/-?languageId=1). The postgraduate training comprises four years of full time studies and entitles the holder to salary according to local salary rules and full social benefits. The position can be combined with up to 20% of teaching assistantship, which will then prolong the position accordingly.

The environment The Evolutionary Biology Centre (EBC, http://www.ebc.uu.se/) is one of the worlds leading research institutions in evolutionary biology and part of Uppsala University ' the oldest university in

Scandinavia. Uppsala University, ranked top among European Universities in the subject of biology (CHE European ranking), attracts approximately 45.000 students from all over the world, creating an international and stimulating research environment as well as providing a multitude of opportunities for collaboration and socializing. The city of Uppsala is a vibrant college town, less than an hour by train from Stockholm (and even closer to Arlanda International Airport), with beautiful and easily accessible surroundings.

How to apply The application should include (1) a cover letter describing your research interests and experience and outlining your motivation to work on this project, (2) a detailed CV describing your education and listing authored publications (if any), (3) an accredited copy of your MSc degree or equivalent (if available at time of application), and (4), names and contact information (address, email address, and phone number) of two academic references. The application should be written in English or Swedish and should be sent via e-mail as a single pdf file to elisabeth.bolund@ebc.uu.se. Review of applications will start on February 15th, but candidates will be considered until the position is filled. The starting date can be discussed but ideally early this year. If you have any questions, dont hesitate to contact me:

Elisabeth Bolund, PhD Associate Professor Department of Animal Ecology Evolutionary Biology Centre Uppsala University Norbyvägen 18D Uppsala, SE-752 36 Sweden Phone: +46(0)18-4712613 Email: elisabeth.bolund@ebc.uu.se Homepage: http://bolund.wix.com/homepage Elisabeth Bolund <elisabeth.bolund@ebc.uu.se>

UppsalaU SpongeMetabolomics

Ph.D. position on Metabolomics/Genomics of Deep Sea Sponges,

Dept. of Medicinal Chemistry, Uppsala University, SWEDEN.

I am seeking a highly motivated PhD candidate to work within the frame of the newly EU funded SponGES consortium. This consortium will investigate deep-sea north Atlantic sponge grounds. The candidate will develop a suite of genomic and metabolomic resources to investigate the population diversity of key sponge species and assess connectivity between sponge grounds. These resources will also unlock the potential of sponge grounds for drug discovery, in which the candidate will also play a part.

For more info and to apply, use the link below (in Swedish, for the English version click on “English”, upper-right corner). https://mp.uu.se/web/info/vart-uu/lediga-jobb/-/jobb/86997 duration of position: possibly 5 years

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Dr. Paco Cardenas Div. of Pharmacognosy, Dept. of Medicinal Chemistry, Uppsala University BMC Box 574, SE 75123 Uppsala, Sweden paco.cardenas@fkog.uu.se

Paco Cardenas <paco.cardenas@ebc.uu.se>

URhodeIsland BiodiversityGenomics

The Lane Lb at the University of Rhode Island is inviting PhD applicants to work on a recently funded NSF GoLife project. The focus of the project is diversity and genomics within the Stramenopiles, Alveolates and Rhizaria - largely microbial eukaryotic taxa that are underrepresented in traditional databases.

The bulk of eukaryotic diversity is microbial and, when compared to plants, animals and fungi, much of this microbial diversity has been undersampled from the standpoint of morphological, phylogenetic and genomic data. This skew in data not only has consequences for our understanding of the biodiversity of eukaryotic life on Earth, but also how we interpret cellular and evolutionary biology in the broadest sense. One of the most diverse major clades of eukaryotes that has recently emerged from phylogenomic analyses united the Stramenopila, Alveolata and Rhizaria into the ’SAR’ group. Initially this clade was controversial because it forced a re-evaluation of the evolution of several characters, most notably the spread of photosynthesis across eukaryotes. However, additional data have robustly supported SAR as an independent clade. Among the diverse lineages within SAR, genomic-scale data are rare and concentrated in only a few areas, Apicomplexa (e.g. malarial parasites), omycetes (e.g. parasite ’water molds’) and diatoms (e.g. ecologically important phytoplankton). Despite their global ecological importance, fewer than 50% of all SAR clades, and only one third of non-photosynthetic SAR clades, are represented by even a single genome in public databases. This work will add at least 250 novel genomic-scale datasets (transcriptomes, draft genomes, single-cell amplified genomes), focused primarily on capturing diversity within SAR.

Details of the project can be found at http://www.nsf.gov/awardsearch/showAward?AWD_ID=1541510&HistoricalAwardsÃolse Interested applicants are encouraged to contact Chris Lane (clane[at]uri.edu) to express interest and for more details. Information of applying can be found at http://web.uri.edu/graduate-school/apply/ The deadline for full consideration is Jan 15.

Chris Lane Associate Professor Department of Biological Sciences University of Rhode Island 120 Flagg Road Kingston, RI., 02881 Office: CBLS 277 ph (401) 874-2683 fax (401) 874-2065 http://cels.uri.edu/bio/lanelab/ Chris Lane <clane@uri.edu>

USheffield 2 PlantCarnivory

REMINDERof upcoming deadlines: I'm looking for quantitatively oriented, field-experienced*, motivated students for the following projects at University of Sheffield (UK).

The eco-evolutionary dynamics of plant carnivory *field experience is a must https://acce.shef.ac.uk/phd-opportunities/sheffield/ Deadline:Jan 11th

The determinants of optimal life history strategies in a variable world *field experience is not absolutely necessary

https://www.shef.ac.uk/ÂÂ'/graduatÂÂ'/cabmprojects/salguerogomez< https://www.shef.ac.uk/aps/prospectivepg/phd/graduate-opportunities/cabmprojects/salguerogomez > Deadline:Jan 15th

"Aliuditer ad prosperitatem nos est: id est omnibus rebus vincere"

RobSalguero-GÂÂmez, PhD ARCDECRA fellow Guestresearcher of the Max Planck Institute for Demographic Research http://sites.google.com/site/RobResearchSite/ Salguero@demogr.mpg.de

USheffield EvolutionaryGenomics

A NERC funded PhD (3.5 years) is available with Prof Jon Slate (University of Sheffield, http://jon-slate.staff.shef.ac.uk/) and Dr Kanchon Dasmahapatara (University of York, http://goo.gl/RFxuOI). The project is on the evolutionary genomics of great tits (Parus major) but the candidate will have considerable flexibility to develop the specific questions. Details of the project can be found here: https://goo.gl/twC09h . We have typed approximately 2000 birds from >20 populations at a 500K SNP chip. Approximately half of the samples come from an intensively studied population at Wytham Woods near Oxford. The great tit genome has recently been assembled and annotated (to a high quality), and we collaborate with groups in Oxford (Ben Sheldon), Wageningen (Martien Groenen) and the Netherlands Institute of Ecology (Marcel Visser).

The lab is interested in a broad set of evolutionary quantitative genetic questions, and the project could focus on one or more of the following topics: understanding the genetic architecture of quantitative traits; identifying genes driving adaptive evolution; exploring the role of copy number and structural variation in evolutionary processes; using genomics tools to understand inbreeding and inbreeding depression; prediction of phenotype from genomic data. The project does not involve lab or field work, and is ideally suited to an evolutionary biologist that enjoys data analysis or other scientist with strong quantitative skills.

The project is part of the ACCE (Adapting to the Challenges of a Changing Environment) doctoral training program run by the Universities of Sheffield, Liverpool and York (see https://acce.shef.ac.uk/phd-opportunities/sheffield/). Note that the projects which are funded will be decided by open competition between the best candidates put forward by each supervisor.

Unfortunately NERC studentships have quite restrictive conditions. Applicants can be from the UK or EU, but non-UK applicants do not receive any living allowance (effectively ruling them out). Applications MUST be made through the University of Sheffield online system outlined on the ACCE webpage (URL above). However, Jon Slate welcomes informal enquiries (j.slate@sheffield.ac.uk). The closing date is Monday 11th January.

Versailles France InsectBehavioralEvolution

Master Student research fellowship for 6 months on Moths' Pheromone differentiation at the Institute for Agricultural Research (INRA), Versailles, France

Our general interests are insects' behavioral evolution and functional genomics. The aim of the project is to find the genetic basis of the differentiation of Ostrinia nubilalis moth species in two pheromone strains. This will be done by using in situ hybridization and the latest methods in transgenesis i.e. CRISPR/Cas9 genome editing system. Thus the project represents a unique opportunity to gain experience in an area which is of high demand in the research field.

We are looking for a highly motivated student with BSc degree in biology and experience in molecular biology. Experience on insects' manipulation and physiology are a plus. This project is a collaboration between the University of Amsterdam (Institute for Biodiversity and Evolutionary Dynamics, IBED), Netherlands and the INRA in Versailles, France. Therefore, communication skills in English (oral and written) are necessary and knowledge of French is a plus.

There will be a monthly salary of 550 euros, for every complete month worked, for 6 months maximum. The salary is paid by the Institute of Ecology and Environnemental Sciences (iEES) - Paris, France, with the obligation for the student to administratively subscribe to the iEES (no subscription fees).The group has excellent laboratory facilities with all state of the art equipment.

Recent/representative papers:

1. Lassance, J.M., Groot, A.T., et al. (2010). Allelic variation in a fatty-acyl reductase gene causes divergence in moth sex pheromones. Nature 466, 486-489.

2. Koutroumpa, F. A. et al. (2014) Shifts in sensory neuron identity parallel differences in pheromone preference in the European corn borer. Frontiers in Ecology and Evolution. 2.

3. Koutroumpa, F. A. & Jacquin-Joly, E. (2014) Sex in the night: Fatty acid-derived sex pheromones and corresponding membrane pheromone receptors in insects. Biochimie. 107, 15-21.

For more information contact Fotini KOUTROUMPA or Astrid T. GROOT at the address below. To apply please send us a letter of interest, bachelor scores and CV (including contact information for 2 references). Deadline for application 30 of February 2016.

Contact information:

Fotini Koutroumpa, PhD, Marie Curie SkÄ^{1}âodowska postdoctoral Fellow

Astrid T. Groot, group leader

IBED, University of Amsterdam, Science Park 904, 1098 XH Amsterdam Phone: +31 20 5255400 Fax: +31 20 5257832 F.Koutroumpa@uva.nl or a.t.groot@uva.nl

http://www.science.uva.nl/ibed/home.cfm Address in France:

INRA of Versailles - UMR 1392 - iEES-Paris RD 10 - route de Saint-Cyr, 78026 VERSAILLES Cedex Tel : 0033 (0)1 30 83 31 63 Fax : 0033 (0)1 30 83 31 19

Vienna 2 InsectEvolution

> The two grad-positions advertised are intended for grad students > interested in evolution. The successful candidates will be involved in > SIT and IIT and also genomics of mass reared insects.

Two PhD assistantships in applied entomology are available at Boku (University of Natural Resources and Life Sciences, Vienna, Austria). The three year project is in close cooperation with the Insect Pest Control Laboratory (IPCL) from the Joint FAO/IAEA Division (Seibersdorf, Austria), University of Lyon 1, France and the University of Rennes.

Two highly motivated and creative doctoral students are sought to join the French Research National Agency (ANR) and Austrian Science Fund (FWF) funded project to conduct research on developing control strategies for the spotted wing Drosophila fly, Drosophila suzukii. The recent invasion of D. suzukii is a major concern for Europe's soft fruit production sector. The objective of the project is to develop an alternative approach for controlling D. suzukii through the release of sterile insects produced via Sterile Insect Technique (SIT) and Incompatible Insect Technique (IIT). Protocols for mass-rearing and sterilization of D. suzukii using radiation as well as cytoplasmic incompatible CI Wolbachia strains shall be developed and validated.

- One PhD candidate will be responsible for developing the mass rearing protocol for D. suzukii and establish

SIT by applying different irradiation protocols for reaching optimal male sterility. Thus, quality control analysis including male mating competitiveness besides others will be performed.

- The second PhD candidate will be responsible for the characterization of available Wolbachia-infected lines in respect to cytoplasmic incompatibility levels and fitness. The most suitable line(s) will be further assessed for the development and application of a combined SIT and IIT approach in the absence of an efficient sex separation system. The selected PhD candidate will also be responsible to assess genetic changes occurring during domestication and/or mass-rearing.

The supervisors of these project are at IPCL Rui Cardoso Pereira, Carlos Caceres, Kostas Bourtzis, at the University Lyon 1 Laurence Mouton, Patricia Gibert and Fabrice Vavre and at Boku Christian Stauffer.

General requirements for the position: We ask a MSc degree in Plant Sciences, Biotechnology, Biology or Evolution with multidisciplinary profile. In addition to the specific skills required, the candidates should be team players with demonstrable experience in collaboration with ecologists and/or entomologists. The candidates should have excellent communication skills and should be fluent in English. The project is expected to start in spring 2016 and PhD candidates have to enroll at Boku www.boku.ac.at/en/. Monthly salary of the successful candidates will be according to the regulations of the Austrian Science Fund FWF www.fwf.ac.at/en/ . Please send applications to Christian Stauffer christian.stauffer@boku.ac.at until 21st of February, 2016 including at least two reference letters, CV, cover letter expressing motivation and the preferred PhD work. Please indicate "SUZUKILL PhD Application" as subject of the mail.

Christian Stauffer <christian.stauffer@boku.ac.at>

WageningenU PlantInsectEvolutionaryEcol

PhDposition "Insect Community Ecology"

Thegoal of the research project is to unravel plant adaptations to attackby multiple insect herbivore species. Plants respond to insect herbivoryby changing their defence phenotype specifically for the identityof the attacker. It has been hypothesized that specificity in inducedplant responses is a plant adaptation to deal with unpredictabilityof insect attack. However, a response to one attacker maymake plants more susceptible to attack by other herbivore species. Anoptimal defence strategy should thus incorporate the consequences of theinduced response. As PhD student you will study whether various Brassicaceousplant species differ in the predictability of exposure to insectattack, such as when, by which species and in which order herbivoreattack takes place and if these patterns of attack are reflectedin specific plant defence adaptations to dynamic processes in multi-herbivoreattack. You will combine field experiments on the structureof insect communities with plant performance measurements as wellas laboratory experiments on insect behaviour. Within the project youwill be closely collaborating with a PhD student who focusses on plantphysiological responses to multi-herbivore attack, a technician andpost-doc as well as researchers at international institutes with expertisein ecology, entomology and plant sciences.

Welook for

Thesuccessful candidate will have an MSc degree in Biology with a specializationin Ecology or similar, with experience in community ecology,behavioural studies on insects and statistical analyses of multivariatedatasets. We are looking for a highly motivated field ecologistwho can work in a multidisciplinary team in a collaborative spirit.The candidate will be proficient in the English language. Withinthe Laboratory of Entomology, PhD students are encouraged to superviseMSc thesis students when such opportunities arise.

Organisation

Theresearch on plant adaptations to multi-herbivore attack is embedded inthe research team of Dr. Poelman at the Laboratory of Entomology WageningenUniversity. Our team studies community ecology of plant-insectinteractions and consists of ecologists, entomologists, molecularbiologists and computational modellers. At the Laboratory of Entomologythe research teams consist of ambitious scientists and we aimat an interdisciplinary approach from cellular to community level tounravel biological phenomena underlying the functioning of plant-insectcommunities, insect vectored diseases, insect neurobiology andinsects as food and feed. The Laboratory of Entomology is part of thePlant Sciences Group of the Wageningen University and Research Centre.

WageningenUniversity and Research Centre

Deliveringa substantial contribution to the quality of life. That's ourfocus - each and every day. Within our domain, healthy food and livingenvironment, we search for answers to issues affecting society - suchas sustainable food production, climate change and alternative energy.Of course, we don't do this alone. Every day, 6,500 people work onâthe quality of life', turning ideas into reality, on a global scale.

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Weoffer

Weoffer a full-time position (38 hours), initially for 1 year after whicha go/no go decision will be taken on extension with another three years.Gross salary per month euro 2174,- in the first year rising to

euro2779,- per month in the fourth year, for a fulltime appointment. The candidatewill be based at the Laboratory of Entomology in Wageningen.

Toapply

Informationon the research: Dr. Erik H. Poelman , +31(0)317 485433, erik.poelman@wur.nl

Informationon the selection procedure: Mrs. Dorien Wissink (dorien.wissink@wur.nl).

Youcan apply up and until 10 February 2016 Forthis position you can only apply on line: http://www.wageningenur.nl/career Don'temail directly to the people mentioned above but use the website toapply.

Stuuruw sollicitatie niet naar de genoemde contactpersoon, maar solliciteervia de website.

Dr.Erik H. Poelman

AssistantProfessor

Laboratoryof Entomology

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internet - http://www.wageningenur.nl/en/Expertise-Services/Chair-groups/Plant-Sci ences/Laboratory-of-Entomology/Research/Erik-Poelmans-research.htm

www.disclaimer-uk.wur.nl "Poelman,Erik" <erik.poelman@wur.nl>

WesternWashingtonU EvolBiol

The Biology Department at Western Washington University has openings for graduate students starting Fall 2016. Faculty members in the department offer a wide range of expertise, from molecular biology to ecology. Graduate students are eligible for teaching assistantships, which fund the majority of tuition and provide a stipend of $12,116 per year. WWU is located in Bellingham, WA, a coastal city north of Seattle at the base of Mt. Baker in the northwestern part of the state.

More information can be found at: http://www.biol.wwu.edu/biology/gradprog_brochure.shtml or by contacting Dr. Ben Miner, Graduate Program Advisor, at benjamin.miner at wwu.edu

Potential advisors

Marion Brodhagen: Microbiology, molecular biology, and chemical ecology. Our lab studies the plant pathogenic fungus Aspergillus and aflatoxin, a potent toxin produced by this fungus. Our current projects involve the ability of certain plant secondary metabolites to stop growth and/or toxin production by Aspergillus. Future research directions will include investigations of the molecular mechanisms by which these plant compounds alter fungal metabolism. We also are interested in the role of Aspergillus in colonization of plastics labeled biodegradable, in agricultural settings. Aspergillus is a key colonizer of such plastics but its ability to break down polymers is unclear, as is the extent of toxin formation during plastic colonization.

Dave Hooper: Plant Community and Ecosystem Ecology. I will be accepting one graduate student in fall 2015. My local research is currently focused on assessing ecosystem services associated with different scenarios of riparian restoration in Whatcom County. Student work would combine GIS analyses of ecosystem services and field work, particularly on nutrient retention, to validate modeling results. I also have opportunities focused on analyzing large data sets to understand aspects of biodiversity loss and assembly of plant communities.

Robin Kodner: Marine Microbial Metagenomics. The Kodner lab does interdisciplinary work integrating marine microbial ecology with comparative genomics and bioinformatics for metagenomes. I am recruiting for one student for work on bioinformatics projects. Some experience with sequence analysis and programming required.

Craig Moyer: My interests are marine microbiology and geomicrobiology focusing on molecular approaches for exploring microbial diversity, community structure and ecological interactions. Presently, my lab and I are focused on the study of iron-oxidizing Zetaproteobacteria acting as the ecosystem engineers in microbial mats found at strong redox boundaries, including seep, spring and vent habitats. We are also examining the evolutionary divergence of surface and deep subsurface Zetaproteobacteria in hydrothermal systems.

Lynn Pillitteri: Plant Molecular and Developmental Biology. A potential graduate project in my lab would be aimed at understanding the molecular mechanisms driving cell type differentiation in the model organism, Arabidopsis thaliana.

Dan Pollard: Cellular Systems Genetics and Genomics. The Pollard lab has opportunities to study the molecular mechanisms of natural variation in protein expression dynamics in budding yeasts on an NSF supported project. The lab integrates microscopy, molecular biology, quantitative genetics, genomics, and computational biology, providing a broad and diverse graduate training experience.

Dietmar Schwarz: Ecological and Evolutionary Genetics and Genomics, Evolutionary Ecology. Schwarz's lab offers opportunities to study speciation, hybridization, and adaptation in host specific insects (apple maggot flies and relatives) on a USDA supported project.

Anu Singh-Cundy: Plant Cell Biology and Biochemistry. We study cell-cell interactions at the physiological, cellular, and molecular levels. Current projects are focused on understanding the role of HD-AGPs, which are extracellular glycoproteins that are expressed in the transmitting tissue of the pistil and in the vasculature of roots and shoots. We also study pectins and pectin-modifying enzymes found in the pistil of solanaceous species.

Benjamin Miner Associate Professor Biology Department, MS 9160 Western Washington University 516 High St. Bellingham, WA 98225-9160

Tel: 360-650-3640 Fax: 360-650-3148

Benjamin Miner <Benjamin.Miner@wwu.edu>

Jobs

ArizonaStateU EvolutionaryGenomicsProgrammer

The Human and Comparative Genomics laboratory at the Biodesign Institute is looking for a Software Application Associate who will work in a collaborative environment to design, construct, test, document and maintain software packages. Typical projects involve implementing high performance algorithms for the statistical analysis of large genomic datasets for studying questions related to evolution and population genetics.

To apply visit http://links.asu.edu/job19991BR or search for ID 19991BR at https://cfo.asu.edu/hr-applicant . If you have any questions about the opening, please email Reed A. Cartwright <cartwright@asu.edu> and visit http://cartwrig.ht/ . ESSENTIAL DUTIES: Develops and documents requirements of software applications. Participates in on-the-job and formal training sessions concerning the design, writing, and testing of software application programs. Participates in and/or independently performs the design, testing, and documentation phases of programs. Translates predetermined logic into appropriate programming language and operating systems. Utilizes standard reference, resource, and/or procedural materials to resolve problems. Integrates multiple tools into a single, user-friendly software package, as well as providing support for the software. Operates on-line terminals and related computing equipment as required.

MINIMUM QUALIFICATIONS: Bachelor's degree in Statistics, Mathematics, Computer Science or related field AND two years of experience in software application development, including writing computer code in one or more programming languages; OR, any equivalent combination of experience and/or education from which comparable knowledge, skills and abilities have been achieved.

DESIRED QUALIFICATIONS: Experience in translating software prototypes from Perl, Python, Java, etc into C/C++ preferred. Experience with JavaScript. Experience with databases query tools including, but not limited to, SQL, as well as programming languages including, but not limited to, C++ python, XML, HTML.

DEPARTMENT STATEMENT: The Biodesign Institute addresses today's critical global challenges in healthcare, sustainability, and security by developing solutions inspired from natural systems and translating those solutions into commercially viable products and clinical practices. The Cartwright Lab is based in the Human and Comparative Genomics Laboratory in the Biodesign Institute at Arizona State University. Our research focuses on various topics in the field of computational evolutionary genetics. We develop methods and software to analyze large genomic datasets and "big data". The majority of our research is related to the detection and analysis of mutations and variation from next-generation sequencing. We are species-neutral and work on taxa across the tree of life. Recent work involves humans, cancer, bonobos, ciliates, maize, Plasmodium, Leishmania, E. coli, archaea, Solanaceae, strawberries, and Anolis.

– Reed A. Cartwright, PhD Barrett Honors Faculty Assistant Professor of Genomics, Evolution, and Bioinformatics School of Life Sciences Human and Comparative Genomics Laboratory The Biodesign Institute Arizona State University

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

AuburnU 2 ViralPlantOmics

Beloware two positions At Auburn University as part of an -Omics and Informatics Cluster hire

Oneis virology/viromics in the Department of Biological Sciences and the other is molecular ecology in a the department of Plant Pathology.

Deadlinesare soon.

1)Virology/Viromics TheDepartment of Biological Sciences at Auburn University invites applications for a tenure-track faculty position (9-month) at the level of Assistant or Associate Professor beginning Fall of 2016. This position is part of an Auburn University cluster hire in "omics" and informatics and will strengthen our departmental research core area of host-microbial interactions. The successful candidate is expected to establish an extramurally funded, internationally recognized research program. Instructional responsibilities include development of graduate and/or undergraduate courses in virology including informatics and related topics.

TheOmics and Informatics Cluster represents an interdisciplinary research initiative at Auburn University which has made a significant financial commitment to hiring multiple new faculty. The successful candidate for this position will be expected to participate actively in Auburn University's multidisciplinary Cluster Hires Initiative in the Omics and Informatics cluster. New faculty with expertise in viromics will complement the University's considerable existing expertise in these areas to form the core of this innovative multidisciplinary initiative. Participation in the Omics and Informatics cluster will be an important component in faculty annual reviews. For more information regarding the Cluster Hires please click on the following link: http://www.auburn.edu/academic/provost/strategic_hire.html Applicantsshould submit a 1 page cover letter emphasizing specific qualifications, a curriculum vitae, a description of research interests, a statement of teaching philosophy/experience, and names and contact information of at least 3 references.

Moreinformation can be found at: http://www.auburn.edu/biology MinimumQualifications Applicantsmust have a Ph.D. in an appropriate discipline and experience in virology and informatics. Excellent written and interpersonal communications skills are required. Qualifications include postdoctoral or professional experience, a strong record of publication and potential for funding. The candidate selected for this position must be able to meet eligibility requirements for work in the United States at the time the appointment is scheduled to begin and continue working legally for the proposed term of employment.

DesiredQualifications Applicantsat the level of Associate Professor are expected to have current funding. Applicants studying host-viral interactions using informatics are encouraged to apply.

SpecialInstructions to Applicants Reviewof applications will begin January 8th, 2016 and will continue until the position is filled.

2)Plant Pathology - Molecular ecology

TheDepartment of Entomology and Plant Pathology at Auburn University and Auburn University's Cluster Hiring Initiative (CHI) Omics and Informatics Cluster is seeking applicants for the position of Assistant Professor in MOLECULARECOLOGY of PLANT and SOIL SYSTEMS. The expected start date is August 16, 2016.

Responsibilities:This is a 9 month tenure-track position with 75% research and 25% instruction responsibilities. The successful candidate for this position will be expected to participate actively in Auburn University multidisciplinary Cluster Hires Initiative in the cluster of Omics and Informatics. New faculty with expertise in Molecular Ecology of Plant and Soil Systems will complement the University's considerable existing expertise in these areas to form the core of this innovative multidisciplinary initiative. Participation in the Omics and Informatics will be an important component in faculty annual reviews. For more information regarding the Cluster Hires please click on the following link: http://www.auburn.edu/academic/provost/strategic_hire.html Thesuccessful candidate will also be expected to build and lead an extramurally-funded research program focused on fundamental aspects of Molecular Ecology of Plant and Soil Systems. The successful candidate (Research/Teaching) selected for this position will lead a research program based on understanding population dynamics of microbes associated with crops of agricultural importance for Alabama and the U.S. The candidate will use diverse bioinformatic approaches such as genomics, metagenomics, population genomics and/or phylogenomics to understand microbiome/plant interactions. Understanding the microbiome (including pathogenic, beneficial and saprophytic microorganisms) is

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at http://life.biology.-

mcmaster.ca/~brian/evoldir.html

CCMAR Portugal ComputationalBiologist RevisedDeadline

Apologies: the deadline for applications is 15th February 2016 (not 28th Feb as originally advertised).

Computational Biologist position [M/F] 1 vacancy*

Post reference: CCMAR/CB/01/2016

The Algarve Centre for Marine Sciences (CCMAR), a non-profit scientific organization at the University of Algarve, Faro, Portugal, is seeking to recruit a Computational Biologist (M/F) to complement and grow the existing bioinformatics capacity within the institute. The successful candidate will be expected to provide bioinformatic expertise and training to diverse institutional research groups, and to contribute to current European computational infrastructure projects (ELIXIR-EXCELERATE) and to advance the institutional strategic plan (UID/Multi/04326/2013) approved for the period 2015-2020. The position represents an excellent opportunity for an outstanding candidate to contribute to advancing the biocomputational competencies and infrastructure at a leading marine research centre.

Candidates with interests in bioinformatics, computational genomics, and other areas of computational biology are encouraged to apply.

Duties and Responsibilities of the position: 1) develop novel programmatic solutions to common computation problems experienced at the leading-edge of marine biological research, 2) contribute to existing research projects and develop new research opportunities, 3) provide training and expertise to research laboratories, 4) provide expertise and guidance for the implementation of infrastructure projects and future data management and computational resource requirements.

Professional Profile: 1) a Ph.D in Computational Biology or related subject; 2) demonstrable research capability through internationally recognized journals within the field of computational biology; 3) demonstrable skills in the administration of UNIX(-like) systems, proficiency in a scripting languages such as Python, Perl, and/or Java, and a familiarity with relational databases, SQL, and other relevant technologies; 4) experience of analyzing large life science data sets, such as genomic data and/or physical measurement data, using bioinformatics tools and web-based resources; 5) a high proficient in English (spoken and written).

Working Conditions: The position is a full-time, term appointment contract at CCMAR subject to satisfactory performance up to the end of the projects (approximately 48 months). The normal place of work is building 7, Campus de Gambelas, University of Algarve, Portugal. The gross annual salary will be approximately 44,500 euro with funding from the National Foundation for Science and Technology, project reference UID/ Multi/04326/2013, and the European Commission Horizonte 2020 project Elixir-Excelerate.

Application period: between 18 of January and 15 of February 2016

*Selection committee: *Professor Adelino Canário (President), Professor Maria Ester SerrÃ£o and Dr. Cymon J. Cox.

Expected start date: 1 April 2016

Application and Selection Procedure: Applications should be addressed to the Selection Committee through the e-mail: ccmar@ualg.pt Any queries should be sent to the same address. Applications should be submitted in a single pdf. file in English language with a motivation letter and CV. Candidates should only consider their application as validated after receiving written confirmation from CCMAR.

CCMARs non-discrimination and equal access opportunities policy No candidate can be privileged, benefited, jeopardised or private of any right or exempt of any claim in regards to descendent, age, gender, sexual orientation, marital status, economic situation, origin, social economy, genetic heritage, disability, chronic disease, nationality, ethnicity, territory of origin, language, religion, politics and ideological beliefs and union membership.

January 18th 2016

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Cymon J. Cox Orcid ID: 0000-0002-4927-979X < http://orcid.org/0000-0002-4927-979X >

cymon.cox@googlemail.com

ColumbiaU NeuronalEvolution

Columbia University's Mortimer B. Zuckerman Mind Brain Behavior Institute Announces Search for Tenure Track Faculty The Zuckerman Institute invites applications for tenure-track positions at the Assistant Professor level in the following Columbia University Arts & Sciences Departments to begin as early as July 1, 2016: Biological Sciences Chemistry Ecology, Environment and Evolutionary Biology (E3B) Physics The Zuckerman Institute brings together researchers to explore aspects of mind and brain, from crystallography through functional imaging. The Zuckerman Institute's new home will be the Jerome L. Greene Science Center on Columbia's Manhattanville campus. The building will form a creative hub where Columbia scientists can exchange ideas and forge collaborations. Individuals conducting research in the following areas are of particular interest: - Structural biology of relevant neuronal molecules - Genetic and chemical genomic approaches to the analysis of neural circuits - Comparative, genomic or evolutionary approaches to the neural basis of behavior - Computational and statistical approaches for analysis of large neural datasets - Imaging methods to probe neural circuit function - Tools to visualize and/or manipulate neuronal activity

We expect that successful candidates will develop vigorous research programs and also participate in undergraduate and graduate teaching. Women and minorities are very strongly encouraged to apply. All applications must be submitted through Columbia University's online Recruitment of Academic Personnel System (RAPS). Please enclose CV, statement of research interests and names of three referees. Review of applications will begin on February 8, 2016 and continue until positions are filled. For more information and to apply, please visit: academicjobs.columbia.edu/applicants/Central?quickFinda998 Columbia University is an Equal Opportunity/Affirmative Action employer.

Lourdes A. Gautier Director of Administration and Finance Department of Ecology, Evolution & Environmental Biology (E3B) Columbia University 1200 Amsterdam Avenue New York, NY 10027 212-854-9987

Lourdes Gautier <lg2019@columbia.edu> Lourdes Gautier <lg2019@columbia.edu>

CRITFC Idaho FishGenetics

Fisheries Geneticist - Columbia River Inter-Tribal Fish Commission (CRITFC)

http://www.critfc.org/jobs/fisheries-geneticist Salary: $55,952-$72,737 DOQ, plus benefits

Closes on: March 15, 2016

The Columbia River Inter-Tribal Fish Commission (CRITFC) is seeking Fisheries Geneticists with experience in population genomics, association mapping, and mixed stock analysis. Positions are part of the Fishery Science Department, but will be located with the genetics group at the Hagerman Fish Culture Experiment Station in Hagerman, ID. This research group is involved in testing conservation, evolution, and ecological theories related to salmonids and other fishes. The employee will work under the Lead Geneticist, in association with CRITFC geneticists and technicians, as well as staff of the Fishery Science Department in Portland, OR. Efforts will focus on applying empirical genetics/genomics data to address questions related to conservation and recovery of steelhead, Chinook, sockeye, and coho salmon, sturgeon, lamprey, and other fishes of the Columbia River Basin.

See more at: http://www.critfc.org/jobs/fisheries-geneticist Shawn Narum <nars@critfc.org>

DenverBotanicGardens AssistCuratorMycology

Job Title: Assistant Curator of Mycology

Job Summary: Coordinates the growth and improvement of Denver Botanic Gardens mycology program, advocate biodiversity science and natural history collections, develop an active externally funded research program that incorporates postdoctoral fellows, graduate students and undergraduates, and oversees volunteers.

Career Type: Full-time

Location: York Street

Qualifications: Ph. D. in mycology, evolution, or equivalent with interest in developing field and collection orientated research projects related to the study and conservation of natural ecosystems within our region and show leadership in science communication and engagement; or minimum 6 years related experience and/or training; or equivalent combination of education and experience. Must demonstrate a strong record of research accomplishments and acquisition of funding. Experience with fungal identification, specimen digitization and curation techniques and interest in formal and informal science education, preferred. Must possess strong communication skills, both written and spoken, needs excellent time management skills, and good interpersonal skills.

Benefits: Major benefits include choice of medical plans, dental, vision and life insurance, medical and daycare Flexible Spending Account (FSA) and Healthcare Spending Account (HSA) ; a generous retirement plan plus paid holidays, vacation, personal and sick time and access to personal lines of insurance. Additional benefits include short-term and long-term disability coverage, an Employee Assistance Program (EAP), an ECO pass and a complimentary Denver Botanic Gardens membership, access to Gardens education classes and summer concert tickets.

*Additional Information: *

Review of applications will begin April 2016 and continue until the position is filled with an anticipated start date of September 1, 2016. Applications should include a curriculum vitae and statement of research interests (3 pages maximum).

Send resume and/or application to *Human Resources, Denver Botanic Gardens, 1007 York St., Denver CO 80206*, or *e-mail your resume to hr@botanicgardens.org*. We are a nonprofit, EOE.

Rebecca Hufft <becky.h.kao@gmail.com>

DukeU ResTech EvolAnthro Genomics

An Associate in Research/Laboratory Research Analyst position available, starting immediately, in the Tung lab at Duke University. The Tung lab studies the relationship between behavior, the social environment, and genetics and genomics, with a focus on nonhuman primate populations. 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, 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 individuals age, color, disability, genetic information, gender, gender identity, national origin, race, religion, sexual orientation, or veteran status.

voyles.tn@gmail.com

FordhamU SummerREU EvolutionaryGenetics

REU at Fordham University- Summer 2016

An NSF-funded REU to study Y-chromosome diversity and sex-biased dispersal in wild brown rats (Rattus norvegicus) is available in the Munshi-South Lab at Fordham University. Our lab is currently investigating rat evolution at scales ranging from landscape genetics of individual cities to global patterns of diversity. Development of resources for investigating Y-chromosome diversity will support many of these studies. The REU student will work with the lab to bioinformatically identify Y-chromosome SNPs, design SNPtype assays, extract DNA, genotype samples, and analyze data.

We seek applicants interested in bioinformatics, evolutionary biology, and related disciplines. Applicants must have taken a college-level genetics course. This REU will require attention to detail, reliability, independence, and critical thinking.

This position is based at Fordham University's field station, the Louis Calder Center, in Armonk, NY. The Calder Center is located approximately 25 miles north of New York City in a protected woodland area. Housing will be provided at the Calder Center for the duration of the REU (May 23 to Aug 12, 2016). Additionally, the student will receive a $6,000 stipend. The selected student will participate in professional development activities through the Calder Centers REU program, including presentation of results at a research colloquium at the end of the summer.

To apply, please send a one page personal statement about your scientific interests and how this REU will support your professional goals, unofficial transcripts including a list of Spring 2016 courses, and names of two professional references (including title, address, phone number, and email address) as a single pdf (with your last name in the file name) to Dr. Jason Munshi-South (jmunshisouth@fordham.edu). Applications are due March 4th, 2016.

Jason Munshi-South <jason@nycevolution.org>

GrinnellCollege 2 Biology 2yearTerm

We welcome applications for either position from those with expertise in evolution.

https://jobs.grinnell.edu/postings/1496 GRINNELL COLLEGE V DEPARTMENT OF BIOLOGY V TWO 2-YEAR POSITIONS (START FALL 2016)

The Department of Biology invites applications for two 2-year leave-replacement positions beginning Fall 2016, one in the area of Cell/Molecular Biology and a second in Ecology/Evolution/Behavior. Assistant Professor (Ph.D.) preferred; Instructor (ABD) possible. Teaching will include one intermediate-level course, either , Cells, and Organisms or , Evolution, and Ecology, and one or more advanced courses in the area of specialty. Other teaching possibilities may include our innovative, research-based introductory course or biochemistry lab instruction, as appropriate to the applicant.

Grinnell College is a highly selective undergraduate liberal arts college with a strong tradition of social responsibility. In letters of application, candidates should discuss their potential to contribute to a college community that maintains a diversity of people and perspectives as one of its core values. To be assured of full consideration, all application materials should be received by February 11, 2016. Please visit our website at https://jobs.grinnell.edu to find more details about the job and submit applications online. Candidates will need to upload a letter of application, curriculum vitae, transcripts (copies are acceptable), statements of teaching and research interests, and provide email addresses for three references. Questions about this search should be directed to the search chair, Professor Jackie Brown, at [BiologySearch@grinnell.edu] or 641-269-3169.

Grinnell College is committed to providing a safe and inclusivestatus, veteran status, religion, disability, creed, or any other protected class.

Jackie (Jonathan M.) Brown Professor of Biology Grinnell College brownj@grinnell.edu

"Brown, Jonathan" <BROWNJ@Grinnell.EDU>

HarvardU ResAssist MolEvol DeadlineUpdate

A research fellow (research assistant) position is available within the Department of Organismic and Evolutionary Biology, Edwards Lab at Harvard University.

The researcher will contribute to the development of a new experimental and synthetic approach that involves reconstructing ancient molecular components and observing their biological function in modern bacterial cells through experimental evolution. This will generate experimental systems consisting of viable modern-ancient hybrid bacterial organisms amenable to biological, biochemical and genetic characterization.

The position will be based at the main campus of Harvard University, and will include access to resources available through the Organismic and Evolutionary Department and the FAS Center for Systems Biology.

The application packet should include a cover letter, CV and list of references. In the cover letter, please describe your prior knowledge or experience with specific molecular biology and bacterial genetics techniques including bacterial genomic engineering, experimental evolution, molecular cloning, protein expression and purification, as well as experience with whole genome sequencing library preparation methods and data analysis. The planned starting date for the position is on or about March 15th, 2016; the cover letter should also indicate the applicant's intended starting date.

The position includes competitive salary and full benefits, and is for 1 year with potential extension to 2 or more years. The minimum academic requirement for this position is a masters degree in molecular and cell biology, genetics, biology, or a closely related field. Applicants with at least 2 years of research experience or an equivalent combination of education and experience will also be considered.

Direct all questions and application materials to the team leader Betul Kacar, kacar@g.harvard.edu. For further information visit http://kacarlab.org, for OEB visit http://www.oeb.harvard.edu.

Application Deadline: February 1st 2016

Harvard University 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.

"Kacar, Betul" <kacar@fas.harvard.edu>

IAST Toulouse EvolBiol

"The Institute for Advanced Study in Toulouse (IAST) and Université Toulouse I Capitole, France, seek candidates for one open rank tenure-track or tenured position, open to Evolutionary Biologists. Rank and tenure status will be commensurate with experience and qualifications. Anticipated start date: September 1st, 2016. For more information and send your application please visit: www.iast.fr, and select "Applications" - Tenured or Tenure-track position in Social Sciences. You can also contact Ingela Alger, Director of the program in Biology at the IAST. Application materials should be sent as soon as possible, and no later than 29th February 2016."

Delphine POUTS Assistante de Direction Executive Assistant

IAST 21 allée de Brienne 31015 Toulouse Cedex 6

PhÂ: 0033 5 61 12 86 27 Delphine.pouts@iast.fr

Delphine Pouts <delphine.pouts@iast.fr>

INRA RennesFrance EvolutionaryBiol

INRA, the French National Institute for Agricultural Research, invites applications for a permanent position at the Junior Research Scientist level, in the area of evolutionary biology and ecotoxicology. The position will be based within the Research Unit "Ecology and Ecosystem Health" http://www6.rennes.inra.fr/ese_eng/ Description: Molecular and evolutionary ecotoxicology The long-term impact of chemical contaminants on natural populations represents a current challenge of importance to ecotoxicology and ecological risk assessment. The recruited scientist will study the evolutionary and non-genetic transgenerational effects of pollutants on aquatic populations, and in particular the unintentional effects of plant protection products. To this end, he/she will implement experimental evolution and ecotoxicological protocols using organisms with short generation times, and will investigate the relative role of selection and adaptive plasticity, as well as the influence of the genetic load on the response of the populations exposed. Strong expertise in evolutionary biology, with an interest in issues related to xenobiotic stress would be appreciated. Experience in genomic analysis (transcriptomics and/or epigenetics) is recommended. Experience in quantitative genetics would be a bonus. Training required PhD or equivalent. Candidates should have a good command of English, and long-term international experience would also be desirable. Successful candidates who have not yet acquired postdoctoral training will be required to do so, preferably abroad, after their probationary period (1st year) and before being eligible for promotion to an Experienced Research Scientist position (CR1). Submission deadline for application package: 1st March 2016 Pre-selections: April-May 2016 Final selections: June-July 2016 Starting date for appointments: from 1st of July 2016 Scientific contact: marie-agnes.coutellec@rennes.inra.fr

more information at: http://jobs.inra.fr/en/-offers/emploi_perm/open-competitions/cr2/-?concours$348&campagne#129&domaine=&region=-&corps=&entite_rattachement=&discipline=-&annonce=16175&annonce_id=15#annonce Marie-Agnès Coutellec INRA/Agrocampus-Ouest UMR0985 Ecology and Ecosystem Health Ecotoxicology and Quality of Aquatic Environments 65 rue de Saint-Brieuc

35042 Rennes cedex - FRANCE phone: +33 223 485 248 http://www6.rennes.inra.fr/ese_eng/ INRA - coutellec <marie-agnes.coutellec@rennes.inra.fr>

InstitutPasteur 10 Bioinformatics

Ten Permanent Positions in Bioinformatics and Biostatistics at Institut Pasteur (Paris)

Bioinformatics, biostatistics and integrative biology have emerged as strategic priorities for the Institut Pasteur. A new Center for Bioinformatics, Biostatistics and Integrative Biology (C3BI - https://c3bi.pasteur.fr) has been created in 2015 on the Parisian campus. The objective of this center is to federate and strengthen capacities in bioinformatics and biostatistics in the different research areas developed within the institute, around biology and health.

In this framework and after 20 recruitments in 2014-2015, Institut Pasteur proposes this year again 10 permanent positions in bioinformatics and biostatistics for 2016. Successful applicants will be affiliated to the C3BI and to the Hub of bioinformatics and biostatistics and will be supervised by the director of the Center. They may be assigned for most of their time to research units and/or technological platforms. Teaching activities will also be possible, both at Paris and in the Institut Pasteur International Network.

TASKS AND RESPONSIBILITIES

The main objective is to provide support to research units and platforms, for the analysis of their data using bioinformatics and statistics approaches. This support will be provided in various ways:

* advising and guiding in the use of existing methods and tools,

* maintaining an active bibliographical survey and evaluate existing tools and methods,

* developing new methods and tools when necessary,

* collaborating with research units and platforms to analyze their data,

* helping, defining and implementing collaborative projects such as ANR, ERC ,

* transferring knowledge and tools towards research units and platforms, and provide training in bioinformatics and biostatistics,

* perpetuating and maintaining methods and tools developed by research units, and ensuring their integration within open platforms such as Galaxy, Mobyle

* actively participating to the implementation of the web portal of the Pasteur Institute bioinformatics platform, to be open to the international community,

* interacting with the Institut Pasteur International Network (IPIN, 33 institutes all around the world), mainly for setting up trainings and analyzing data.

AVAILABLE POSITIONS

This year positions will mostly focus on the following domains:

* Statistical analysis and modeling of omics data

* Statistical analysis of genetic data

* Statistical and molecular epidemiology

* News HTS data (epigenetics, single cell, long reads)

* Eukaryotic genomics

* Human genomics

* Proteomics and mass-spectrometry data

* Annotation of proteomes, sequence/structure/function relationships

* Development, maintenance and use of bioinformatics software

EXPECTED PROFILES

In order to postulate, you need to:

* hold an engineer or master degree in (bio)informatics, (bio)statistics, applied mathematics or any other related domain, followed by at least 3 years of professional experience in bioinformatics and/or biostatistics in research or support to research activity,

* or hold a PhD in bioinformatics, biostatistics, applied mathematics or any other related domain, followed by at least 2 years of professional experience in bioinformatics and/or biostatistics in research or support to research activity.

Strong experience in teaching bioinformatics/biostatistics will be a plus.

TO APPLY

Applications (cover letter, detailed CV and referees addresses) have to be filled on line at the following URL: https://c3bi.pasteur.fr/c3bi-2016-job-application-post/ The deadline for applications is February 15th, 2016. Candidate pre-selection will take place around March 25th, 2016. Short-listed candidates will be called for an interview between the 11th and 15th of April 2016 (dates to be reserved absolutely). Internal HR reference :

16005ES PLEASE DIFFUSE THIS ANNOUNCEMENT !!

Olivier Gascuel <olivier.gascuel@pasteur.fr>

IZW Germany BiodiversityTechnician

The Leibniz Institute for Zoo and Wildlife Research (IZW) in the Forschungsverbund Berlin e. V. (www.izw-berlin.de) together with the Freie Universität Berlin, the Technical University of Berlin, the University of Potsdam, and the other partners in the Berlin-Brandenburg Institute for Advanced Biodiversity Research (BBIB, www.bbib.org) have formed a consortium to implement a major new interdisciplinary research initiative, the Bridging in Biodiversity Science (http://www.bbib.org/-bridging-in-biodiversity-science.html) project funded by the Federal Ministry of Research and Education (BMBF).

Within the work package Rural-urban coupling, the IZW, together with its partner, the Technical University Berlin (TUB), seek to fill the following positions:

1 ecological modeler/ quantitative ecologist, with focus on spatial analyses (postdoc) - IZW & TU Berlin

Tasks: The research initiative will focus on quantifying and modelling the biodiversity impacts of human-mediated ecological processes and socioeconomic drivers, investigating processes at the expanding human-wildlife interface, and accounting for past and current landscape configuration. We are looking for a highly motivated researcher keen to work in the fields of urban ecology, spatial modelling and simulation. The goal of the project will be to develop species habitat models (flora, fauna), and to link these models to urban and rural matrix heterogeneity and patch configuration.

Requirements: The successful candidate will have a strong expertise in the development of spatial models, spatial statistics and species distribution modelling. A sound knowledge in geographic information systems (GIS) and remote sensing, programming (e.g., Python, R) and geodatabase management is required. Applicants must hold a doctoral degree, have proven publication skills and should be able to work independently. Organisational skills, high motivation and the willingness to work as part of a team within an interdisciplinary project are essential.

1 doctoral student in urban ecology / hedgehogs - IZW

Tasks: As part of this research initiative, the doctoral student will study the life history, movements, and population structure of European hedgehogs (Erinaceus europaeus) along a rural-urban gradient, by using radio-collaring and telemetry, collection and analysis of genetic samples to assess population structure in a landscape context and participating in the citizen science module of the project.

Requirements: Completed master's/diploma degree in biological sciences, a degree in veterinary medicine or similar life sciences; competence in statistical methods (particularly R) and a sound knowledge in geographic information systems (GIS); an open and communicative attitude towards stakeholders and members of the public; sound German and English language skill (spoken and written); an excellent ability to work as part of a team and interact fruitfully with scientists from a wide variety of fields; a background in ecology, previous experience with wildlife, biotelemetry, experience in field research and a valid driving licence would be highly advantageous.

Applications and working environment: We offer state-of-the-art methodology and a stimulating research environment within an interdisciplinary, collaborative context. Both positions are limited to three years and start on March 1st, 2016, with salary according to TVöD (50% for doctoral student, 100% for postdoc). As a member of the Leibniz Association the IZW is an equal opportunity employer, determined to increase the proportion of women in successful scientific careers, and particularly encourages women to apply. Preference will be given to disabled applicants with the same qualifications. Enquiries or questions should be directed to (a) postdoc: Dr Stephanie Kramer-Schadt (kramer@izw-berlin.de<mailto:kramer@izw-berlin.de>), or Prof. Ingo Kowarik (kowarik@tu-berlin.de<mailto:kowarik@tu-berlin.de>); (b) doctoral student: Dr Anne Berger (berger@izw-berlin.de<mailto:berger@izw-berlin.de>).

Please email complete application documents including a letter of motivation, CV, copies of relevant degrees, and names and contact details of two referees as soon as possible but no later than January 24th, 2016 via the IZW's (www.izw-berlin.de< http://www.izw-berlin.de >) online-job-market (button "Apply online"). Please note: Interviews will take place at the IZW on January 28th and January 29th 2016.

"Vollberg, Stephanie" <vollberg@izw-berlin.de>

LausanneU ComputationalBiology

Tenure-Track Assistant Professor or Associate Professor at the upcoming Department Computational Biology of the University of Lausanne, Switzerland

The University of Lausanne (UNIL), Switzerland, brings together more than 14,000 students and nearly 4,000 employees, professors and researchers from 120 nationalities. Its Faculty of Biology and Medicine (FBM) intends to strengthen its research program in computational biology, and thus invites *applications for two positions* as :

Tenure-Track Assistant Professor or Associate Professor at the upcoming Department Computational Biology

Starting date: to be agreed.

*The rank of the positions - which come with competitive starting packages and running budget - will be determined according to the level of the selected candidates. At UNIL, Tenure-Track Assistant Professors are appointed for a period of six years with the prospect of performance-based advancement to a permanent Associate Professorship position.

Qualifications and requirements:

- PhD, MD, or MD/PhD degree with a track record of scientific excellence.

- Strong, internationally competitive research program.

- Ability to attract external funding and to promote an interactive and synergistic research environment.

- Management experience, as well as vision and motivation to participate in the transition of the Department of Medical Genetics into a new Department of Computational Biology.

Job description:

- Lead a research team in computational biology.

- Teach at the School of Biology and Medicine.

The Department is embedded in a highly active and expanding research community in the Lake Geneva area, offering interactions with eight other UNIL biology departments (e.g. Dpt of Ecology and Evolution (http://www.unil.ch/dee/home.html) and the Center for Integrative Genomics (http://www.unil.ch/-cig/en/home.html)), the University Hospital (CHUV) in Lausanne, as well as the Swiss Institute of Bioinformatics (https://www.isb-sib.ch/), the Ecole Polytechnique Fédérale de Lausanne (https://www.epfl.ch/-index.en.html) and the University of Geneva (e.g. Dpt of Genetic Medicine and Development; Dpt of Genetics and Evolution).

Areas of particular interest for this position include but are not limited to population genetics, genomics, systems biology, modeling and bioinformatics.

The job description is available on the internet site www.unil.ch/emplois ≪Postes académiques≫.

Further information may be obtained from Prof. Alexandre Reymond (Alexandre.Reymond@unil.ch), chairman of the search committee.

Applications, in English, will include a motivation letter, the curriculum vitae, the list of publications highlighting the five most significant ones, a brief statement of the past and future research, a summary of previous teaching experience (if any), and contact information of at least 3 referees.

The full application should be submitted online by March 15th, 2016 as a single pdf file to www.unil.ch/-iafbm/application . Seeking to promote an equitable representation of men and women among its staff, the University encourages applications from women.

Jérôme Goudet <Jerome.Goudet@unil.ch>

MaxPlanckInst Cologne Bioinformatics

Bioinformatics Position

The Department of Comparative Development and Genetics at the Max Planck Institute for Plant Breeding Research (MPIPZ) in Cologne is seeking a Bioinformatician to contribute to high throughput sequence data analyses for the purpose of understanding trait development and diversification in plants. The candidate will work in the group of the Director Prof. Dr. MiltosTsiantis and will also enjoy opportunities for collaborating with the new bioinformatics group of Dr. Xiangchao Gan. Tasks will involve analysis and interpretation of high throughput sequencing data including RNAseq, ChIPseq and DNAseq generated predominantly but not exclusively on the Illumina platform. Outstanding teamwork and communication skills as well as willingness and ability to work collaboratively towards common goals are essential. Recent work by the group can be seen in Rast-Somssich, (2015) Alternate wiring of a KNOXI genetic network underlies differences in leaf development of A. thaliana and C. hirsuta Genes and Development in press; Cartolano et al (2015) Heterochrony underpins natural variation in Cardamine hirsutaleaf form PNAS 112, 10539-10544; Vlad et al (2014) Leaf shape evolution through duplication, regulatory diversification, and loss of a homeobox gene Science 343, 780-3. The position will suit creative, highly motivated individuals who can interact productively with biologists and are interested in the genetic basis for natural variation and evolutionary change.

Your profile

The basic qualifications for the outlined position are:

- PhD/masters degree in bioinformatics or equivalent background - expertise in next-generation sequencing data analysis - excellent skills in statistics - proficiency in programming in at least one script language: Perl/Python/Ruby/R - proficiency in Unix (Linux), scripting and bioinformatics tools and databases - strong interest in and understanding of molecular biology and evolution of gene function - excellent communication skills in English (spoken and written) - high quality publications that provide evidence for the skill set outlined above.

Any of the following additional qualifications would be an advantage: - expertise in population genetics - expertise in phylogenetic and evolutionary analyses - knowledge of C++

The position will be for one year at first with good possibilities of extension.

The Max Planck Institute for Plant Breeding Research (MPIPZ) is one of the world's premier sites committed to research into fundamental processes and training in plant biology. There are four science departments plus independent research groups and specialist support.

The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply. 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.

Applications in English can be sent to Ms. Ina Fourre (fourre@mpipz.mpg.de) as a single PDF file and should include a short letter of motivation, explaining how the applicant's profile and aspirations fit with the group, a list of publications and names and contact details of two academic referees. The search will continue until a suitable candidate is identified. Only shortlisted candidates will be contacted.

Stefan Schueller <schueller@mpipz.mpg.de>

NatureCommunications EvolGenetics Editor

Nature Communications is seeking to recruit a genetics editor. Candidates with expertise in bioinformatics, population genetics, statistical genetics and evolutionary genetics are particularly encouraged to apply. Application deadline is 8th February 2016. Full details can be found here: http://www.nature.com/naturejobs/science/jobs/567327-assistant-associate-or-senior-editor Simon Harold PhD Associate Editor Nature Communications The Macmillan Building 4 Crinan Street London, N1 9XW UK

simon.harold@nature.com

"Harold, Simon" <Simon.Harold@nature.com>

OldDominionU ChairPlantEvolution

The Department of Biological Sciences at Old Dominion University invites applications for the J. Robert Stiffler Distinguished Professorship in Botany at the Professor or Associate Professor level.

Minimum requirements include a Ph.D. in Plant Science or a related area, experience in molecular techniques in plant research, substantial research accomplishments with an established record of publications and independent peer-reviewed funding, active competitive grants, and a successful graduate and undergraduate teaching and student mentoring record. We are especially interested in applicants whose research expands the department's expertise in the area of molecular plant systematics and advanced genomics. State salary support and a competitive start-up package are available; additional annual research support funds are provided by the J. Robert Stiffler Professorship endowment.

The department has strong graduate programs, including a Ph.D. in Ecological Sciences, and has four (two endowed) faculty positions in the Plant Sciences (http://ww2.sci.odu.edu/biology/). The incumbent will play a critical role in the future development of botanical sciences in the department. Additional resources available include the Norfolk Botanical Garden, Kaplan Orchid Conservatory, Blackwater Ecological Preserve, and the University's herbarium. Old Dominion University (http://www.odu.edu/) is a state-supported, Carnegie doctoral research extensive institution enrolling approximately 25,000 students.

Applicants should submit a curriculum vitae, a statement of research and teaching interests, and names, telephone numbers, and addresses (postal and email) of four references electronically to https://jobs.odu.edu by clicking on Teaching and Administrative Faculty Opportunities. For full consideration, please apply by January 30, 2016. Questions about the position can be directed to Lytton John Musselman, Mary Payne Hogan Professor of Botany (lmusselm@odu.edu).

Old Dominion University is an equal opportunity, affirmative action institution. Minorities, women, veterans, and individuals with disabilities are encouraged to apply.

https://www.higheredjobs.com/details.cfm?JobCode=176181421&utm_source=12_08_15&utm_medium=email&utm_campaign=JobAgentEmail –

Daniel Barshis, Ph.D. Assistant Professor Department of Biological Sciences Old Dominion University Mills Godwin Building 302J Norfolk, VA 23529 Office: 757-683-3614 Lab: 757-683-5755 Web: www.odu.edu/~dbarshis Dan Barshis <barshis@gmail.com>

Sheffield Bioinformatics

Sheffield Diagnostic Genetics Service (SDGS) is seeking to appoint a Lead Bioinformatician primarily to handle next generation sequencing data from DNA. SDGS is an NHS regional Diagnostic Genetics laboratory providing a wide range of genetic specialist services to the public and private sectors with a number of key areas of service provision, including a full oncology service (sheffieldchildrens.nhs.uk, ukgtn.nhs.uk). The Laboratory Services section provides analytical services to the 2 clinical sections (Oncology and Constitutional Genetics), oversees and contributes to research and development, and has a developing business in providing analytical services to Clinical Trials and research.

SDGS is part of the Division of Pharmacy, Diagnostics and Genetics in Sheffield Children's NHS Foundation Trust and has an established record of integrated service development across the Pathology disciplines both within the Trust and with other Trusts in the region. The trust has invested in Next Generation Sequencing technologies (HiSeq 2500, MiSeq and PGM) which are being substantially used for patient diagnosis to improve healthcare. We are looking for the Lead bioinformatician to build on an existing pipeline for variant detection, extend the range of analyses and improve data processing by using computational tools. A critical part of the job is to support the work of clinical scientists who are responsible for a diagnosis. We will soon have new high-end hardware with substantial processing power and storage space to support the ongoing developments and clinical needs.

You will have a range of experience of developing and implementing bioinformatics tools to assist data handling and processing of sequencing data ideally delivered in a highly regulated healthcare environment. You will be proficient at programming in a language such as Perl and have an understanding of Linux and bash scripting. Experience with R is desirable. You will have knowledge of next generation sequencing technologies and statistical techniques used in data analysis. . You will have an understanding of Laboratory Information management systems and IT. Excellent communication skills are required to be successful in this role. You must be able to present and convey complex bioinformatics ideas to a wide audience and facilitate their understanding. You will have demonstrable leadership skills, but be self motivated and proactive in seeking resolutions to problems.

The Lead bioinformatician will be a key part of laboratory services for delivery of next generation sequencing results and will be expected to interact with many different partners on a variety of projects. You need to be willing to tackle a wide range of tasks including in areas that you may be unfamiliar with. The Lead bioinformatician will also be responsible for a clinical bioinformatician and this is the start of a growing group of staff. This is a rapidly changing time for the NHS and represents an exciting opportunity for the right candidate to make their mark.

Darren Grafham Head of Laboratory Services Sheffield Diagnostics Genetics Service C Floor Blue Wing Sheffield Children's NHS Foundation Trust Western Bank Sheffield S10 2TH Tel: 0114 2717005

Sheffield Children's NHS Foundation Trust Western Bank Sheffield. S10 2TH www: http://www.sheffieldchildrens.nhs.uk The Children's Hospital Charity http://www.tchc.org.uk/ Donate here http://www.justgiving.com/tchc/donate Darren Grafham <Darren.Grafham@sch.nhs.uk>

StJohnsU EvolutionaryBiol

Assistant/Associate Professor, Ecology, Evolutionary Biology or Environmental Sciences, Tenure Track

St. John's College of Liberal Arts and Sciences

Department of Biological Sciences

The Department of Biological Sciences at St. John's University invites applications for a tenure-track faculty position of Assistant or Associate Professor in the area of ecology, evolutionary biology or environmental sciences. Preference will be given to candidates who use tools of bioinformatics.

The successful candidate will posses a doctoral degree plus postdoctoral experience, and will be expected to develop externally funded research program and mentor graduate and undergraduate research students. The candidate will teach on a rotating basis in our Fundamentals of Biology course and an upper level/graduate course in his/her specialty.

Applicants should submit a cover letter, curriculum vitae and statement of research and teaching interests to Dr. A. Vancura at vancuraa@stjohns.edu. All documents should be submitted as a single pdf file. Applicants should also arrange to have three letters of recommendation sent as an e-mail attachment to the same email address. Review of applications will commence immediately and continue until the position is filled.

St. John's University is an Equal Opportunity Employer and encourages applications from women and minorities.

Dianella Howarth <howarthd@stjohns.edu>

UCalifornia Merced ComputationalBiol

University of California Merced is recruiting for four Assistant Professor Positions as part of a cluster hire in the area of Computational Sciences and Data Analytics. Topics of interest include, but are not limited to: statistical inference from comparative or population analysis of high-throughput omics data to address fundamental problems in molecular and cellular biology. Full details are available at https://aprecruit.ucmerced.edu/apply/ Emilia Huerta-Sanchez (ehuerta-sanchez@ucmerced.edu) Assistant Professor, School of Natural Sciences

"ehuerta-sanchez@ucmerced.edu" <ehuerta-sanchez@ucmerced.edu>

UCentralFlorida SeniorLabTech MolecularBiol

The Department of Biology at the University of Central Florida is recruiting a permanent Senior Lab Technician to maintain and operate a core molecular lab facility. The position will involve basic DNA skills (DNA/RNA extraction, PCR and standard DNA sequencing, fragment purification, gel electrophoresis, restriction enzyme digestion), as well as next-generation sequencing (Illumina) methods, included but not limited to: whole genome library preparation, microbial metagenomics, reduced representation libraries using probe hybridization, and RNAseq/whole transcriptome library preparation. The technician will maintain, troubleshoot and perform day-to-day lab upkeep and coordinate sample shipment for sequencing at off-site core Illumina facilities. S/he will also help design and execute next-generation sequencing data generation workflows; oversee sequencing projects conducted in the lab as part of undergraduate courses and faculty research; analyze current process procedures and provide feedback for their optimization and improvement; document processes and improvements to methods; perform Quality Control on samples and raw sequence data; consult on research projects with other laboratories; develop, assess and adapt new technologies, protocols and software; supervise and train graduate and undergraduate students; and conduct other laboratory work as needed.

Complete details on salary, benefits, eligibility and how to apply can be found at:

http://www.jobswithucf.com:80/postings/44207 Note: the revised close date for this position is Friday, January 22, 2016 (5pm EST).

For additional information, please contact Anna Savage at Anna.Savage@ucf.edu

Anna Savage <Anna.Savage@ucf.edu>

UHaifa LabManagerEvolution

Biology, mathematics, computer science and bioinformatics students/researchers are needed

Dr. Livnat's new lab for the study of evolution at the University of Haifa in Israel is seeking applications for Ph.D, postdoc, lab manager and other positions from individuals with a background in biology, mathematics, computer science or bioinformatics and a record of past excellence.

We study the deep principles of how evolution works both theoretically and experimentally. 1) Students with a background in theoretical computer science or other branches of mathematics may participate in work at the interface of evolutionary biology and theoretical computer science whose goal is to form a new mathematical framework for evolution. Our lab works in collaboration with leading computer scientists abroad and in Israel. 2) Students with a background in bioinformatics and students with molecular biology lab skills may participate in evolutionary research involving cutting-edge sequencing methods. 3) Students interested in the evolution of behavior are also encouraged to apply.

Applicants should send a cover letter and a CV to alivnat@univ.haifa.ac.il, including the names of 2-3 references. More info at http://sci3.haifa.ac.il/˜alivnat/
adi.livnat@gmail.com

UHull ResAssist VertebrateInvasion

NERC Research Associate/Assistant in Phylogenetic Comparative Analyses of Vertebrate Invasion Success (1 Post)

School of Biological, Biomedical and Environmental Sciences

We are looking to appoint a Research Associate suitably qualified and experienced in the areas required or a Research Assistant that is presently working towards completing their PhD and looking to develop their experience in this field. The post is funded for 1 year by a NERC New Investigator Award to Dr Isabella Capellini, entitled 'Understanding biological invasions: a phylogenetic comparative approach'.

The RA will be a member of the Evolutionary Comparative Ecology Group (http:/tinyurl.com/kswc4ac) led by Dr Isabella Capellini (http:/tinyurl.com/icapellini). The group offers a dynamic research environment where the successful applicant will be member of a team using state of the art phylogenetic comparative approaches to answer an array of fundamental questions in biology and ecology.

Using alien (non-native) vertebrates as model organisms and cutting edge phylogenetic comparative methods, the project's goal is to test which biological characteristics promote species success in space and time, as predicted by key hypotheses in macroecology and evolution. The proposed work for this position will extend the results of the paper we recently published (Capellini et al 2015 Ecology Letters), by either investigating invasion success in fish or ecological species' traits promoting success in terrestrial vertebrates. The RA will help completing an extensive database of vertebrate invasion success at the global scale and species characteristics, and is expected to work together with the other postdoctoral researcher on the project, in constructing, updating and maintaining the project database of vertebrate invasions. The post holder will also contribute to the dissemination of the results to the scientific community through presentation at international conferences and workshops, and to the general public through public lectures and interviews with the media where appropriate.

Within the School, the RA will benefit from a rich and diverse research environment that includes the Ecology and Environment Group and the Evolutionary Biology Group. The University of Hull also offers a comprehensive Staff Development Programme.

Essential: PhD in biology or related discipline near completion, BSc in Biology or related discipline, knowledge of modern phylogenetic comparative methods, strong quantitative skills, evidence of work of publishable quality, excellent oral and written communication skills, demonstrable ability to work as an effective team member, and be reliable, self-motivated and well organized.

Desirable: PhD in biology or related discipline, experience with phylogenetic comparative methods, experience in testing hypotheses in macroecology and phenotypic evolution across species, strong publication record, experience with R.

The position is fixed term for 1 year. The start date of the project is fixed to 1ˆst April 2016.

Salary range: Â£26,537 to Â£31,656 pa - Starting salary according to qualification and experience.

You can learn more about this position and apply online at: www.hull.ac.uk/jobs (Vacancy ref: FS0214) Informal enquiries to Dr Isabella Capellini (I.Capellini@hull.ac.uk)

Closing date: 21^st February 2016

Interviews: 1^st March 2016

Dr Isabella Capellini School of Biological, Biomedical and Environmental Sciences University of Hull Cottingham Road, Hull HU6 7RX (UK) Personal webpage & NERC/BBSRC projects: http:/tinyurl.com/icapellini Evolutionary Comparative Ecology Group: http:/tinyurl.com/kswc4ac Isabella Capellini <I.Capellini@hull.ac.uk>

UMontreal PlantEvoDevol

2ndannouncement

DeÌpartementde sciences biologiques FaculteÌ des arts et des sciences

Professorin Molecular development of plants

TheDeÌpartement de sciences biologiques is seeking applications for a full-timetenure-track position at the rank of Assistant Professor in Moleculardevelopment of plants, including evolutionary developmental biology.

* ïResponsibilities

Theappointed candidate will be expected to teach at all three levels of thecurriculum, supervise graduate students, engage in ongoing research andpublication, and contribute to the academic life and reputation of theUniversity.

* ïRequirements

* Ph.D. in molecular biology or in a related field

* Postdoctoral experiences in relevant fields

* High quality publication record in international journals with very good impact factor

* Interest in cross-disciplinary research and capacity to develop collaborations with members of

theDeÌpartement de sciences biologiques and other departments of UniversiteÌde MontreÌal

* Excellent abilities to teach at the undergraduate and graduate levels

* Elaboration of a novel research programme that uses molecular genetic approaches to study plant development for a model system

* Priority will be given to candidates using advanced imaging approaches and possessing a good knowledge of plant anatomy and morphology

* Proficiency in French within a reasonable period

LinguisticPolicy : UniversiteÌ de MontreÌal is a QueÌbec universitywith an international reputation. French is the languageof instruction. To renew its teaching faculty, theUniversity is intensively recruitingthe world's best specialists.In accordance with the institution's language policy [http://secretariatgeneral.umontreal.ca/fileadmin/user_upload/secretariat/doc_officiels/reglements/administration/adm10-34_politique-linguistique.pdf], UniversiteÌ de MontreÌal providessupport for newly-recruited faculty to attain proficiency inFrench.

* ïSalary UniversiteÌde MontreÌal offers a competitive salary and a complete rangeof employee benefits. Salary scale

* ïStarting Date Onor after June 1st, 2016.

ïConstitution of application

* The application must include the following documents: - a cover letter -a curriculum vitÃ -copies of three recent publications and research

-a description of the teaching philosophy - a description of the research programme

* Three letters of recommendation are also to be sent directly to the Chair of the DeÌpartement de sciences biologiques by the referees.

ïDeadline Applicationand letters of recommendation must be sent to the Chair of theDeÌpartement de

sciencesbiologiques by March 1st, 2016 at the following address :

M.Daniel Boisclair, Chair DeÌpartement de sciences biologiques FaculteÌ desarts et des sciences UniversiteÌ de MontreÌal C. P. 6128, succursale Centre-villeMontreÌal (QC) H3C 3J7

Thecomplete application may also be sent at the following e-mail : daniel.boisclair@umontreal.ca.For more information about the Department, pleaseconsult its website at :

http://www.bio.umontreal.ca/.____________
ï

TheUniversiteÌ de MontreÌal application process allows all regular professorsin the Department to have access to all documents unless theapplicant explicitly states in her or his cover letter that access tothe application should be limited to the selection committee. This restrictionon accessibility will be lifted if the applicant is invited foran interview.

ïAccess Employment Program

UniversiteÌde MontreÌal promotes diversity in its workforce and encouragesmembers of visible and ethnic minorities as well as women, Aboriginalpeople, persons with disabilities and people of all sexual orientationsand gender identities to apply.

ïRequirements Weinvite all qualified candidates to apply at UniversiteÌ de MontreÌal.However, in accordance with immigration requirements in Canada,please note that priority will be given to Canadian citizens andpermanent residents.

ChristopherB. Cameron

https://www.webdepot.umontreal.ca/Usagers/-cameroc/MonDepotPublic/Cameron/index.htm

http://en.wikipedia.org/wiki/Université_de_Montréal twitter:@InvertEvo

CameronChristopher <c.cameron@umontreal.ca>

UNSW Australia Professor Bioinformatics Systems

The University of New South Wales, Australia invites applications for Professor (Level E) in the School of Biotechnology and Biomolecular Sciences in the field of Bioinformatics, Systems Biology and/or Medical Genomics.

For more information and instructions for applying please visit

https://www.jobs.unsw.edu.au/professor-bioinformatics-systems-biology-andor-medical-genomics The School of Biotechnology and Biomolecular Sciences (BABS) is part of the Science Faculty at UNSW Australia and is located on our Kensington campus in Sydney. BABS hosts the Ramaciotti Centre for Genomics, which has world class facilities for sequencing (including MiSeq, NextSeq, PacBio and access to Illumina X-Ten), microfluidics (including single cell genomics) and microarray analysis. The School hosts the New South Wales Systems Biology Initiative, supported by high-performance computing facilities, including national supercomputers. The School also has access to outstanding proteomics and metabolomics facilities at the UNSW Bioanalytical Mass Spectrometry Facility. Additional major facilities at the University provide capacity for biochemical, biophysical and chemical analyses, electron microscopy and animal breeding.

For more information about the School, please visit: http://www.babs.unsw.edu.au/ Application close: 26 February 2016

"m.tanaka@unsw.edu.au" <m.tanaka@unsw.edu.au>

UWisconsin Madison ResTech EvolBiol

A technician position is available in the Hittinger Lab and the DOE Great Lakes Bioenergy Research Center.

The full Position Vacancy Listing (PVL) can be viewed here: https://www.ohr.wisc.edu/Weblisting/External/-PVLSummary.aspx?pvl_num=85167 .

Applications must be received by 31st January 2016. Please follow the application instructions in the PVL.

Chris Todd Hittinger, Assistant Professor of Genetics DOE Great Lakes Bioenergy Research Center University of Wisconsin-Madison 425-G Henry Mall, 4102 Genetics/Biotechnology Center Madison, WI 53706-1580 cthittinger@wisc.edu http://hittinger.genetics.wisc.edu "cthittinger@wisc.edu" <cthittinger@wisc.edu>

UZurich PlantEvoBio

University of Zurich Faculty of Science

The Faculty of Science of the University of Zurich invites applications for an Assistant Professorship in Plant Evolutionary Biology in the framework of the University Research Priority Program "Evolution in Action: from Genomes to Ecosystems".

Evolutionary biology is a core area of biology, and understanding the mechanisms underlying evolutionary processes is of crucial importance for both basic and applied aspects of biology and medicine. Beyond the biological and medical fields, evolutionary concepts are an important theme in the social sciences and in economics. The University Research Priority Program (URPP) "Evolution in Action" is set within this wide area of research. It brings together multiple research groups of the Faculty of Science, the Faculty of Medicine, and the Faculty of Arts and plays an important integrative role for diverse disciplines at the University of Zurich (UZH). In the Plant Sciences, UZH conducts pioneering basic research and is strongly involved in the integrative, interdisciplinary structure of the URPP Evolution in Action.

We seek an innovative scientist with an outstanding track record in research and teaching, as well as the leadership skills and enthusiasm to build on the integrative structure of the URPP Evolution in Action and to further strengthen the integration of diverse disciplines. The successful candidate will establish a strong research group with a focus on Plant Evolutionary Biology, using novel approaches based on sequencing data and genome-wide analyses to address evolutionary questions. Possible research areas are: i) genetic and genomic studies at the population level, ii) molecular basis of adaptation and speciation, iii) evolution of developmental processes, iv) evolution of genomes and regulatory networks. In teaching, the successful candidate will contribute at the advanced level to graduate and undergraduate education (in English or German) in Biology.

The position will be filled as a non-tenure track Assistant Professorship but previous holders of such positions have subsequently obtained a permanent professorship at UZH. The UZH is an equal opportunity employer.

The UZH provides generous research support, including funds for personnel and running expenses. Zurich offers a stimulating scientific environment and extensive opportunities for collaborations within UZH and with ETH Zurich. Switzerland provides excellent research funding opportunities.

Application packages should be uploaded to http://www.mnf.uzh.ch/APPEB in a single file containing a one-page summary; motivation letter; a full curriculum vitae; a vision statement of research and teaching interests outlining major unsolved problems and how they could be tackled; and the names and addresses of three potential referees. Application guidelines can be found on the above page. The deadline for applications is 29 February 2016. For further information, please contact Prof. Dr. Ueli Grossniklaus at grossnik@botinst.uzh.ch.

mfrani@botinst.uzh.ch

WelcomeTrustCenterHumanGenomics Bioinformatics

*Senior Software Developer in Bioinformatics** * Applications to be received by 12pm on Wednesday 2nd of March 2016

Grade 8: Â£38,896 - Â£46,414 with a discretionary range to Â£50,702 p.a.

Applications are invited for a Senior Software Developer in Bioinformatics to join the Bioinformatics Core group at the Wellcome Trust Centre for Human Genetics.

We are seeking an expert and highly experienced software developer to lead the design and implementation of a system for the efficient automation of our existing pipelines for processing genomic data. You will take day-to-day responsibility for a vital aspect of our work and should have strong technical abilities combined with highly-developed decision-making and problem-solving skills, ideally gained through extensive experience in either academia or industry. Leadership and project management skills will also be highly valued. This role offers some freedom to bring your own expertise and ideas while working closely with colleagues to ensure the system meets all requirements.

You will have at least degree-level, and preferably postgraduate-level, qualifications in a relevant quantitative discipline, such as computer science or bioinformatics, with additional and substantial relevant experience. You will have excellent programming and scripting skills, and have extensive experience in Linux/Unix environments and databases. You will be aware of and adhere to best practice software development principles and have been involved with (ideally leading) large software-development projects. You will also be an excellent team player able to interact and communicate effectively with colleagues with a wide variety of backgrounds.

The position is fixed-term for 2 years in the first instance, with expected extension for at least a further 3 years (with the anticipated renewal of the WTCHG's core funding at the end of 2016), and is funded by the Wellcome Trust.

Please quote reference 121441 on all correspondence. You will be required to upload a CV and supporting statement as part of your online application.

Only applications received before 12.00 midday on

Wednesday 2 March 2016 can be considered.

The full Job Description can be downloaded from the link at: http://www.ndm.ox.ac.uk/current-job-vacancies/vacancy/121441-Senior-Software-Developer-in-Bioinformatics%20%0D%0DMike-%20Bioinformatics%0D "camilla.ip@well.ox.ac.uk" <camilla.ip@well.ox.ac.uk>

WelcomeTrustCenterHumanGenomics SingleCellBioinformatics

*Senior Bioinformatician in Single Cell Genomics** * Applications to be received by 12pm on Wednesday 24th of February 2016

Grade 8: Â£38,896 - Â£46,414 with a discretionary range to Â£50,702 p.a.

Applications are invited for a Senior Bioinformatician in Single Cell Genomics to join the Bioinformatics Core Group at the Wellcome Trust Centre for Human Genetics (WTCHG). The group primarily supports the centre's high throughput sequencing facility, providing pipelines for data processing and analysis.

We are seeking a highly-skilled and proactive bioinformatician to co-ordinate our expanding single-cell genomics activities. You will have primary responsibility for building, developing and maintaining pipelines that are tailored to single cell data for a diverse range of projects. Anticipating and responding to new developments in this fast-moving technology will be key. You will play a pivotal role in initiating communications with colleagues in both scientific computing and the wet lab, requiring specialist knowledge and technical discussions on a regular basis. You will also be closely involved in supervising the work of other members of the group implementing the pipelines and analysing the data.

You will have a MSc or higher degree in computer science, bioinformatics or another quantitative discipline together with experience in the analysis of next generation sequencing data and high-level programming skills, preferably in more than one language. You will have experience of leading specific projects or supervising others, and the ability to work largely independently. You will also have excellent communication skills and enjoy working as part of a multidisciplinary team.

The position is fixed-term for 2 years in the first instance, with expected extension for at least a further 3 years (with the anticipated renewal of the WTCHG's core funding at the end of 2016), and is funded by the Wellcome Trust.

An appointment at Grade 7 (Â£30,738 - Â£37,768 p.a.) may also be considered for a less experienced candidate with suitable adjustment of the responsibilities.

Please quote ref. 121147 on all correspondence. You will be required to upload a CV and supporting statement as part of your online application.

Only applications received before 12.00 midday on Wednesday 24 February 2016 will be considered.

The full Job Description can be downloaded from the link found at: http://www.ndm.ox.ac.uk/current-job-vacancies/vacancy/121147-Senior-Bioinformatician-in-Single-Cell-Genomics%20%0D%0D For more information, please contact: Helen Lockstone Acting Head, Bioinformatics and Statistical Genetics Core Wellcome Trust Centre for Human Genetics University of Oxford Roosevelt Drive, Oxford, OX3 7BN, UK Email: hel23@well.ox.ac.uk

"camilla.ip@well.ox.ac.uk" <camilla.ip@well.ox.ac.uk>

Other

2016 EvolutionFilmVideo Contest

2016 Evolution Film Festival/Video Contest

Scientists and science educators of all stripes “students, postdocs, faculty, and full- or part-time science communicators” are invited to enter the Sixth Annual Evolution Video Competition, sponsored by the Duke Initiative for Science & Society, the Howard Hughes Medical Institute (HHMI), the Society for the Study of Evolution (SSE) and the BEACON Center for the Study of Evolution in Action.

To enter, please submit a video that explains a fun fact, key concept, compelling question, or exciting area of evolution research in THREE MINUTES OR LESS. Entries may be related or unrelated to your own research, and should be suitable for use in a classroom (K-12, undergraduate, graduateâyour choice). Videos should be both informative and entertaining. (In other words, no taped lectures or narrated Powerpoint presentations!) Animations, music videos, and mini documentaries are all fair game. The finalists will be screened at the 2016 Evolution meeting in Austin, TX. (You do not need to attend the conference in order to enter a video.) First- and second-place winners will receive up to $1,000 and $500, respectively. The deadline to submit your video(s) is TUESDAY, MAY 31st, 2016 (11:00 PM, EST). For more information (and to see entries from previous years) please visit evolutionfilmfestival.org or contact Jory Weintraub (jory@duke.edu)

Jory P. Weintraub, Ph.D. Science Communication Director, Duke Initiative for Science & Society Senior Lecturing Fellow Duke University 304 Research Drive Box 90222 Durham, NC 27708-0222 (919) 668-0792 jory@duke.edu Skype: jory.weintraub

Jory Weintraub <jory@duke.edu>

BlackHills SouthDakota REU Summer

Summer 2016 REU Position: Black Hills, South Dakota.

Project Title:

Individual variation in seasonal timing of breeding in dark-eyed juncos- Katie Needham and Jessica Graham

(Ph.D. Candidates, under advisement of Dr. Timothy Greives, Biological Sciences Department, North Dakota State University).

Description:

This project will focus on the driving forces behind why some individuals breed earlier or later in the season than the majority of the population. Previous research with songbirds has shown that earlier breeding individuals have higher reproductive success and optimize timing with peak food abundance. While reproductive success is higher for individuals that breed earlier, selection is not shifting towards earlier reproduction, suggesting there are costs associated with breeding early, but the underlying physiological mechanisms of individual variation require further exploration. Working with the population of Dark-eyed Juncos near Hanna, South Dakota, we hope to uncover 1) What ecological factors affect increased reproductive success? 2) How variation in parental care affects reproductive success? Possible REU projects will focus on the nesting period and include observing how bacteria (presence-absence manipulation), parental care, or other ecological factors of interest that may affect reproductive success across the season.

Expectations:

REU will be expected to develop an independent project related to the ongoing research with guidance from mentors. Student will take leadership roles in all aspects of the study; they design the study, prepare a proposal, collect data and perform analysis, interpret the results, prepare a written manuscript, and complete an oral presentation at their home institution or conference. In the field we will work long hours in all weather conditions. We are looking for a motivated individual who is able to hike through steep terrain for long hours beginning early in the morning.

In order for the REU position to be considered complete, the following must be done:

1. Write a project proposal prior to beginning the field research season.

2. Participate in field work for duration of season.

3. Write a project report in manuscript form that has potential to be submitted for publication.

4. Present independent research in poster or talk format. Location and event for this requirement is open for discussion. There may be funding available for a national meeting, but presenting at own university is also acceptable.

Compensation:

A stipend, per diem, housing and travel are all provided. After completion of the REU, you can expect to be well trained in the ability to trap, handle, band, and process songbirds, as well as analyze and interpret data.

Timeline:

Deadline to apply is February 15, 2016. Skype interviews will be offered to top candidates by February 19, 2016. REU will begin project development soon after accepting position. REU is expected to join research mentors at the field site after completion of finals and remain for 10 weeks past arrival date. Completion of the REU project will depend on date of oral presentation.

Requirements:

To apply, email a cover letter that outlines professional goals and research interests that fall within the project, a resume or CV, and 1 letter of recommendation from an instructor, research mentor, or someone who can comment on how you would contribute to vigorous field research and work as an independent researcher. We are willing to train individuals, so previous work with birds is not required. Preferred applicants should have course experience in fields such as ecology, behavior, and evolution. Participants are chosen for their readiness to take on original creative field-based biological research and for their interest in, and potential for, a career based in science. Applicant must plan to be enrolled in an undergraduate program in the fall of 2016.

Application Deadline: February 15, 2016

Contact Information:

Jessica L. Graham (jessica.l.graham@ndsu.edu)

Katie Needham (katie.needham@ndsu.edu)

"jessica.l.graham@ndsu.edu"
<jessica.l.graham@ndsu.edu>

Bootstrapping Trees answers

Hi,

Following my question about bootstraping a distance matrix to produce a phylogenetic tree with bootstrap confidence values, I got many useful replies. My original question is below and the replies summary is further down this message.

On 15-12-18 10:57 AM, Eric Normandeau wrote: > Hi, > > I'm creating a tree from a distance matrix using phylip neighbor and > phylib drawgram. I would like to have bootstrap values for the > branches but all I have is this one distance matrix. Is this possible? > > The distance matrix is calculated from a Genotyping by Sequencing > (GBS) dataset with a few thousand SNPs. For each individual pair, the > distance is basically the proportion of genotypes that differ for loci > where both individuals are genotyped. > > I could easily create different distance matrices by randomly sampling > only some of the SNPs to calculate the distances, but that would not > make much sense. For example, if I use a low proportion of the SNPs > (ie: 5%), the bootstrap values will end up being lower because the > matrices will be more different from one another than if I use a high > proportion of the SNPs (ie: 50+%). It feels like I can control the > bootstrap values artificially, so that is not a good avenue. > > Is there a way, given a single distance matrix, to create a tree with > bootstrap values? > > I'll be happy to summarize the answers and post them back on EvolDir. > > Eric > Here is the summary of the very useful replies:

1) I cannot bootstrap the distance matrix 2) I can bootstrap the markers (random choice with replacement) and produce 1000 distances matrices 3) I was describing a jackknife procedure, not a bootstrap procedure

David Remington also suggested that I could use a nucleotide substitution model to calculate a more appropriate distance metric. However, he mentions that this approach wouldn't work if the SNP dataset has been pre-filtered, for example by retaining only the variable markers, as it would make the nucleotide substitution model incorrect. In our case, we have to work with preselected SNPs, otherwise we would be using hundreds of thousands of SNPs with a lot of missing data and most of which would be variable in only one individual, thus more probably sequencing errors.

David also asked if this was a within-species study and it is not. It uses specimens from a variety of related species with low numbers of samples per species. That is why we went for a phylogenetic approach.

Jack Cameron suggested using a Canberra distance, which is a robust Manhattan metric and then to use Pvclust to bootstrap once I have the distance matrices. The Canberra distance computes a distance between two vectors P an Q of numbers by computing the sum of, for each index i, (|Pi - Qi|) / (|Pi| + |Qi|). Since my pairwise comparisons between two samples use all the loci for which both samples were genotyped, and that the length of the the P and Q vectors vary among the pairwise comparisons, I would then divide by the length to normalize them. This leaves the problem of encoding the possible genotypes (AA, AB, BB) as numbers, probably with AA=1, AB=2 and BB=3. In this context, however, I do not see how dividing by (Pi + Qi) makes any sense. It basically gives more weight to a case of AA-AB than to a case of AB-BB since the later will be divided by 5, compared to 3 for the former. My implementation of the distance is equivalent to using only the numerator (|Pi - Qi|) part of the Canberra distance and then dividing the sum by the length of the vectors.

Any further thoughts on using a different distance metric would be highly welcome!

I will then implement the following:

1) Use my VCF file with my SNP markers and bootstrap it 1000 times 2) Use Phylip to compute the concensus tree and bootstrap confidence values 3) Keep an eye out for how to use a different distance metric

Many thanks to all who replied to my question (in chronological order of replies):

- Bernhard Haubold - Peter Smouse - Francisco Bilbao Moore - David Remington - Murray Cox - Jack Cameron - Frank E. Anderson - Mary Kuhner - Miguel NavascuÃÂ©s - Louis Ranjard

Eric Normandeau - Bioinformaticien Laboratoire de Louis Bernatchez Ressources Aquatiques QuÃÂ©bec (RAQ)

Institut de Biologie IntÃÂ©grative et des SystÃÂmes (IBIS) Pavillon Charles-EugÃÂne-Marchand 1030, Avenue de la MÃÂ©decine Local 1143 UniversitÃÂ© Laval QuÃÂ©bec (QuÃÂ©bec) G1V 0A6 Canada

TÃÂ©l: 418 656-2131 poste 8455 Courriel: eric.normandeau@bio.ulaval.ca

eric.normandeau@bio.ulaval.ca

Botany AdvocacyLeadership Grant

The American Society of Plant Taxonomists (ASPT) and Botanical Society of America (BSA) have teamed up to craft a NEW grant opportunity - the Botany Advocacy Leadership Grant!

Please find the call for proposals at the following link: http://cms.botany.org/file.php?file=3D3DSiteAssets/awards/BSA_BAL_Call.pdf One successful applicant for this award will receive $1,000 toward developing new (or enhancing existing!) botanical advocacy projects - apply or encourage others you know to submit an application.

DEADLINE: 16 March 2015

gostelm@gmail.com

ChicagoBotanicGarden REUSummerInternship

Hello,

This summer the Chicago Botanic Garden and affiliated institutions will host 10 REU interns (Research Experience for Undergraduates) with the theme of plant biology and conservation, spanning genomics to ecosystem levels of inquiry. Projects range from restorations, seed biology, genomics, phylogenetics, soil fungal communities, plant reproduction and community ecology. Students will gain both laboratory and field experience in addition to professional development opportunities. We'd like your help spreading the word to exceptional undergraduates who are excited about scientific inquiry and research.

Our program website http://www.cbgreu.org has information on program background, application process, and contact information. Participants should be U.S. citizens who will be enrolled as undergraduates in fall 2016. They will receive a stipend of $5,000 in addition to assistance travelling to Chicago. Room and board is at university center downtown Chicago. The application deadline is February 1st , 2016 and the 10-week program starts June 13th, 2016. We encourage applications from students at non-PhD granting universities and minorities that are under-represented in biological fields.

Students can find more information and apply at http://www.cbgreu.org, and questions can be directed to info@cbgreu.org.

Thanks! Chicago Botanic Garden REU Experience info@cbgreu.org

Genetics Lab <Lab@chicagobotanic.org>

Chromonomer Software

Hi All,

I'm pleased to release the Chromonomer software package today:

http://catchenlab.life.illinois.edu/chromonomer/ Chromonomer is software to integrate a genome assembly with a genetic map to create a 'chromonome' (1). The software will order and orient scaffolds from a genome assembly according to the markers from a genetic map. Chromonomer was designed around RADseq genetic maps but should work with any genetic map where the markers can be aligned to the genome sequence.

Chromonomer will break scaffolds to fill gaps in the assembly with smaller scaffolds or to correct mis-joins in the assembly. It will also identify markers that are out of order with respect to the assembly. In this way the software uses the assembly order on the small scale and the map order on the large scale to integrate an assembly and a map together.

Chromonomer generates extensive documentation of where any incompatibilities occur between the assembly and the map, including (optional) web-based visualizations.

The software is released under the GPL free software license.

Please try it and let us know your experience with it.

Best wishes,

julian

(1) http://onlinelibrary.wiley.com/doi/10.1002/jez.b.22589/abstract – Julian M Catchen, Ph.D. Assistant Professor Department of Animal Biology University of Illinois, Urbana-Champaign – jcatchen@illinois.edu; @jcatchen

DukeU AEOP UndergradSummer

The Patek Lab in the Biology Department at Duke University is recruiting one high school and one undergraduate student researcher through the US Army Educational Outreach Program (AEOP) during the summer of 2016. The students will participate in projects examining fast, impulsive movements of animals in the natural environment. The focal systems for the project are catapult jumping in froghopper insects and underwater foraging attacks in dragonfly larvae. Responsibilities of the student researchers may include collecting study organisms from local habitats, obtaining high-speed videos of animals, analyzing high-speed videos using computer software, performing statistical analyses and scientific writing. The details of responsibilities and tasks will be determined based on mutual interests of the students and the mentors. There are also possibilities for the students to develop individual projects under our mentorship.

We are looking for motivated, reliable students who are excited about having first-hand research experience at the intersection of biology and physics. Skills to perform the above-mentioned tasks are not required. We especially value students who are curious, hard-working and have an open mind about the possibilities of basic, scientific research. For more information about The Patek Lab, please visit our website: www.thepateklab.org DEADLINE: January 30, 2016, 11:59 pm. All applicants must submit two letters of recommendation, transcripts and must have maintained a cumulative GPA of at least 3.2 in their coursework. Applicants must also include a brief essay that explains their interest in this research and how it relates to their future goals.

Go to the below links and: Click "Apply" at the bottom of the page * Fill out the forms * When you get to "Please select your 1st preference of URAP location.", Select "BDNC53 Duke University"

For high school students, please apply through the HSAP program:

http://www.cvent.com/events/2016-high-school-research-apprenticeship-program-hsap-/event-summary-bfd469afd55b4a91a548ab27f32e560e.aspx For undergraduate students, please apply through the URAP program:

http://www.cvent.com/events/2016-undergraduate-research-apprenticeship-program-urap-/event-summary-bb5f13ee0df7493ab0e4518d15080d8e.aspx Chi-Yun Kuo <chi.yun.kuo@duke.edu>

EmoryU URAP StudentApprenticeship DNAbarcoding

A student apprenticeship position is available in the laboratory of Dr Berry Brosi at Emory University during Summer 2016 on "Development of Mixed-Sample DNA Barcoding of Pollen for Security-Related Forensic Palynology".

This position is within the Undergraduate Research Apprenticeship Program (URAP) sponsored by the Army Research Office.

Student activity will focus on understanding and correcting quantitative biases in pollen metabarcoding, including DNA extraction bias, amplification bias, and copy number bias. Students with a strong background in basic biology (including molecular biology), some previous molecular biology lab experience (including DNA extraction and PCR), a GPA of 3.0 or above, the ability to work independently and precisely, and a strong work ethic are encouraged to apply.

More information about the program, and instructions for applying, can be found here: http://www.usaeop.com/programs/apprenticeships/urap/ For more information about the research project, please contact Dr Karen Bell karen.bell@emory.edu or Dr Berry Brosi bbrosi@emory.edu

Karen L. Bell, Ph.D. Postdoctoral Fellow Emory University Department of Environmental Sciences 400 Dowman Drive Atlanta, GA 30322, USA Phone: +1 (404) 727-5126

"Bell, Karen L." <karen.bell@emory.edu>

ESEB CallConferenceTravelAwards

ESEB CONFERENCE TRAVEL AWARDS 2016

The European Society of Evolutionary Biology (ESEB) is pleased to announce the call for applications for conference travel awards 2016. These stipends are for students and young scientists to attend the Evolution 2016 conference in Austin, Texas, USA, in June 17-21, 2016 (http://www.evolutionmeetings.org/evolution-2016—austin-texas.html). The stipend will contribute to covering travel, living expenses and congress registration fees. The award will be paid out as a reimbursement after the congress, based on specification of the expenses.

ELIGIBILITY: - Applicants must be ESEB members (for becoming an ESEB member, please visit www.eseb.org). - Applications can be submitted by scientists at various stages of their professional career (e.g., Masters and PhD students, postdocs, and lecturers). - Scientists working in a country with high GDP are not eligible (for the list of excluded countries see below). - People who received an ESEB travel stipend in the last five years are not eligible. - Applicants must submit to present either an oral communication or a poster to be eligible for the stipend. This will be verified before the reimbursement, but no proof that a poster or talk is accepted is necessary at the application stage.

PLEASE NOTE THAT THESE STIPENDS ARE GIVEN IN CONJUNCTION WITH ANALOGOUS STIPENDS OFFERED BY THE SSE (separate call), SO THERE IS NO NEED TO APPLY TO BOTH

HOW TO APPLY: Send your application by email to the ESEB Travel Bursary Committee, c/o Dr. Martijn Egas, Email: egas@uva.nl The application should be no more than 2 pages long and include:

- Name of the applicant; - Budget, including sources of additional support; - An explanation of how attendance to the meeting will support the attendant's professional goals; - and a CV.

Please submit the application as a single PDF-file. A support letter from the applicant advisor/mentor/senior colleague is also required. Support letters should be sent to the same email address (egas@uva.nl) by the applicant's mentor.

Deadline: 29 February 2016 24:00 GMT.

Members professionally based in the following countries are not eligible for the travel stipend: Australia, Austria, Belgium, Canada, China, Croatia, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Israel, Italy, Japan, Luxembourg, Malta, Netherlands, New Zealand, Norway, Poland, Portugal, Singapore, Slovakia, Slovenia, South Korea, Spain, Sweden, Switzerland , United Kingdom, United States of America.

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

ESEB OutreachFund DeadlineMar15

ESEB Outreach Fund

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

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

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

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

Ethiopia VolFieldAssist PrimateResearch

FIELD ASSISTANT / CAMP MANAGER POSITION AVAILABLE STUDYING WILD PRIMATE BEHAVIOR IN THE ETHIOPIAN HIGHLANDS

ONE field assistant / camp manager needed for The University of Michigan Gelada Research Project, a study of the evolutionary biology, behavior, communication, endocrinology, and conservation of wild geladas (Theropithecus gelada) - a close relative of baboons. All research is conducted at a remote field station located in the Simien Mountains National Park of Ethiopia. Directors of the project are Dr. Thore Bergman and

Dr. Jacinta Beehner, faculty at the University of Michigan. The successful candidate will be responsible for (a) collecting basic demographic and reproductive data as part of routine monitoring of the well-habituated study population, (b) conducting focal animal samples, taking growth photos, and collecting fecal and urine samples from individually-recognized geladas (for later laboratory steroid hormone analysis in the USA), (c) downloading the data each day to a computer and sending this data back to the U.S. on a monthly basis, and (d) maintaining camp equipment and managing personnel. The gelada population has been studied on a near-daily basis since 2006, and we currently recognize approximately 250 individuals (that you will learn to identify and love).

Our field station is a stone hut located deep within the national park that is shared with 0-3 American graduate students (depending on the time of year). The project employs 3 Ethiopian field assistants, and 1-2 Ethiopian staff (for cooking and cleaning) who live down the path from the project hut in the Park outpost that consists of 4-5 rangers and their families. The hut has 3 bedrooms (sleeps 6 comfortably), a full kitchen set-up (including a propane-powered freezer, and a propane-powered stove and oven), a propane-powered hot shower, solar panels to power computers and lights, a generator (for electricity during the rainy season), a satellite telephone and modem (for email), and a Toyota 4x4 pickup truck. There is no running water at the fieldsite, but fresh water is brought to the camp daily from a nearby spring (and filtered at the camp). For more information on the project directors, the project publications, and some photos of the fieldsite, please see the project website: http://www.umich.edu/~gelada/UMGRP/Home.html . Qualified applicants will have a B.S. or B.A in Biology, Zoology, Biological Anthropology, or a related field. Prior travel and/or field experience in Africa or mountainous regions of Asia or South America preferred. Applicants must be fluent in English and eager to learn Amharic (the national language of Ethiopia). Good physical fitness is absolutely essential - the terrain is hilly, the air is thin (due to the high elevation), and the temperatures can get quite cold during the rainy season (nights are sometimes below freezing and days can be cold). Good organizational skills and experience with basic database management a must. Must be able to drive a stick-shift 4x4 truck over rough terrain. Experience with leadership also a plus - as you will be working closely with several graduate students and field assistants.

Salary/funding: This is a volunteer position, so there is no salary. However, round-trip airfare and living support will be provided for the volunteer (visa expenses, travel, meals, lodging). Additionally, volunteer will be provided with basic accommodation, food and other basic supplies while at the field site. The volunteer is responsible for any additional expenses incurred while traveling in Ethiopia. The project will provide emergency travel health insurance, but the volunteer is required to have basic health care coverage and must acquire the necessary vaccinations prior to entry to Ethiopia. The volunteer will need to provide their own winter/alpine condition clothing, footwear and sleeping bag. Advice about what items are necessary for life in the Simien Mountains will be provided to the successful applicant.

Appointment: 1-2 years beginning early-May, 2016. Because the training process requires 2-4 months (mostly learning the animals), the successful applicant must be willing to work for a minimum of 1 year. Applicants committing to a longer period will receive one round-trip flight to their home country halfway through their internship. Note that 4 (out of 5) previous camp managers have found this experience quite rewarding and have signed on to a second year. Ethiopia is a safe and extremely friendly country to live in.

Deadline: Position will remain open until filled. Earlier applications will receive priority. We hope to fill the position before the end of February, 2016.

Application: Please email the following materials to Dr. Jacinta Beehner at jbeehner@umich.edu: (1) a letter of interest stating how and why this position satisfies your interest and future career goals,

— / —

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

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Evolution2016 Art

Attention artists! The deadline for submission of evolution-themed works (or proposed-works) for the 'Evolution 2016 Art Exhibit' is quickly approaching (Jan. 18).

The 2016 Evolution conference (the annual meeting of theSociety for the Study of Evolution, theSociety of Systematic Biologists, and theAmerican Society of Naturalists) will be held from June 17-21 in beautiful Austin, TX. In conjunction with the meeting, the societies and a local art gallery (Art.Science.Gallery) are co-sponsoring an evolution-themed art exhibit. The exhibit will provide an opportunity for meeting attendees and others to showcase their creative talents, increase the visibility of the meeting and the societies to the local community, and provide opportunities for public education about evolutionary biology through the exciting lens of visual arts. The exhibit will run at the Art.Science.Gallery leading up to, and during, the conference, and a selection of the works will be on display at the Austin Convention Center as a pop-up exhibit during the evening of the opening reception of the meeting.

Art.Science.Gallery has issued an open call seeking submissions for this exhibition. Works may explore (but are not limited to) the sub-disciplines within evolutionary biology, notable evolutionary biologists, current research topics, important discoveries and concepts, and the history of evolutionary thought. You need not be a member of any of the societies to submit something for consideration.

Pass the word along and, if you're at all artistically inclined, consider submitting something. Additional details can be found on our permanent meeting website (www.evolutionmeetings.org) under the 'News' heading, or on Art.Science.Gallery's website (http://-artsciencegallery.com/opencall).

The open call closes on Jan. 18.

Sincerely, Your Evolution2016 organizers

howard.rundle@uottawa.ca

Evolution2016 Art Extended

NOTICE: THE OPEN CALL HAS BEEN EXTENDED UNTIL JAN. 31.

Attention artists!

The 2016 Evolution conference (the annual meeting of theÂSociety for the Study of Evolution, theÂSociety of Systematic Biologists, and theÂAmerican Society of Naturalists) will be held from June 17-21 in beautiful Austin, TX. In conjunction with the meeting, the societies and a local art gallery (Art.Science.Gallery) are co-sponsoring an evolution-themed art exhibit. The exhibit will provide an opportunity for meeting attendees and others to showcase their creative talents, increase the visibility of the meeting and the societies to the local community, and provide opportunities for public education about evolutionary biology through the exciting lens of visual arts. The exhibit will run at the Art.Science.Gallery leading up to, and during, the conference and a selection of the works will be on display at the Austin Convention Center as a pop-up exhibit during the opening reception for the meeting.

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The open call closes on Jan. 31, 2016.

Sincerely, Your Evolution 2016 organizers

howard.rundle@uottawa.ca

Evolution Honors Textbook

Hello list!

I was hoping that some of you might have a suggestion for me. I am fortunate enough to be teaching a one credit honors seminar this coming semester tied to my intro level evolution, diversity, and physiology course. During the second half of the semester we will be reading Neil Shubin's Your Inner Fish to connect the physiology we are covering in lecture to evolutionary principles.

During the first half of the semester I would like to dive a little into evolutionary theory. I'm looking for a "popular" text that is approachable to a group of eighteen and nineteen year olds. Suggestions are greatly appreciated and can be sent me to off list.

I thought of reading Darwin but I want to avoid the issues of "translating English into English" that I can already foresee. I like Dawkins, but given the population I want to avoid anyone feeling patronized and turned off.

Thanks for any help.

Sean

"Beckmann, Sean" <sb135893@Rockford.edu>

Fis variability question

Hi, I am actually working on a relict population of a marine fish which is considered as almost extinct. Reproduction is supposed to be very rare or even absent in the wild, and the survival of the specie is thus dependant upon a captive stock of around 40 individuals captured three decades ago in the wild. The specie reproduced at around 10 years.

Using 18 microsatellites markers, I analysed the genetic variability of breeders issued from the wild and found that the genetic variability is very low (mean=4 alleles/locus), which is not surprising given the demographic history of the specie (with sharp declines due to overfishing and degradation of its habitat during the last century) and the founder event (capture of these subset of individuals for captive breeding). The Bottleneck test from Cornuet is also significant.

BUT, I also found also that the observed heterozygosity is higher than expected for almost all loci, and that Fis values are negative. My question is how these last results could match with the evidence of low diversity, population size and strong bottlenecks ??

Many thanks for your answers and help on that,

Cheers, Séverine"

Séverine Roques Irstea

UR "Ecosystèmes aquatiques et changements globaux"

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33612 Cestas

Tel : + 33 (0)782826649

severine roques <severineroques@hotmail.com>

GeorgetownU REU summer2016

REU Site: Environmental Science and Policy in the Nation's Capital Georgetown University Summer 2016

We anticipate that Georgetown University's Research Experience for Undergraduates (REU) Site program " Environmental Science and Policy in the Nation's Capital " will be funded by a grant from the National Science Foundation (award is pending). This ten-week program will bring a cohort of students to Washington DC to conduct research in environmental science at Georgetown University and to take part in a mini-curriculum that explores the intersections of science and policy. Participating research mentors have expertise in various aspects of environmental science and policy.

The 2016 program will run from May 31 - August 5. Students will be housed on campus and will receive a $5250 stipend plus a $750 allowance for food. We are striving for a diverse group, so students from populations typically underrepresented in STEM fields are strongly encouraged to apply. Review of applications will begin on February 15, 2016.

For more information on the program and to apply, visit: biology.georgetown.edu/REU

For other inquiries, contact Dr. Manus Patten (mmp64@georgetown.edu)

"mmp64@georgetown.edu" <mmp64@georgetown.edu>

Greifswald RESPONSE ExchangeGrants

20-01-2016

Call: RESPONSE Exchange Grants

The DFG funded Research Training Group RESPONSE (Biological Responses to Novel and Changing Environments; www.uni-greifswald.de/RESPONSE/) invites applications for Exchange Grants. In order to foster collaborations between RESPONSE members and other scientists, researchers are invited to spend a period of 2-12 weeks at one of the RESPONSE labs in Greifswald, Germany. Exchange Grants should involve the execution of a collaborative research project relevant to RESPONSE, i.e. on issues related to environmental change. We particularly aim to integrate research across multiple levels of investigation, including ecology, evolution, genetics, physiology, behaviour, theory or modelling. The deadline for grant applications is April 15^th 2016.

Eligibility

Grantees must hold a MSc degree or equivalent, be hosted by a participating researcher of RESPONSE (www.uni-greifswald.de/RESPONSE/), and undertake high quality scientific research at the University of Greifswald. Funding by RESPONSE must be acknowledged in publications resulting from the grantees work in relation to the Exchange Grant.

Application Procedure

Applications for RESPONSE Exchange Grants should include the following information: * scientific CV including a publication list, * letter of acceptance from the prospective RESPONSE host, * project title and short description of the proposed project (max. 1200 words), * proposed starting date and duration, * estimated travel costs.

Applications should be submitted as one PDF file to the spokesperson of the research training network (email to klaus.fischer@uni-greifswald.de). Funding decisions will be made by the RESPONSE Executive Board based on scientific quality and relevance to the aims of RESONSE.

Allowance

Exchange Grants are reimbursed on the basis of an allowance of up to 400 EUR (depending on experience) per week (for 2-12 weeks) plus actual travel expenses up to a maximum of 500 EUR. The grants do not cover health insurance, taxes, or retirement scheme contributions.

Prof. Dr. Klaus Fischer Zoological Institute & Museum Greifswald University J.-S.-Bach-Str. 11/12 D-17489 Greifswald Phone: +49-3834-864266 Fax: +49-3834-864252

“kfischer@uni-greifswald.de” <kfischer@uni-greifswald.de>

HumanPopGenomics OnlineTeaching

We have written an online educational module that examines human, Neanderthal and chimpanzee genome sequences for chromosome 6p with an eye to discovering:

(a) what the overall variability of the genome says about human prehistory,

(b) what anomalous regions of the genome say about specific forces (population admixture, natural selection) acting on genes in those regions.

The module is intended for college undergraduates in biology and related fields (a reviewer thought it was also relevant to anthropology students) and is free to use. We'd appreciate feedback from anyone who uses it in a class.

It can be found at:

http://evolution.gs.washington.edu/module1/-index.html Best wishes, Mary Kuhner mkkuhner@uw.edu

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IIASA Austria SummerFellowships EvolModeling

Summer Fellowships for Young Scientists at the International Institute for Applied Systems Analysis, Austria

Funding is available for PhD students interested in three months of collaborative research during June-August 2016 on

Evolutionary and Ecological Modeling

at the International Institute for Applied Systems Analysis (IIASA) in Laxenburg, Austria.

Young scientists from all countries are eligible for stipends provided by IIASA's Evolution and Ecology Program (EEP) that contribute to travel and accommodation costs. Students from Australia, Austria, Brazil, China, Egypt, Finland, Germany, India, Indonesia, Japan, Korea, Malaysia, Mexico, the Netherlands, Norway, Pakistan, Russia, South Africa, Sweden, Ukraine, the United Kingdom, USA, and Vietnam are furthermore eligible for fellowships that provide full coverage of travel, accommodation, and living expenses.

Model-based summer research projects are invited in the following indicative areas:

Evolution of cooperation Governance of common goods Systemic risk and network dynamics Eco-evolutionary dynamics Evolutionary community ecology Food-web evolution Vegetation dynamics Adaptive speciation Disease ecology and evolution Evolutionary conservation biology Fisheries management Fisheries-induced evolution Adaptive dynamics theory and models Spatial models in ecology and evolution

Applicants are encouraged to prepare a research proposal that corresponds to their scientific interests and to EEP's research agenda. Accepted applicants will begin work before the summer, by planning their research in collaboration with their IIASA supervisors. Previous experiences with implementing and studying evolutionary or ecological models are important assets for working in EEP. To improve chances of being selected, potential applicants are welcome to send informal inquiries regarding their specific research interests and plans to EEP's program director Ulf Dieckmann (dieckmann@iiasa.ac.at).

Online applications will be accepted until Monday, January 11, 2016 (24:00 CET).

Since 1977, IIASA's annual Young Scientists Summer Program (YSSP), has attracted 1750+ students from 80+ countries. The YSSP 2016 will take place from June 1 to August 31. IIASA is located in the former summer palace of Austria's royal family, ca. 15 km south of Vienna. IIASA's summer program offers exceptional opportunities for acquiring experience in an international and interdisciplinary research environment. Research training is based on regular personal interaction with advising scientists, and typically leads to a publication in an international journal, as well as to a chapter in a candidate's PhD thesis.

Some useful links:

+ Details about the summer program, and online application http://www.iiasa.ac.at/web/home/education/yssp/Apply/ConditionsEligibility/Conditions-and-Eligibility.en.html + Information about IIASA's Evolution and Ecology Program http://www.iiasa.ac.at/web/home/research/researchPrograms/EvolutionandEcology/New-page.en.html + Examples of successful YSSP projects http://www.iiasa.ac.at/web/home/research/researchPrograms/EvolutionandEcology/AbouttheProgram/Student-Participation-in-EEP.en.html + General information about IIASA http://www.iiasa.ac.at/web/home/about/whatisiiasa/what_is_iiasa.html Ulf Dieckmann Program Director Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

Email dieckmann@iiasa.ac.at Phone +43 2236 807 386 Phone secretary +43 2236 807 231 Fax +43 2236 807 466 or +43 2236 71313 Web http://www.iiasa.ac.at/Research/EEP Online reprints http://www.iiasa.ac.at/~dieckman FroSpects Network http://www.iiasa.ac.at/Research/EEP/FroSpects FinE Network http://www.iiasa.ac.at/Research/EEP/FinE FishACE Network http://www.iiasa.ac.at/Research/EEP/FishACE DIECKMANN Ulf <dieckmann@iiasa.ac.at>

KansasStateU SummerREU

Summer 2016 REU at Kansas State University

The REU Site program at Kansas State University 'Ecology and Evolutionary Biology of Changing Environments: Integrating from Genomes to Biomes' invites applicants for a 10-week summer program, which will provide a foundation in mechanistic and integrative research in ecology and evolutionary biology. We have a diverse set of research projects addressing biological patterns observed in changing environments and their underlying genetic, developmental, physiological, or ecological mechanisms.

The program is hosted by the Ecological Genomics Institute, Konza Prairie Biological Station, and the Division of Biology at K-State. Over 30 faculty from the Division of Biology and Departments of Entomology, and Plant Pathology serve as potential mentors. Participants will gain practical research skills in molecular techniques, field methods, experimental design, and data analysis; attend professional development seminars; travel to important ecological sites and genomic centers; and have two opportunities to present their research. The program covers costs of accommodations. Participants will also receive a generous stipend and food allowance.

Application deadline is 1 March 2016.

Complete information about the program is available by visiting http://www.ksu.edu/reu . Specific questions can be directed to the PIs (Dr. Bruce A. Snyder and Dr. Theodore J. Morgan) at biologyreu@ksu.edu.

Theodore J Morgan, Associate Professor Mail: Division of Biology, 116 Ackert Hall, Kansas State University, Manhattan, KS 66506

Phone: 785.532.6126, Email: tjmorgan@k-state.edu, Skype: morganlab.ksu, www.ksu.edu/morganlab "tjmorgan@ksu.edu" <tjmorgan@ksu.edu>

LearningEvolution Survey

Dear Colleagues,

My name is Mindi Summers and I am a postdoc working with Michelle Smith at the University of Maine. We are part of a multi-institutional team developing a diagnostic assessment, called Eco/Evo-MAPS (Measuring Achievement and Progression in Science) for departments to use to better understand and improve studentsÂ understanding of big ideas in evolution and ecology. We have used feedback from over 70 experts, data from more than 75 student interviews, and pilot results from over 3000 students at 27 institutions to revise our tool to its current state.

We are looking for a few additional institutions that would be willing to give the assessment to their students this spring to help us ensure the questions are working for a diverse set of students and institutions. The assessment is taken online outside of class and typically takes students 30-40 minutes to complete. Students are usually given a few participation points for their efforts.

Eco/Evo-MAPS questions are organized so that each consists of a prompt followed by a series of statements that students will answer as likely or unlikely - a variation on true/false. To give you a sense of the instrument, I have included below a link to one of the ten total questions.

https://umaine.qualtrics.com//SE/?SID=-3DSV_bIQlMb8EvIa2vFH Once the students have completed the Eco/Evo-MAPS assessment, we will send you a score report. The overall averages are reported plus a breakdown of questions by core concepts in ecology and evolution and the five Vision and Change core concepts. We will also work with your IRB office to make sure we have the proper permission to survey your students.

Thank you for considering this request! We hope you are interested in being part of the development process.

Thank you,

Mindi Summers mindi.summers@maine.edu

– Mindi Summers Postdoctoral Research Associate University of Maine School of Biology and Ecology Rise Center 311 Murray Hall (207) 581-2520 mindi.summers@maine.edu

mindi.summers@maine.edu

Malaysia VolFieldAssist WaspSocialityEvolution

A volunteer field assistant is required to help with a field-based project on behaviour in social wasps. The position is a fantastic opportunity to gain tropical field experience working in a vibrant research group, led by Dr. Seirian Sumner, from the University of Bristol, UK (http://www.sumnerlab.co.uk/). This exciting project combines behavioural experiments with the latest sequencing techniques to understand the molecular mechanisms behind sociality. The fieldwork will be conducted in Frasers Hill, Malaysia for three months between July and September 2016. The work involves marking wasps, manipulations, conducting censuses, sample collections, and behavioural observations.

Assistants are generally expected to be biological science graduates with a good degree (2:1 or equivalent) or Masters graduates. A background in molecular biology is not necessary as fieldwork is behavioural based - a keen interest in behavioural ecology, social evolution, and/or entomology is required. Applicants should be fit, enthusiastic, hard working and happy living in shared accommodation and working in challenging conditions. Previous experience of working on social insects would be an advantage. The applicant must be able to commit to the full field season. These wasps can sting when provoked, so applicant must have no know previous allergies to wasp/bee stings. Due to the nature of work you may also be required to work up ladders, and must have full colour vision.

Work-related costs in Malaysia will be paid for, including accommodation and flights (up to Â£500). Worldwide applicants are supported, although must be fluent in English. Costs related to food are expected to be self-funded (Malaysian prices are much cheaper than UK) and the balance towards flights over Â£500.

Please contact Dr. Daisy Taylor (daisy.taylor@bristol.ac.uk) for more details. Applications should include a CV with email addresses for two referees and a 1-page cover letter explaining why you would like to work on the project. Applications should be submitted by e-mail to Dr. Daisy Taylor . Shortlisted applications will be notified by email, and will be invited for interview either in person or over skype/phone.

Dr Daisy Taylor Post-doctoral Research Assistant School of Biological Sciences 24 Tyndall Avenue Bristol BS8 1TQ UK daisy.taylor@bristol.ac.uk

daisy.taylor@bristol.ac.uk

MaxPlanckInst Munich FieldAssist Crickets

EXPERIENCED FIELD ASSISTANT

Needed in for Field Cricket Project at the Max Planck Institute for Ornithology. Websites: http://www.behavioural-ecology.bio.lmu.de/people/postdocs/niemela/index.html & https://www.orn.mpg.de/159079/Research_Group_Dingemanse Where: Munich (LMU) and Seewiesen, Bayern, Germany. When: End of March 2016 - End of June 2016

Job description: The field assistants will help to collect life-history data on Field Crickets (Gryllus Campestris) in the wild from end of March to the end of June 2016. The research focuses primarily on identifying how the social environment (ie. other individuals) generate and maintain individual differences in behaviour and behavioural plasticity. Research is also concentrated on identifying how environmental conditions affect the expression of behavioural variation. Assistants will work closely with an international team consisting of one post-doc, two field assistants and various students. The research project is intense and will have typically only 1-2 days off per week. Duties include behavioural observations, cricket handling (marking, measuring), data entry and data management.

Qualifications/Experience: Candidates should have a BSc in Biology or a related field. Candidates should have experience with handling small insects and working as part of a research group. Ideal candidates are highly motivated, well organized and able to work independently, while at the same time able to function well in a group.

A small financial compensation and accommodation will be provided. Accepted assistants should be vaccinated against Tick Borne Encephalitis (TBE or FSME) before arriving in Seewiesen. Applicants should also be aware that Lyme disease (carried by ticks) is prevalent in the area and should inform themselves about this disease beforehand.

Applications: Review of the applications will begin February and continue until the position is filled. To apply, please send (1) a statement of relevant experience, (2) a short resume or CV, and (3) contact information for two references to Dr. Petri Niemela (eMail: niemela@biologie.uni-muenchen.de).

“Niemela, Petri” <niemela@biologie.uni-muenchen.de>

Minnesota SummerResearchInternships

Are you interested in field research experience and learning about the ecology and evolution of plants and plant-animal interactions in fragmented prairies? We are looking for 3-6 summer researchers for an NSF-funded project investigating how habitat fragmentation influences inbreeding, pollination, herbivory, and demography in purple coneflower, Echinacea angustifolia, populations in western Minnesota. We anticipate hiring 2-3 REUs, 2-3 summer field assistants, and a 12-month research intern. This is a great opportunity for aspiring ecologists, conservation biologists, and evolutionary biologists to gain research experience and learn about the ecology and evolution of plants in fragmented prairies!

No experience is necessary, but you must be enthusiastic and hard-working. During the summer, you will monitor natural plant populations, observe and collect bees, measure plant traits in experimental plots, and assist in all aspects of research. Undergraduate students will have the opportunity to pursue an independent project as an REU participant. Potential projects could involve observing & collecting insects, monitoring flowering phenology, conducting statistical analyses, or computer programming.

If you would like more information or wish to apply, please visit this website http://echinaceaProject.org/opportunities/ or contact Stuart Wagenius. Applications will be reviewed starting 26 February 2014 for REU positions and 4 March for other positions.

echinaceaproject@gmail.com

OmmenPrize EvolutionAndMedicine NominateYourArticle

The International Society for Evolution, Medicine, & Public Health invites nominations for the Omenn Prize of $5000 for the best article published in 2015 in any scientific journal on a topic related to evolution in the context of medicine and public health. It will be awarded on June 25th at the 2016 ISEMPH Meeting in Durham, NC. The prize, provided by the generosity of Gilbert S Omenn, will be awarded to the first author of the winning article. Authors are encouraged to nominate their own articles, but nominations of articles by others are also welcome. Nominations must be submitted by 31 March, 2016

Information on the Society and its June 22-25 meeting in Durham NC is here: http://evolutionarymedicine.org —The abstract deadline is January 31 —CEM is available —Travel Awards are available

Full information on the Prize is here: http://-evolutionarymedicine.org/funding-and-awards/gil-omenn-prize/ The Prize Committee for this year is chaired by Andrew Read, and its members are David Haig and Grazyna Jasienska. Papers by committee members, their students and lab group members are not eligible, and articles by their co-authors or close associates are subject to special conditions. The winner will be invited to present a talk at the June 22-25 meeting of the International Society for Evolution and Medicine in Durham, North Carolina.

rmnesse@gmail.com

Passing T J Case

It is with great sadness we inform his friends and colleagues that Prof. Ted J. Case passed away on Thursday, December 31, 2015, at the age of 68. Ted was a renowned island biogeographer, community ecologist, and herpetologist. He retired in 2004 after more than 25 years of service in the Biology Department at UC San Diego. David Quammen captured the essence of Ted exceptionally well in his book 'The Song of the Dodo'. A further obituary will follow.

Robert Fisher U.S. Geological Survey San Diego Field Station 4165 Spruance Road, Suite 200 San Diego, CA 92101-0812

Phone: 619-225-6422 Phone (Admin): 619-225-6451 Fax: 619-225-6436

rfisher@usgs.gov

"Fisher, Robert" <rfisher@usgs.gov>

PeregrineFalcon article

Dear evoldir community,

I'm looking for a paper entitled: Genetic evidence for global dispersal in the peregrine falcon (Falco peregrinus) and affinity with the taita falcon (Falco fasciinucha). Journal of Raptor Research 48(1):44-53. 2014. If anybody here has it on pdf I would be grateful if you can send it to me at jfo@tinet.cat.

Thank you very much,

Joan

Joan Ferrer Obiol PhD student

Departament de GenÃÂtica Facultat de Biologia Av. Diagonal, 643 08028 BARCELONA, Spain Tel. +34 93 402 17 46

"jfo@tinet.cat" <jfo@tinet.cat>

Phyloseminar VladimirMinin Feb8

Preferential sampling through time when estimating changes in effective population size Vladimir Minin University of Washington Monday, February 8, 2016, 10:00 AM PST

Phylodynamics seeks to estimate effective population size fluctuations from molecular sequences of individuals sampled from a population of interest. However, when analyzing sequences sampled serially through time, current methods implicitly assume either that sampling times are fixed deterministically by the data collection protocol or that their distribution does not depend on the size of the population. Through simulation, we first show that, when sampling times do probabilistically depend on effective population size, estimation methods may be systematically biased. To correct for this deficiency, we propose a new model that explicitly accounts for preferential sampling by modeling the sampling times as an inhomogeneous Poisson process dependent on effective population size. We demonstrate that in the presence of preferential sampling our new model not only reduces bias, but also improves estimation precision. Finally, we compare the performance of the currently used phylodynamic methods with our proposed model through seasonal human influenza examples. Our analysis demonstrates that influenza data sets constructed by mining sequence databases do contain strong preferential sampling signal. Accounting for this preferential sampling produces a markedly cleaner picture of influenza population dynamics.

Frederick "Erick" Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ matsen@fredhutch.org

Portugal VolFieldAssist Magpies Correction

We are looking for a motivated field worker to assist in a research project that is investigating social networks and cooperative breeding in Iberian magpies (/Cyanopica cooki/) in Extremadura, SW Spain. The work involves daily monitoring of nests in the two study colonies, running experiments and conducting behavioural observation. The work will be conducted from early April to the end of June. All expenses are paid (travelling, food and accommodation). This is a great opportunity to gain fieldwork experience, practice essential field techniques (ringing, measuring and bleeding birds) and learn about field-based behavioural studies, while working on a fascinating social species in a beautiful environment.

For more information please contact Juliana Valencia: jvalencia@cibio.up.pt

CIBIO - InBIO University of Porto

Campus Agrário de VairÃ£o Rua Padre Armando Quintas 4485-661 VairÃ£o Portugal

rita.covas@gmail.com

RobertKeithSelander Obituary

My former colleague Robert K. Selander died last June, but I have not seen an obituary in journals or elsewhere. The following is an obituary that I wrote for our departmental web site and I share it now with the evolutionary biology community now.

Robert Keith Selander, emeritus faculty member of the Biology Department, died on June 14, 2015 at the age of 87. He received his B.S. in Zoology from the University of Utah in 1950, his M.S. in Zoology from the University of Utah in 1951, and his Ph.D. in Zoology from the University of California at Berkeley in 1956. He was a member of the faculty at the University of Texas at Austin from 1956 to 1974 and moved to the University of Rochester in 1974. He received numerous honors over his career which culminated with his election into the National Academy of Sciences in 1982. In 1987, he joined the biology faculty at Penn State where he helped to assemble a group of molecular evolutionary geneticists. Dr. Selander held the Eberly Chair in Biology from 1987 until his retirement from Penn State in 1999.

Dr. Selander published over 200 papers in his career. During the early part of his career, he focused on behavior and evolution in birds. He was a pioneer in applying molecular genetic approaches to the study of genetic structure of populations that included classic studies of genetic structure in house mouse populations as well as work on the origins of blind cave fishes. In the 1980s, Dr. Selander began to apply molecular genetic approaches to understand the structure of bacterial populations including many pathogenic organisms that were responsible for human disease outbreaks. This included work on Salmonella, an agent that leads to food borne illnesses, and Neisseria meningitidis, the bacterial species that causes meningitis. Dr. Selander trained and mentored many talented graduate students and postdocs. His work has been cited over 17,000 times showing the profound impact that his scientific work has had in the field of evolutionary genetics. Dr. Selander loved music of all types from classical music and opera to contemporary standards. He was an accomplished pianist and musical arranger. He also had important insights into modern culture. He once opined that one only needs to watch the last two minutes of a basketball game to see the salient aspects of the contest.

Stephen W. Schaeffer, Ph.D. Department of Biology The

Pennsylvania State University 208 Erwin W. Mueller Laboratory University Park, PA 16802-5301 Telephone: 814 865-3269 FAX: 814 865-9131 URL: www.bio.psu.edu
STEPHEN SCHAEFFER <sws4@psu.edu>

SouthAfrica VolResAssist SocialMoleRats

SouthAfrica.VolResearchAssistant.SocialMoleRats

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

Voluntary field research assistant: Mid-February to Mid-May 2016 (3 months)

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

Applicants should be enthusiastic, willing to work hard and keen to get involved in an ecological research project in the African bush. The research assistants are expected to be willing to work at night when trapping schedules require it and need to be fit as capturing mole-rats requires the capacity to do hard physical work (digging) in a challenging environment. Applicants must be holders of a driving license. A zoology related degree and/or previous field experience will be considered an asset. The successful applicant will work in a small team of 2 persons and hence need to be a team player and generally a person that enjoys collaboration under sometimes challenging and isolated circumstances.

What you will learn:

Conduct field research in a remote area in the African bush.

Capture-mark and recapture techniques of small rodents.

Biological sampling and processing of scientific samples (blood, tissue and morphometrics).

Accommodation is provided, and research assistants are paid a weekly allowance to cover their personal costs and food. Costs for travelling from Johannesburg to the field site will be covered. We have no funding to cove overseas travel to South Africa.

Applications received until the 15th of January 2016 are ensured full consideration. Later applications can be considered.

To apply (CV + cover letter) or enquire further information:

Dr Markus Zöttl

Research associate

University of Cambridge

+441223336673

Mz338@cam.ac.uk

Markus Zoettl <mz338@cam.ac.uk>

Spain VolFieldAssist MagpieEvolution

Volunteer field assistant needed: Cooperation in Iberian magpies We are looking for a motivated field worker to assist in a research project that is investigating social networks and cooperative breeding in Iberian magpies (Cyanopica cooki) in Extremadura, SW Spain. The work involves daily monitoring of nests in the two study colonies, running experiments and conducting behavioural observation. The work will be conducted from early April to the end of June. All expenses are paid (travelling, food and accommodation). This is a great opportunity to gain fieldwork experience, practice essential field techniques (ringing, measuring and bleeding birds) and learn about field-based behavioural studies, while working on a fascinating social species in a beautiful environment. For more information please contact Juliana Valencia: j.valencia@cibio.up.pt

Rita Covas <rita.covas@gmail.com>

Statistics withOrdinalResponsePlusPhylogeny

Dear evoldir community,

I would like to conduct a simple statistical analysis, where I test the effect of a categorial variable on an ordinal one, but correcting for phylogeny. The problems are :

- regarding the phylogeny, I have no information about branch lengths and it also presents several polytomies

-> from what I read, it would appear that a classical PGLS method can deal with those problems

- the response (dependent) variable is ordinal(around 6 categories)

-> PGLS can be used for continuous or discrete explanatory variables, but I found nothing about ordinal ones... I saw that for ordinal response variables, "cumulative logit models" could be used, but they do not make use of the phylogenetic information. The best would probably be a mix of the two, but since I do not know a lot about those kind of analyses, maybe I just miss something?

Any help or advice would be much appreciated!

Thank you all very much in advance.

Best regards,

GwennaÃ≪l Bataille

– GwennaÃ≪l BATAILLE, PhD student - Teaching assistant

Earth and Life Institute Université Catholique de Louvain SST/ELI/ELIB BÃtiment Carnoy, c.145 Croix du sud 4-5, bte L7.07.04 1348 Louvain-la-Neuve BELGIUM

GwennaÃ≪l Bataille <gwennael.bataille@uclouvain.be>

Summer Wildlife FieldWork

Position Title: Crew Member Position Type: Full-time, temporary, 24 weeks Location: Based out of the Taos, NM or Las Cruces, NM Field Office Salary: $350-480/week Benefits: Uniform, training, $800 travel stipend for training and camp rate per diem; AmeriCorps Education Award, if eligible Program Dates: TBD, around May 2nd, 2016 - September 30th, 2016

Program Overview: Interns will work in a crew of 2 - 3 people to monitor land health on National Monument lands, vegetation treatments, rangeland allotments, or reference areas. Participants will manage all aspects of vegetation monitoring using the Assessment, Inventory, and Monitoring (AIM) methodology. Experience with identifying vegetation to species is essential for the position. Within all plots, vegetation will be identified to species; line-point intercept will be used to gather species cover and composition data; shrub density will be measured; and soil descriptions will be required. All point data will be gathered using a GPS unit and stored in an ArcGIS geodatabase. Data are entered into Database for Inventory, Monitoring, and Assessment (DIMA) on site with ruggedized tablets and are further analyzed and synthesized into various reports for future land management planning. DIMA requires a high level of Quality Assurance/Quality Control (QA/QC), therefore attention to detail is paramount for these positions. Subsequent, professional reports must be completed and will involve the presentation of scientific data and pre and post treatment analysis. Crew may be camping 1-4 nights/week, depending on location.

General Qualifications: Applicants should have a degree in ecology, botany, range science, soil science, wildlife biology, natural resource management, biology, conservation biology, or a related field. Identifying plants to species and experience with a taxonomic key is essential to the position. Familiarity with northern New Mexico flora is beneficial. The successful applicant must be self-motivated and able to work independently with limited supervision after the initial training period. Applicants with previous AIM or Indicators of Rangeland Health training are highly preferred. Background in statistics/Microsoft Suite, including Access, is additionally useful. The applicant must be able to maneuver and operate in a mixture of office and field work, which can include long periods of standing or walking on rough, uneven ground; bending, crouching, stooping, stretching or reaching to observe occurrences or place and retrieve equipment or devices; lifting and moving moderately heavy items. Applicant must be physically fit, able to stand and walk for long periods of time (at a minimum 6 miles/day) and lift items that weigh up to 40 pounds in upwards of 100 degree heat. A government vehicle will be used for work travel but a personal vehicle is highly recommended for travel to and from the duty station and for personal time. There is potential for working in adverse conditions including extreme heat and monsoonal rains and hazardous wildlife (i.e. rattlesnakes, scorpions), so field safety skills and risk management are important. The successful applicant will also attend CPR, First Aid training and Defensive Driving (or provide certification if still current). Applicant must have a valid driver's license and a good driving record. Prior to starting this position a government security background clearance will be required.

To Apply: Complete the Online Application, which can be found at http://sccorps.org/join/internships, under the New Mexico Bureau of Land Management Vegetation Monitoring Internship title. Contact Natalie Pyrooz at 970-403-0137 or natalie(at)conservationlegacy.org with any questions.

Position Title: Crew Leader Position Type: Full-time, temporary, 52 weeks Location: Based out of the Taos, NM or Las Cruces, NM Field Office Salary: $550 - 700/week, DOE Benefits: Uniform, training, $800 travel stipend for training and camp rate per diem Program Dates: TBD, around May 2nd, 2016 - April 28, 2017

Program Overview: Interns will work in a crew of 2 - 3 people to monitor land health on National Monument lands, vegetation treatments, rangeland allotments, or reference areas. Participants will manage all aspects of vegetation monitoring using the Assessment, Inventory, and Monitoring (AIM) methodology. Experience with identifying vegetation to species is essential for the position. Within all plots, vegetation will be identified to species; line-point intercept will be used to gather species cover and composition data; shrub density will be measured; and soil descriptions will be required. All point data will be gathered using a GPS unit and stored in an ArcGIS geodatabase. Data are entered into Database for Inventory, Monitoring, and Assessment (DIMA) on site

— / —

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

Switzerland Internship BatLifeHistoryEvol

Internship for undergraduate/ Master's degree student for the bat project

Topic: Impact of early life condition on alternative reproductive tactics in bats.

Context: Oxidative stress is considered to be a major mechanism impacting on life history trade-offs. Carollia perspicillata, a neo-tropical bat, shows two reproductive tactics, with harem males defending a territory, and bachelor males.

Early life experiences have long lasting consequences on an individual. To understand how early conditions impact the future "choice" of the reproductive tactic, we will manipulate the growth rate of babies, using food restriction.

The project is based at the university of Neuchâtel, Switzerland. We study a captive bat colony (Papiliorama http://www.papiliorama.ch). Bats can fly freely under a 40m-diameter dome, which includes an artificial cave. The light cycle is reversed, allowing us to work during the day. Therefore, it is a unique opportunity to study bats, animals still largely unknown.

Tasks of the intern, in collaboration with the PhD student working on the project:

- Planning of the experiment
- Help to feed the bas that are in cages during the experiment
- Regular trapping of new gravid females
- Participation in blood collection
- Behavioral observation
- Possibility of lab work

About the position:

- It can be part of your studies. Therefore, the candidate is welcome to conduct a personal research project linked to the main project.
- Unfortunately it is not paid, but a grant is available via the University of Neuchâtel with an internship agreement (420 swiss francs per month).
- Minimum duration of two months, if possible starting in March. The starting/ending dates are very flexible, as this experiment will last a long time.

Please feel free to contact me if you have any questions. To apply, please send a CV and a cover letter to magali.meniri@unine.ch with "application bat internship" as a subject.

magali.meniri@unine.ch

TrainingGrants PlantEvoDevo

microMORPH Cross-Disciplinary Visits and Training Grant in plant eve-devo

microMORPH promotes and fosters cross-disciplinary interaction through a series of small grants that allow graduate students, post-doctoral researchers, and early career faculty to visit labs and botanical gardens with the aim of enriching their scientific research on plants. Successfully funded proposals directly address plant evolution and development as related to processes of microevolution. These grants are available to support cross-disciplinary visits between labs or institutions for a period of a few weeks to an entire semester.

Award Amount: this grant can fund graduate student, post-doctoral, or early career faculty cross-training research opportunities for up to $3,500 to cover travel, lodging, and pier diem.

Submission Deadline: The next microMORPH Cross Disciplinary Training Grant deadline is 11:30 pm on March 15th, 2016.

Eligibility: To be eligible for a microMORPH training grant you must fulfill one or more of the following requirements: 1) you must be a U.S. citizen or, 2) you must be affiliated with a U.S. university or institution (in a graduate program or working as a post-doc or faculty member), or 3) the lab you plan to visit for your training experience must be at a U.S. university of institution.

How to Apply: For full application instructions and to submit applications, please visit the microMORPH website (http://projects.iq.harvard.edu/micromorph).

Pamela Diggle

Professor Department of Ecology and Evolutionary Biology University of Connecticut

860-486-4788<tel:860-486-4788>

"diggle@colorado.edu" <diggle@colorado.edu>

TrainingGrants Undergrad PlantEvoDevo

microMORPH Undergraduate Summer Internships/Training Grants for plant eve-devo

microMORPH promotes and fosters cross-disciplinary training and interaction through a series of small grants that allows undergraduates to visit labs and botanical gardens as well as gain invaluable laboratory experience while contributing to scientific research on plants. These grants are available to support training visits for a period of a summer (or summer semester equivalent). Successfully funded proposals address plant evolution and development as related to processes of microevolution.

Award Amount: this grant can fund 10-week research internships/training grants for undergraduates. $5,000 is available per grant, which can be used for travel and housing for the period of the internship.

Submission Deadline: Undergraduate training grant proposals are due on 11:30 pm on March 15th, 2016.

Eligibility: To be eligible for a microMORPH undergraduate training grant you must fulfill one or more of the following requirements: 1) you must be a U.S. citizen or, 2) you must be affiliated with a U.S. college, university, or institution (in an undergraduate program), or 3) the lab you plan to visit for your training experience must be at a U.S. university of institution.

How to Apply: For full application instructions and to submit applications, please visit the microMORPH website (http://projects.iq.harvard.edu/micromorph).

Pamela Diggle

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860-486-4788<tel:860-486-4788>

"pamela.diggle@uconn.edu"
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Trinidad VolFieldAssist GuppyEvolution

Research Internships - Evolutionary Biology Research interns are needed to assist in a multi-disciplinary, multi-investigator, experimental study of the interactions between ecology and evolution in Trinidad. The research is led by Professor David Reznick at the University of California, Riverside in collaboration with Joseph Travis (Florida State), Tim Coulson (Oxford), Paul Bentzen (Dalhousie U.) and Andres Lopez-Sepulcre (CNRS-Universite Pierre et Marie Curie, Paris). We seek to integrate multiple biological fields for the study of these interactions in experimental populations of guppies in Trinidad. Duties include assisting in monthly censuses of guppy populations in montane streams. The monthly censuses include long hours in the field and laboratory. There will also be two weeks off during successive censuses when interns will pursue an independent project.

Qualifications: We seek interns who are entertaining the possibility of pursuing graduate studies in some area of ecology and evolution and who wish to gain some additional field research experience. Research will take place in semi-remote areas of Trinidad sometimes under bad weather conditions. Applicants must be able to live and work well with others.

Research will involve carrying heavy packs over slippery and steep terrain. Applicants must be in good physical condition and be able to meet the demands of field research under these conditions. Ability to drive a standard transmission vehicle is desirable but not required. Applicants with first-aid/first responder training, skills in automobile maintenance, and construction skills are highly desirable. Please address these skills when applying.

Interns will be required to spend a minimum of 3-months in Trinidad, with possibility of extension. Starting dates are as early as August 2015. We will cover all travel and living expenses and provide housing. We will cover all travel and living expenses. Please see our website <cnas.ucr.edu/guppy> for more information on the project and access to reprints. Our video menu includes a guppy censuses submenu that details the main tasks associated with the internship. Applicants should send cover letter, CV and the names, phone numbers and e-mail addresses of three or more professional references to David Reznick (gupy@ucr.edu). At least two of the references should be academics.

Andres Lopez-Sepulcre http://www.faculty.ucr.edu/~gupy/Andres/ Andres Lopez Sepulcre <lopezsepulcre@gmail.com>

UIdaho-Galapagos SummerREU EvolutionaryEcol

The Parent lab (http://parentlab.weebly.com) is looking for an undergraduate student to assist with field research in the Galapagos Islands. The undergraduate student will spend 10 weeks (May 30th - August 5th, within the NSF-funded REU program in the Department of Biological Sciences at University of Idaho) conducting research under the guidance of two graduate students investigating island biogeography, invertebrate physiology, and biomechanics.

The research will involve traveling to the Galapagos Islands, hiking long distances with field equipment on difficult terrain, backpacking and camping in remote locations, and working long hours in the laboratory to measure physiological response and biomechanical variables in terrestrial invertebrates. The student will also have the opportunity to conduct independent research and present the results in the form of a poster at a research symposium at the end of the program.

We are looking for applicants with some or all of the following experience and skills: - Prior research in biology, ecology, wildlife management, or physiology - Ability to travel internationally (passport) - Ability to speak Spanish - Experience backpacking and camping in remote locations - Patience and attention to details.

To apply, follow instructions here: https://www.uidaho.edu/sci/biology/research/summer-reu/application-process The deadline to submit an application is Feb 15, 2016.

If you have questions, please contact: Dr. Christine Parent Department of Biological Sciences University of Idaho Email: parentlabatuidaho@gmail.com

"Parent, Christine (ceparent@uidaho.edu)" <ceparent@uidaho.edu>

UMichigan BiologicalStation ResearchFunding

The University of Michigan Biological Station (UMBS) has funding opportunities for students of all levels (undergraduate through doctoral) who conduct research at the Station.

Our fellowships page (http://goo.gl/hhBGSs) has all of our research funding information, including eligibility requirements, the application process and deadline (February 15, 2016), and contact information.

Prospective applicants should browse our Research Gateway (http://umbs.lsa.umich.edu/research/) to learn about the breadth of research that takes place at the Biological Station, the variety of habitats and research sites we have access to, and our specialized facilities. The Station has over a century of data in many fields and an equally long history of supporting regionally and nationally important field work.

Interested students should direct questions to UMBS Associate Director Karie Slavik, slavik@umich.edu.

– Alicia Farmer, Communications Coordinator University of Michigan Biological Station 734-764-5212

www.lsa.umich.edu/umbs/ "farmeral@umich.edu" <farmeral@umich.edu>

UMichiganBiolStation PaidSummerResearch

The University of Michigan Biological Station is now accepting applications for its Research Experience for Undergraduates (REU) program, "Biosphere-Athmosphere-Hydrosphere Interactions in a Changing Global Environment."

Our REU summer program runs for nine weeks (June 21 - August 20, 2016) at the UM Biological Station on Douglas Lake in beautiful northern Michigan. Each REU participant will

– Work closely with a research mentor on a project of mutual interest. – Design, conduct, analyze, and report on their research project, with guidance from the mentor and the two program co-directors. – Participate in workshops and group discussions designed to provide the background knowledge and technical tools needed to carry out interdisciplinary scientific research. – Contribute to the body of knowledge that can help address many of Earth's most important environmental challenges.

COMPENSATION: Participants receive a stipend of $5,000 plus free room and board at the Station.

DEADLINE: The deadline to apply is Monday, February 1, 2016.

Application and details at: http://goo.gl/GwYGNx . The University of Michigan Biological Station is located on Douglas Lake near Pellston, Michigan at the tip of the lower peninsula. Its campus is situated amid 10,000 undeveloped acres owned by the Station. Students have quick access to many unique habitats in the region including dune, alvar, bog, and old-growth forest. The Station also has 2 atmospheric gas sensing towers for monitoring forest and atmospheric gas. More information about the Station is available at http://www.lsa.umich.edu/umbs . – Alicia Farmer, Communications Coordinator University of Michigan Biological Station 734-764-5212

www.lsa.umich.edu/umbs/ "farmeral@umich.edu" <farmeral@umich.edu>

UMissouri REU InsideDinosaurs

Research Experience for Undergraduate positions are available at the University of Missouri Integrative Anatomy program for the summer of 2016. THE REU students will design and conduct studies that explore the anatomy and biomechanics of birds, dinosaurs, and reptiles as part of the NSF-sponsored Inside Dinosaurs program to better understand the evolution of vertebrate feeding biomechanics and the origins of avian cranial kinesis. The REU students will work with a team of researchers under the supervision of Drs. Casey Holliday and Kevin Middleton. We are particularly interested in students interested in conducting projects in comparative biomechanics, vertebrate paleontology and skeletal tissue biology. The REU students will be involved in all components of their project as well as a variety of related projects being conducted by other researchers.

The REU students will join a broader summer internship program through the University of Missouri. In addition to a full-time faculty-mentored research experience, students engage in educational programming including professional development, topical small group seminars, 14 evening lectures given by University of Missouri faculty and staff, and social activities. All students participating in the Summer Program develop a research abstract and create a poster to present at the Summer Forum.

Candidates must be available for May 31-July 30th. We will provide transportation fees, room and board at University of Missouri dormitory and dining facilities, transportation fees, support for their research and a $3500 stipend.

The ideal candidate should be interested in pursuing a career in anatomy, paleontology or biomechanics, creative, industrious, detail-oriented and comfortable working as part of a research team. Experience with field, collections, or laboratory work in these areas is a plus but not necessary. Background or at least coursework in biology, anatomy, physiology, mathematics, or geology is required. To be eligible you must not have received your degree before January 2016.

Application deadline: March 1, 2016

Applications should include: copy of unofficial transcripts, contact information for two academic references, CV/resume and an one page statement that describes your interest in the REU position, academic goals and any previous research experiences.

Applications should be sent to Dr. Casey Holliday at hollidayca@missouri.edu with '2016 REU application' in the subject line. Please feel free to contact Casey Holliday or Kevin Middleton (middletonk@missouri.edu) if you have any questions.

"middletonk@health.missouri.edu"
<middletonk@health.missouri.edu>

UPittsburgh SummerREU EvolutionChytridiomycosis

The Richards-Zawacki lab at the University of Pittsburgh invites undergraduate applicants for a 10-week summer research experience at the Pymatuning Lab of Ecology in northwestern Pennsylvania (http://www.biology.pitt.edu/facilities/pymatuning). This position is part of the National Science Foundation's Research Experiences for Undergraduates (REU) program.

Ongoing work in the Richards-Zawacki lab aims to clarify the relationship between climate and the dynamics of chytridiomycosis, a fungal disease that threatens amphibian populations on several continents. The successful applicant will design and carry out a study using physical models deployed in the field to investigate differences in the thermal biology of co-occurring amphibian hosts and how these differences might translate to differences in susceptibility to chytridiomycosis. The student will also work collaboratively with other members of the Richards-Zawacki lab to survey local amphibians for *Batrachochytrium* pathogens, the fungi that cause chytridiomycosis.

Room and board at the Pymatuning Lab of Ecology will be provided, along with transportation and a stipend of $500/week.

To apply, please send a one page personal statement (about your scientific interests and how this REU will support your professional goals), your resume or cv, unofficial transcripts, and the names of two professional references (including title, address, phone number and email address) to Dr. Cori Richards-Zawacki (cori.zawacki@pitt.edu). Applications are due March 4, 2016.

Please direct any questions you may have about the program to Dr. Richards-Zawacki (cori.zawacki@pitt.edu).

Corinne L. Richards Zawacki, Ph.D. email: cori.zawacki@pitt.edu <email%3Acori@tulane.edu>
Associate Professor, Department of Biological Sciences
and Director, Pymatuning Laboratory of Ecology
University of Pittsburgh

"At night I went out into the dark and saw a glimmering star and heard a frog and nature seemed to say, well do not these suffice?" - Ralph Waldo Emerson

"cori.zawacki@pitt.edu" <cori.zawacki@pitt.edu>

UTelAviv VolResAssistMarch RoyalIrisEvolution

Opportunity available to participate in an ongoing project on Floral Evolution and Ecology of the Royal Irises in Dr. Yuval SapirÂs lab (http://labsapir.wix.com/labsapir) at Tel Aviv University, Israel. We are seeking one or two motivated volunteer research assistants to help with field data collection, to perform experimental work at the botanical garden and to assist in data analyses.

The positions are most suitable for graduates in Biology seeking to gain further research experience. Candidates who are still undergraduates will be also considered. Candidates should have good organizational skills, high interest to work in the field and fluent English. International driving license is essential. Positions start early March and will continue until early April, but a partial term of two weeks is also possible.

About Tel Aviv University: Tel Aviv University (https://english.tau.ac.il/) is considered the best university in Israel for life sciences. It is located in the city of Tel Aviv, an international and vibrant coastal city. The University has a wide representation of International students.

Israel is culturally and ecologically diverse. The country has approximately 3000 plant species growing along a climate gradient, from sub-alpine mountain through Mediterranean maquis to extreme desert. Alongside the natural settings, Israel is rich in history, with archaeological sites dated thousands years old and sites that are sacred to three religions.

The volunteer will have an opportunity to travel during the project work and experience the diversity in vegetation, as well as the culture.

If you are interested please e-mail your cv to Dr Yuval Sapir (sapiryuval[at]gmail.com) or to Dr. Mahua Ghara (mahuaghara[at]gmail.com). You could also write to us for further information and queries regarding the opportunity.

PBC Post-Doctoral Research Fellow, Dept. of Molecular Biology and Ecology of Plants Tel-Aviv University, Tel Aviv, 69978 Israel. http://labsapir.wix.com/labsapir Botanical Garden, Tel Aviv University, Ramat Aviv, Tel Aviv 69978 http://botanic.tau.ac.il/ mahuaghara@gmail.com

UTexas SummerResearch SwitchgrassEvolution

Switchgrass (Panicum virgatum) is emerging as an important biofuel candidate in the United States. Our labs (see list of collaborators below) collectively study the ecology, genetics/genomics, physiology and agronomy/plant breeding of Switchgrass. We are seeking a talented and diverse group of undergraduate students interested in conducting a variety of research in Switchgrass biology across the US.

Program description: This program is an opportunity for undergraduate students to participate in mentored independent research on the biology of Switchgrass. The program is funded through the NSF Research Experience for Undergraduates (REU) program and is associated with our ongoing interdisciplinary work on the ecology, physiology, and genomic responses of switchgrass to future climate change. Summer students will be immersed in research and learn basic and applied biology through active participation. Working as part of our research team, they will contribute to group research projects, design short research projects, and present their work in an end-of-summer student symposium.

Each position is supported for 8-10 weeks beginning the first week of June. Students are awarded a $4500 stipend, plus a housing and food allowance, and some funds to help defray the cost of traveling to the designated University.

Who Should Apply: Undergraduates that are not in their senior year (typically 2nd or 3rd year students), who are either U.S. citizens or permanent residents studying in the U.S.

Application process: The application deadline is February 15, 2016. Applicants should submit a cover letter describing any relevant research experience, along with their motivation for joining our research group, and include a copy of their current transcript (unofficial transcript or screenshots are acceptable). Applicants should also ensure that two letters of recommendation are submitted on their behalf. Only applications that are complete will be considered. Applications and requests for further information should be directed to:

Dr. Brandon Campitelli e-mail: brandon.campitelli@utexas.edu Subject: Switchgrass REU 2016

For more information regarding this opportunity, and ongoing research, please visit our website: https://sites.cns.utexas.edu/juenger_lab/summer-research-opportunities Collaborating professors and institutions: Prof. Thomas Juenger; University of Texas at Austin; https://sites.cns.utexas.edu/juenger_lab/home Prof. David Lowry; Michigan State University; https://plantbiology.natsci.msu.edu/directory/david-lowry/ Prof. Felix Fritschi; University of Missouri, Columbia; http://plantsci.missouri.edu/faculty/fritschi.cfm Prof. Yanqi Wu; Oklahoma State University; http://biopec.okstate.edu/?page_id=155 Prof. Rob Mitchell; USDA-ARS, University of Nebraska, Lincoln; http://www.ars.usda.gov/pandp/people/people.htm?personid=31809 Prof. Arvid Boe; South Dakota State University; https://www.sdstate.edu/resources/directory/directory-detail.cfm?view=detail&ci=234 Brandon E Campitelli, PhD Postdoctoral Researcher, Dept. of Integrative Biology College of Natural Sciences Clinical Assistant Professor, Biology of Biofuels Freshmen Research Initiative University of Texas at Austin

brandon.campitelli@utexas.edu

PostDocs

AarhusU EvolutionaryBiology

Marie SkÃÂodowska-Curie Individual Fellowships

We are three scientists (Profs. Volker Loeschcke, Trine Bilde and Michael M. Hansen) from the Section for Genetics, Ecology and Evolution, Dept. of Bioscience, Aarhus University, Denmark who are very interested in collaborating with outstanding postdoctoral researchers on Marie SkÃÂodowska-Curie Individual Fellowships (MSCA IFs) in 2016. Specifically, we are keen to host potential candidates for 2 years working on projects that relate to our current fields of research: Evolutionary biology and adaptation at phenotypic and genomic levels. See below for more specific details on our research.

What can we offer?

Our section provides an excellent, highly ambitious environment, where younger researchers thrive and work on projects of interest to them with active mentoring from senior research staff. In addition, significant application support will be offered as the University will be hosting a Masterclass in May 2016 where potential applicants will have the chance to travel to Aarhus University for 3 days with the following objectives:

- Get an introduction to the MSCA IF programme and application

- Get an introduction to the Section for Genetics, Ecology and Evolution and meet potential colleagues

- Work on the project description with the host group to ensure an excellent starting point and get relevant input to ensure as strong an application as possible

If selected for the event, participants' travel costs and accommodation will be covered.

What do we work with?

Volker LoeschckeÃÂs group:

We study thermal adaptation using Drosophila as a model system. We ask if temperature is the primary driver of adaptation to environmental gradients using experimental evolution approaches as well as studies that are experimentally simulating temperature gradients in climate chambers. We try to connect studies at the DNA level (genomics, transcriptomics, proteomics and metabolomics) with studies on thermal phenotypes and try to create ecologically relevant scenarios. We contrast physiological (plasticity) and evolutionary adaptations and look at fluctuating and unpredictable environments, variation in day length, dietary composition and the role of the microbiome on thermal resistance. We are also interested in other climate-related resistance traits and lifespan, their genetic architecture, phylogenetic constraints and correlations and interactions among traits, and transgenerational effects and epigenetics.

Trine BildeÃÂs group:

We study population genetics, adaptation, and group-living using social spiders as model system. The social spiders are unique among group living animals, as the transition to permanent sociality is associated with strong inbreeding, cooperative breeding, and highly female-biased sex ratios. Our research aims to understand the ecology and evolution of sociality, reproductive division of labour, and population genomic consequences of inbreeding. Social spiders show extremely low genetic variation but occupy wide habitat ranges with strong temperature and humidity clines. We are interested in understanding how plastic and environmentally determined factors (epigenetics, microbiome) influence adaptation. Our research is mainly performed on the African genus Stegodyphus that contains both social and subsocial (pre-social) spiders, which allows comparative studies.

Michael M. HansenÃÂs group:

We investigate how species and populations are adapted to the environments they inhabit. We are interested in if and how they can respond to rapid, anthropogenic environmental change such as climate change, but also analyze adaptation and demographic history on longer, historical time scales. Our primary model organisms are fishes, including Anguillid eels, threespine stickleback, Arctic char, lake whitefish and brown trout, but we are open for suggestions involving other organisms as well. We currently have a strong focus on Greenland, which is one of the regions on Earth experiencing the most drastic climate change. Our research is to a large extent based on whole genome sequencing and various methods for reduced representation genome sequencing (e.g. RAD sequencing), which we integrate with analysis of phenotypic traits. We foresee a major future emphasis on epigenetics and its roles in adaptation.

How does it work?

MSCA fellowships are highly flexible in terms of research focus and pay a generous salary for grant recipients over 2 years. To be eligible to apply with our section as host, the fellow must fulfil to eligibility requirements:

Mobility: For Standard European Fellowships they may not have lived in Denmark for longer than 12 months in the past 3 years at the time of application (14/09/2016). Fellows can move to Denmark from other EU countries as well as non-EU countries.

If the applicant is a citizen of an EU or Associated Country and has

— / —

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

AustralianNaltU BayesianEvolutionaryInference

Dear colleagues

I have an Australian Research Council-funded project to develop Bayesian MCMC methods of evolutionary analyses using short-read sequences obtained from mixed DNA samples of unlabelled individuals. The project provides funds to support one postdoctoral fellow for up to 2.5 years. The ideal candidate will understand the mechanics and mathematics of computational Bayesian evolutionary inference, and will be able to develop new algorithms and code to extend these methods.

The postdoctoral fellow will work at my lab at the Australian National University, and preferably, will be able to begin no later than June 2016. If you are interested to learn more, please email me (allen.rodrigo@anu.edu.au).

Allen Rodrigo

allen.rodrigo@anu.edu.au

ColdSpringHarborLab ComputationalGenomics

The Siepel Lab in the Simons Center for Quantitative Biology at Cold Spring Harbor Laboratory is seeking full-time postdoctoral computational researchers. The Siepel Group specializes in the development of probabilistic models, algorithms for inference, prediction methods, and application of these methods in large-scale genomic data analysis. Of particular interest is research relevant to existing, NIH supported projects in (1) HUMAN POPULATION GENOMICS, including demography inference using Bayesian coalescent-based methods, inference of natural selection on regulatory and other noncoding sequences, and prediction of fitness consequences for noncoding mutations; and (2) TRANSCRIPTIONAL REGULATION in mammals and Drosophila, including the estimation of rates and patterns of transcriptional elongation from GRO-seq data, prediction of transcription factor binding sites from DNase-seq data, and regulatory network inference based on joint patterns of transcription and binding in inducible systems. The research on transcriptional regulation will continue to be carried out in close collaboration with Dr. John Lis at Cornell University.

RELEVANT RECENT PAPERS: Kuhlwilm M, Gronau I, Hubisz MJ, de Filippo C, Prado J, et al. Ancient gene flow from modern humans into Siberian Neandertals. Nature (in press), 2015.

Danko CG, Hyland SL, Core LJ, Martins AL, Waters CT, et al. Identification of active transcriptional regulatory elements from GRO-seq data. Nat. Methods. 2015. 12(5):433-438. PMCID: PMC4507281.

Rasmussen MD, Hubisz MJ, Gronau I, Siepel A. Genome-wide inference of ancestral recombination graphs. PLOS Genet. 2014. 10(5): e1004342. PMCID: PMC4022496.

Freedman AH, Gronau I, Schweizer RM, Ortega-Del Vecchyo D, Han E, et al. (30 co-authors). Genome sequencing highlights the dynamic early history of dogs. PLOS Genet. 2014. 10(1):e1004016. PMCID: PMC3894170.

Core LJ, Martins AL, Danko CG, Waters CT, Siepel A, et al. Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. Nat. Genet. 2014. 46(12):1311-1320 PMCID: PMC4254663.

Capra JA, Hubisz MJ, Kostka D, Pollard KS, Siepel A. A model-based analysis of GC-biased gene conversion in the human and chimpanzee genomes. PLOS Genet. 2013. 9(8):e1003684. PMCID: PMC3744432.

Arbiza L, Gronau I, Aksoy BA, Hubisz MJ, Gulko B, Keinan A, Siepel A. Genome-wide inference of natural selection on human transcription factor binding sites. Nat. Genet. 2013. 45(7):723-729. PMCID: PMC3932982.

Gronau I, Arbiza L, Mohammed J, Siepel A. Inference of natural selection from interspersed genomic elements based on polymorphism and divergence. Mol. Biol. Evol. 2013. 30(5):1159-1171. PMCID: PMC3697874.

Gronau I, Hubisz MJ, Gulko B, Danko CG, Siepel A. Bayesian inference of ancient human demography from individual genome sequences. Nat. Genet. 2011. 43(10):1031-1034. PMCID: PMC3245873.

The ideal candidate will be enthusiastic, highly motivated and independent; will have a strong background in comparative genomics, population genomics, or transcriptional regulation, a serious interest in molecular biology and genetics combined with good skills in mathematics and computer science, and a strong record of accomplishment in research. Postdoctoral associates in the group are expected to participate in both methods development and data analysis, to be comfortable in a fast-moving, interactive, and collaborative research environment, and to actively publish and present results.

REQUIRED QUALIFICATIONS: Ph.D. in bioinformatics, computer science, statistics, genetics, molecular biology, applied mathematics, or a related field; Research experience (with first-author publications) in computational genomics or a closely related field; Fluency in probabilistic modeling and computational statistics; Proficiency in programming, ideally in C or C++, as well as in scripting languages such as python, Perl, mat lab, or R; should be comfortable in a Linux environment, with large data sets, computer clusters, and databases.

TO APPLY: Position Number 01229-R. https://cshl.peopleadmin.com/postings/8866. Informal inquiries are also welcome. Please submit a CV, a short description of research interests and experience, and contact information for three references by e-mail to asiepel@cshl.edu.

Adam Siepel, Ph.D. Simons Center for Quantitative Biology Cold Spring Harbor Laboratory One Bungtown Road Cold Spring Harbor, NY 11724

CSHL is an EO/AA Employer. All qualified applicants will receive consideration for employment and will not be discriminated against on the basis of race, color, religion, sex, sexual orientation, gender identity, national origin, age, disability or protected veteran status. VEVRAA Federal Contractor.

"Gill, Irene" <gill@cshl.edu>

ColdSpringHarborLab EvolutionaryGenomics

Position Description:

Postdoctoral Positions in Computational Genomics are available in Dr. Adam Siepel's research group in its new location at the Simons Center for Quantitative Biology (SCQB) at Cold Spring Harbor Laboratory (CSHL). The Siepel Group specializes in the development of probabilistic models, algorithms for inference, prediction methods, and application of these methods in large-scale genomic data analysis. Of particular interest is research relevant to existing, NIH supported projects in (1) human population genomics, including demography inference using Bayesian coalescent-based methods, inference of natural selection on regulatory and other noncoding sequences, and prediction of fitness consequences for noncoding mutations; and (2) transcriptional regulation in mammals and Drosophila, including the estimation of rates and patterns of transcriptional elongation from GRO-seq data, prediction of transcription factor binding sites from DNase-seq data, and regulatory network inference based on joint patterns of transcription and binding in inducible systems. The research on transcriptional regulation will continue to be carried out in close collaboration with Dr. John Lis at Cornell University.

Relevant recent papers include the following:

Kuhlwilm M, Gronau I, Hubisz MJ, de Filippo C, Prado J, et al. Ancient gene flow from modern humans into Siberian Neandertals. Nature (in press), 2015.

Danko CG, Hyland SL, Core LJ, Martins AL, Waters CT, et al. Identification of active transcriptional regulatory elements from GRO-seq data. Nat. Methods. 2015. 12(5):433-438.

Rasmussen MD, Hubisz MJ, Gronau I, Siepel A. Genome-wide inference of ancestral recombination graphs. PLOS Genet. 2014. 10(5): e1004342.

Freedman AH, Gronau I, Schweizer RM, Ortega-Del Vecchyo D, Han E, et al. (30 co-authors). Genome sequencing highlights the dynamic early history of dogs. PLOS Genet. 2014. 10(1):e1004016.

Core LJ, Martins AL, Danko CG, Waters CT, Siepel A, et al. Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. Nat. Genet. 2014. 46(12):1311-1320.

Capra JA, Hubisz MJ, Kostka D, Pollard KS, Siepel A. A model-based analysis of GC-biased gene conversion in the human and chimpanzee genomes. PLOS Genet. 2013. 9(8):e1003684.

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Gronau I, Arbiza L, Mohammed J, Siepel A. Inference of natural selection from interspersed genomic elements based on polymorphism and divergence. Mol. Biol. Evol. 2013. 30(5):1159-1171.

Gronau I, Hubisz MJ, Gulko B, Danko CG, Siepel A. Bayesian inference of ancient human demography from individual genome sequences. Nat. Genet. 2011. 43(10):1031-1034..

The ideal candidate will be enthusiastic, highly motivated and independent; will have a strong background in comparative genomics, population genomics, or transcriptional regulation, a serious interest in molecular biology and genetics combined with good skills in mathematics and computer science, and a strong record of accomplishment in research. Postdoctoral associates in the group are expected to participate in both methods development and data analysis, to be comfortable in a fast-moving, interactive, and collaborative research environment, and to actively publish and present results.

Required Qualifications:

Ph.D. in bioinformatics, computer science, statistics, genetics, molecular biology, applied mathematics, or a related field; Research experience (with first-author publications) in computational genomics or a closely related field; Fluency in probabilistic modeling and computational statistics; Proficiency in programming, ideally in C or C++, as well as in scripting languages such as python, Perl, mat lab, or R; should be comfortable in a Linux environment, with large data sets, computer clusters, and databases.

Job Location: CSHL, One Bungtown Road, Cold Spring Harbor, NY 11724

TO APPLY: visit the CSHL Careers website at www.cshl.edu/careers .Position Number:01229-R.

“Gill, Irene” <gill@cshl.edu>

Cornell GenomicsSocialWasps

Postdoctoral position in comparative and population genomics of Polistes paper wasps

The Sheehan lab at Cornell University seeks a postdoc for comparative and/or population genomics projects using Polistes paper wasps as a model system. Paper wasps are a diverse group of primitively eusocial insects that have served as a model group in studies of social behavior. Among the notable traits of the group is the presence of substantial variation in the level of cooperation between populations and species. Additionally, complex social is associated with the highly polymorphic color patterns within populations used for individual recognition and quality signaling in different species.

From a population genetics perspective, Polistes wasps are especially appealing for a few reasons including small genome sizes, males are haploid allowing for perfectly phased data and wasps are abundant in a wide variety of habitats making it easy to get large numbers of samples. They can also be reared in the lab.

A 2-3 year position is available (initial 12 month appointment with the possibility of renewal). Start date is flexible. Information about salary and benefits at Cornell can be found here: https://postdocs.cornell.edu/-postdoctoral-associates-benefits . The lab is especially interested in using comparative and population genetic approaches to examine the evolutionary causes and consequences of cooperative nesting and visual recognition in wasps, though postdocs are welcome (and encouraged) to develop independent projects making use of population and comparative genomic data being generated by the lab.

In addition to population and comparative genomics, the postdoc will have the opportunity to conduct fieldwork in the US or abroad, conduct behavioral or cognitive experiments and/or carry out molecular work depending on the nature of the project and the postdoc’s interest.

Required qualifications:

Ph.D. or equivalent degree in biology, evolution, genetics, bioinformatics, or related field. Publication of work based on dissertation. Working knowledge of bioinformatics pipelines and standard population genomic analyses. Proficiency in scripting language (e.g. Python or Perl) and depth in some area of comparative or population genomics is strongly preferred. Prior wet lab or field experience is not required.

To apply please submit a cover letter describing your relevant experience and interest, a CV, the contact information for three references, and 1-2 relevant publications to Dr. Michael Sheehan (msheehan@cornell.edu).

Diversity and inclusion are a part of Cornell University’s heritage. Cornell is a recognized employer and educator valuing AA/EEO, Protected Veterans, and Individuals with Disabilities.

Please feel free to contact me at the above email address with any questions.

Michael J Sheehan

Assistant Professor Neurobiology and Behavior Cornell University 215 Tower Rd Ithaca NY, 14853

(607) 254-4302

msheehan@cornell.edu

CornellU HostMicrobeInteractions

Postdoctoral Associate in host-microbe interactions at Cornell University

The Hendry lab in the Department of Microbiology is seeking a Postdoctoral Associate to study the evolution and ecology of bacteria interacting with hosts. The main focus of the position would be the interactions of Pseudomonas syringae with insects and plants. P. syringae is a widespread environmental and plant-associated bacterium and important plant pathogen. Some strains of P. syringae can also infect plant-associated insects such as aphids. The lab is interested in understanding how these complex interactions in multiple environments impact the evolution and ecology of the bacteria. We also aim to understand how the interaction may influence important crop plants and pest insects.

Specific research questions are flexible and dependent on applicant's experience and interest. Preferred areas include:

1) Comparative genomics/transcriptomics of bacteria 2) Identification and analysis of functionally important genes or 3) Ecology of bacteria in natural environments or laboratory experiments

Additionally the postdoc will have the opportunity to develop independent research projects and those could be outside of this specific system. Other work in the lab involves comparative genomics of unculturable bacteria, bioluminescent symbiosis, and gut microbiomes of insects.

This position is full-time (40 hours/week) and will be located in Ithaca, New York. This is a one year appointment with possible extension depending on funding and performance. Starting date is flexible.

The Department of Microbiology in the College of Agriculture and Life Sciences at Cornell University has eleven active research laboratories. It serves as the home department for the Graduate Field of Microbiology with >40 affiliated faculty members with diverse interests and particularly relevant strengths in host-microbe interactions and plant pathogens. Research within the department is focused on prokaryotic biology, environmental microbiology, and host interactions and includes specific expertise in molecular genetics, gene regulation, genomics, microbial cell biology, bioremediation, symbionts, pathogens, and ecosystems.

Required Qualifications:

Ph.D in Microbiology, Ecology and Evolutionary Biology, or related field; Demonstrated research experience in one of the following areas: comparative genomics/transcriptomics, microbiology, or microbial ecology; Publication record appropriate for career stage; Experience with bacterial culture is preferred but not required; Ability to work and learn new techniques independently is desired.

To apply:

Submit a cover letter describing your research experience and interests, a CV, and the contact information for three references to Dr. Tory Hendry (th572@cornell.edu). Please feel free to contact me by email with any questions.

Tory A. Hendry Research Scientist Department of Microbiology Cornell University 260 Wing Hall Ithaca, NY 14853 (607) 255-1950

Tory Hendry <th572@cornell.edu>

CornellU PopulationGenomics

Postdocin population genomics of hatchery-based population supplementation

Thelaboratory of Matt Hare at Cornell University is looking for a postdoc with diverse skills to lead projects on fitness variation in hatchery-produced F1 vs. wild eastern oysters (Crassostrea virginica). This research is motivated by the need for improved success rates in hatchery-based oyster restoration and more generally to measure within-generation selection and its effects in high-fecundity species. Hatchery production of restoration oysters from wild brood stock typically results in a cohort with low allelic diversity and a broad range of individual heterozygosities compared with wild oysters. The postdoc will take the lead analyzing and publishing existing comparative ddRAD data on wild adults and juveniles, a hatchery-produced F1 cohort from the wild adults, and a commercial aquaculture strain to document genomic changes resulting from aquaculture line improvement versus single-generation domestication selection. The postdoc also will have primary responsibility for field experiments comparing growth, maturation and survivorship of hatchery-produced F1 cohorts (restoration oysters) that differ in genetic diversity to test for differential stress tolerance across environments. Additional projects that could be pursued with existing or anticipated data, depending on interests, include analysis of gene expression plasticity across salinity treatments and genome scans for within-generation selection across habitat heterogeneities.

Qualifications:A PhD in ecological genetics, molecular ecology, or a related field is required. We are looking for a creative and productive scientist with field experience, strong computational skills and good communication abilities. A drivers license and good city driving skills are essential. Ideal candidates will have some previous experience working in the Unix environment analyzing large population genomics data sets. Programming abilities are highly desirable.

Theposition will be based at Cornell University in Ithaca NY and is for 12 months, with possibility for extension based on performance and the availability of funding. The start date is March 1 2016 or as soon as possible thereafter. Information about salary and benefits at Cornell can be found here: https://postdocs.cornell.edu/-postdoctoral-associates-benefits .Interestedcandidates should send a cover letter describing your relevant experience and interest, a CV, the contact information for three references, and 1-2 relevant publications to Matt Hare (mph75@cornell.edu). Review of applications will begin immediately and continue until the position is filled.

MattHare AssociateProfessor Departmentof Natural Resources 205Fernow Hall CornellUniversity Ithaca,NY 14853 mph75@cornell.edu 607-255-5685

mph75@cornell.edu

DartmouthC EvolutionaryBiol

We seek applicants for 1-2 independent postdoctoral fellowships in the Ecology, Evolution, Ecosystems, and Society (EEES) Graduate Program at Dartmouth College. EEES is a diverse community of scholars who conduct innovative research in the natural sciences and interdisciplinary environmental studies, including ecology, evolution, anthropology, environmental economics, geography and earth sciences. Quality candidates will possess a PhD in an appropriate disciplinary or interdisciplinary field and have a strong background in interdisciplinary research, advanced analytical and writing skills, and an interest in undergraduate and graduate level education. The successful candidates will be expected to initiate and develop creative independent research projects. In addition, the fellows will have the opportunity to enhance graduate student education and professional development by leading a seminar course or working group dedicated to developing a research product. The ideal candidate will be a strong contributing member of the vibrant EEES community at Dartmouth and foster productive discourse both within and beyond the program. Applicants should identify in their cover letter one or more potential faculty mentors from the EEES program. (program website: http://sites.dartmouth.edu/EEES/)

Deadline: Review of applications will begin Feb. 12 Starting date: Negotiable Salary: Competitive salary and benefits package Research stipend: TBD Term: up to two years pending satisfactory annual performance

Please submit the following application materials through Interfolio: [apply.interfolio.com/33632] -Cover letter -Curriculum vitae -PDF copies of up to five representative publications or manuscripts -Names and addresses of three references -A one-page prospectus for an interdisciplinary graduate seminar or working group -A statement of scientific purpose that describes your research interests and aspirations

Questions about the fellowships can be directed to: Dr. Doug Bolger (dbolger @dartmouth.edu)

DukeU PlantFungalEvolution

Title: Postdoctoral position in plant-fungal symbiosis and evolution

The Vilgalys Mycology Lab at Duke University seeks a postdoctoral researcher in the area of plant-fungal symbiosis and evolution. The selected candidate will contribute to ongoing studies on ecology and evolution of forest soil fungi and their interactions with trees including *Populus*, *Pinus* and other species. We are especially interested in metagenomic approaches for studying fungal interactions with plants including mycorrhizal fungi and root endophytes.

Major Duties/Responsibilities: Design, conduct and interpret laboratory and field based research; lead and contribute to the development of scientific manuscripts and proposals. The postdoc chosen for this position will also have opportunities to interact with collaborating institutions in the US and abroad. Research is facilitated by state-of-the-art equipment/facilities for microbiology, molecular biology, and genomics, in a professional environment with excellent technical support.

Qualifications Required: Ph.D. degree in plant or fungal biology, microbial genomics, or related fields. Applicant should have demonstrated expertise in modern molecular ecology methods including nextgen sequencing, phylogenomics, phylogentics, and bioinformatics tools for microbiome and metagenomic studies. Demonstrated expertise must include a track record of peer-reviewed publications.

Qualifications Preferred: Priority will be given to applicants with a successful history of interdisciplinary, integrative, and innovative research in this area. Interested applicants should send a cv, research statement, and names of 3 references (preferably in a single pdf) to Dr. Rytas Vilgalys, fungi@duke.edu. The position is available immediately and will remain open until a suitable candidate has been hired. For more information on the Vilgalys Lab see: *http://sites.duke.edu/vilgalyslab/ fungirv@gmail.com

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GeorgeWashingtonU ComputationalBiol

GeorgeWashingtonU. PostdoctoralScientist

The Computational Biology Institute (CBI) brings together GW experts and scholars from partner institutions to conduct cutting edge research, enable broad educational activities in computational biology and provides computational biology services to university researchers and public and private partners. CBI is an interdisciplinary effort, building on GW's strengths in life sciences and computational science, in addition to the wealth of research centers in the Washington, DC area. Additional information on the work of CBI can be found at: http://cbi.gwu.edu/ The GWU CBI is searching for a Postdoctoral Scientist in the Goecks Research Laboratory. The Postdoctoral Scientist will conduct computational biology research in the following areas:

*innovative software development for the Galaxy platform (http://galaxyproject.org) using Python and JavaScript, including new methods for visualization, visual analytics, and parallelization;

*development of new computational methods and pipelines for analyzing large biomedical "-omics" datasets;

*using novel and existing analysis tools to process and extract patterns/information/knowledge from "-omics" datasets, with a potential focus on cancer genomic datasets.

Please send questions to Dr. Jeremy Goecks at jgoecks@gwu.edu

Minimum Qualifications: Requires a PhD in the field or in a related area.

Preferred Qualifications: Demonstrated programming experience, in the form a Github profile (ideal) or code samples is preferred, but not required.

Campus Location: Ashburn, VA

The university is an Equal Employment Opportunity/Affirmative Action employer that does not unlawfully discriminate in any of its programs or activities on the basis of race, color, religion, sex, national origin, age, disability, veteran status, sexual orientation, gender identity or expression, or on any other basis prohibited by applicable law.

Apply here: https://www.gwu.jobs/postings/32317 Thank you,

Veronica Haight Computational Biology Institute 45085 University Drive, Suite 305 Ashburn, VA 20147 vhaight@gwu.edu 571/553-0146

GeorgiaTech MarineMicrobiology

Postdoc in Marine Microbiology and Biogeochemistry

Georgia Tech is looking for a postdoctoral fellow to study the diversity and physiology of marine microbes coupling anaerobic methane oxidation to denitrification. The postdoc will be based in the lab of Dr. Frank Stewart in the School of Biology, but will work jointly between the Stewart lab and the lab of Dr. Jen Glass (Earth and Atmospheric Sciences) on a collaborative NSF-funded project. The work will involve oceanographic cruises (at least one per year) to oxygen minimum zone (OMZ) sites in the Pacific and Gulf of Mexico, shipboard and laboratory experiments, and a blend of biochemical, molecular, and bioinformatic analyses. Research tasks will involve both culture-dependent and independent methods, with the former focused on enrichments of target microbes from OMZs and the latter on comparative analysis of genomic and meta-omic datasets. The postdoc will be encouraged to develop independent lines of research within the broader goals of the project, and will work colla boratively with Dr. Stewart, Dr. Glass, international collaborators, and graduate students to perform research and synthesize results for publication.

The ideal candidate will be enthusiastic, motivated by experimental and analytical challenges, and proficient in biogeochemical and molecular microbiology techniques, ideally with experience in genomic or meta-omic analyses. Candidates should have a Ph.D. focusing on environmental microbiology or bioinformatics (or a related topic). Direct experience with anaerobic methane or nitrogen cycling or marine microbiology is highly desirable.

The School of Biology at Georgia Tech is a dynamic research environment with a strong core of researchers interested in marine systems, microbiology, and genomics. The Institute offers exceptional resources for biomolecular analysis, bioinformatics and high-performance computing, and exciting opportunities for cross-departmental collaboration with earth and atmospheric and computational scientists. Georgia Tech was recently voted one of the best places to work, and Atlanta is consistently ranked among the top ten places to live for young professionals.

This position begins in spring/summer 2016. Funding is available for at least one year, with continuation contingent upon satisfactory progress in year one; applicants should express their ability to commit to the project for at least two years. Application materials should be emailed to Frank Stewart at frank.stewart@biology.gatech.edu and should include a cover letter (describing your interest in the position, work experience, and availability), CV, and contact information (name, email, phone number) for at least three references. Please include the word "Postdoc" in the subject line. Salary will be competitive and commensurate with experience and will include fringe benefits. Review of applications will begin on February 1 and continue until the position is filled.

Informal inquiries about the position can be sent to Frank Stewart at frank.stewart@biology.gatech.edu. Additional details about the Stewart lab can be found at http://marine-micro.biology.gatech.edu/ and the Glass lab at http://www.jenniferglass.com/ Georgia Tech is a unit of the University System of Georgia and an Affirmative Action/Equal Opportunity Employer and requires compliance with the Immigration Control Reform Act of 1986.

– Frank J. Stewart, Ph.D. Assistant Professor School of Biology Georgia Institute of Technology ES&T building, office #1242 311 Ferst Drive Atlanta, GA 30332-0230 office: 404-894-5819 www.fjstewart.org "frank.stewart@biology.gatech.edu"

IndianaU EvoDevo

Postdoctoral position: Genetics and evolution of developmental plasticity, Ragsdale Lab, Indiana University

A postdoctoral position is available in the laboratory of Erik Ragsdale, Department of Biology, Indiana University, Bloomington. Our lab investigates the genetic regulation and evolution of developmental plasticity, specifically a polyphenism that involves novel morphological and ecological traits. The focal species of this research is the nematode Pristionchus pacificus, an emerging model system for evolutionary developmental genetics, which our lab studies using forward and reverse genetics, transgenics, and genome-wide approaches.

P. pacificus alternatively develops into a microbe-feeding or a predatory morph in response to different environmental cues. Recent work has begun to characterize the genes that make up a developmental switch for the polyphenism, providing an entry point into the genetics of a morphological dimorphism in a tractable animal model. Moreover, this species is embedded in a solid phylogenetic infrastructure with a broad range of feeding morphologies and ecologies. Given the laboratory availability of many species and populations of Pristionchus, this system offers a unique opportunity to discover how genetic factors and their interactions evolve to modify developmental plasticity.

The goal of the project is to determine the significance of an increasingly understood polyphenism mechanism in evolutionary process. Approaches will involve population genetics, evolutionary modeling, and/or experimental evolution. For the position, we seek a collegial and intellectually driven individual with a recent Ph.D. in evolutionary biology or a related field. A strong background in population genetics and/or evolutionary modeling is essential. Molecular biology skills are a plus but relevant training will be provided as necessary. The position will be funded for two years, with the potential to extend for an additional year. Salary will be commensurate with experience, and full benefits are included.

To apply, please submit (i) a letter of application, (ii) a full CV, (iii) a statement of research interests, and (iv) contact information for three references electronically to (http://indiana.peopleadmin.com/postings/2209). Review of applications will start immediately and will continue until the position is filled. The exact start date is flexible. Inquiries about the position can be directed to Erik Ragsdale (ragsdale@indiana.edu). Additional information about research in the Ragsdale lab can be found at: http://www.indiana.edu/~ragslab/ Bloomington is a vibrant college town located in scenic southern Indiana, close to several natural parks and wilderness areas, and it enjoys a local culture exceptionally rich in music, art, and theater.

Indiana University is an Equal Employment and Affirmative Action employer and a provider of ADA services. All qualified applicants will receive consideration for employment without regard to age, ethnicity, color, race, religion, sex, sexual orientation or identity, national origin, disability status, or protected veteran status.

Erik J. Ragsdale, PhD Assistant Professor of Biology Indiana University Bloomington, IN 47405, USA www.indiana.edu/ ~ ragslab "Ragsdale, Erik" <ragsdale@indiana.edu>

IowaStateU EvolBioinformatics-DosageCompensation

Bioinformatics PostDoctoral Position in Turtle Dosage Compensation

A postdoctoral position is available to work in the laboratory of Dr. Nicole Valenzuela at Iowa State University on an NSF-funded project to study the evolution of dosage compensation using turtles with independently evolved XX/XY and ZZ/ZW sex chromosome systems.

The project combines bioinformatics, transcriptomics, molecular cytogenetics, and phylogenetic analyses.

*Project description: Species with sex chromosomes face the challenge posed by differential gene dosage between XX and XY individuals (or ZZ and ZW) that may lead to disease, suboptimal phenotypes or death. Dosage compensation is a mechanism to equalize the activity of X- or Z-linked genes between sex chromosomes and autosomes, and between males and females. As part of this NSF-funded project we are leveraging the multiple independently-evolved sex chromosome systems found in turtles to study the evolution of dosage compensation.

The successful candidate will help uncover the full diversity of dosage compensation mechanisms and their molecular underpinnings by contrasting turtles with alternative sex-determining mechanisms, leveraging and augmenting turtle genomic resources.

*Position Requirements: The ideal candidate will have a PhD degree and strong background in bioinformatics, including genome assembly and transcriptome analyses.

Other qualifications such as evolutionary biology background or experience with molecular biology and molecular cytogenetics are a plus but not required.

*Position details: Funding is available for 2-3 years with annual renewal contingent upon performance. The position is available at any time starting February 2016.

*Application deadline: 1 February 2016, or until position is filled.

*How to apply: For inquiries or to apply please email the following to Dr. Nicole Valenzuela at nvalenzu@iastate.edu: 1. Cover letter describing research interests and experience 2. Current CV 3. Copies of up to two relevant publications if available 4. Applicants should arrange to have three letters of recommendation be sent directly to nvalenzu@iastate.edu.

Iowa State University does not discriminate on the basis of race, color, age, religion, national origin, sexual orientation, gender identity, genetic information, sex, marital status, disability, or status as a U.S. veteran.

Dr. Nicole Valenzuela Associate Professor nvalenzu@iastate.edu<mailto:nvalenzu@iastate.edu> Dept. of Ecology, Evolution, and Organismal Biology Iowa State University Office: 239 Bessey Hall 251 Bessey Hall, Ames IA 50011 URL: http://www.public.iastate.edu/~nvalenzu/ "Valenzuela, M. N [EEOBS]" <nvalenzu@iastate.edu>

IowaStateU PopGenomicsFig-FigWasp

Postdoctoral Research Associate Department of Ecology, Evolution, and Organismal Biology Iowa tate University

The Nason and Heath labs are looking to recruit a Postdoctoral Research Associate with expertise in phylo/population genomics. The successful applicant will collaborate with us on a new, NF supported project using sequence capture and GBS data to investigate the coevolutionary history of species interactions in Central American figs and their pollinating (mutualistic) and non-pollinating (antagonistic) fig wasps. Collaborators on the project include Drs. John Nason and Tracy Heath (Iowa State University), Dr. E. Allen Herre (Smithsonian Tropical Research Institute, Panama), Dr.

Charlotte JandÂÂr (Harvard University), Dr. Carlos Machado (University of Maryland), and Dr. Robert Raguso (Cornell University). Required qualifications, terms of employment, application instructions, and a project summary follow below.

Required Qualifications

Education: A PhD degree in biological sciences or bioinformatics, or acceptable equivalent combination of education and experience.

Experience/kills: Experience working with genomic/transcriptomic/GBS datasets; demonstrated experience working in a Linux/Unix shell environment; competency with at least one scripting language (e.g., Perl, Python, R). Demonstrated experience in the phylogenetic and/or population genetic analysis of NGS data, ideally obtained via sequence capture or GBS/RAD-seq methods. Well-developed organizational and time management skills, and leadership ability to direct (with the PIs) a large and productive project.

Terms of Appointment

tarting salary is $45,000 plus benefits. Funds are available for one year and are renewable for up to four years, pending satisfactory progress. The optimal start date is June 1, 2016.

Application Instructions

For consideration, applicants must apply by April 1, 2016. Informal inquiries are encouraged prior to formal application. For formal application, please send 1) a cover letter, 2) a curriculum vitae, 3) a brief statement of research experiences/interests, and 4) names and contact information for three references to Dr. John Nason (jnason@iastate.edu).

Iowa tate University is an Equal Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, age, religion, sex, sexual orientation, gender identity, genetic information, national origin, marital status, disability, or protected veteran status, and will not be discriminated against. Inquiries can be directed to the Director of Equal Opportunity, 3350 Beardshear Hall, (515) 294-7612.

Project ummary

Figs and their fig wasp pollinators and parasites have co-evolved for ˜90 million years to become both highly diverse (>750 species of figs) and ecologically important ÂÂkeystoneÂÂ± components of tropical forest ecosystems. Figs and wasps have long been assumed to represent a case of strict co-speciation, with highly specific pollinator and parasitic (non-pollinator) wasps identifying appropriate hosts via distinctive volatile chemical signals. More recent studies suggest a more complex scenario, however, involving an evolutionary history punctuated by host-shifts by individual wasp species. Although the wasp associations with fig hosts have been widely studied, the genetic consequences for the host figs of host-shifting pollinators and the mechanisms underlying host recognition remain poorly understood.

This project will fill these gaps by producing robust, detailed, many-gene phylogenies for 14 strangling fig (Ficus) species and their associated pollinating (Pegoscapus) and non-pollinating (Idarnes) fig wasps (˜60 species) from the vicinity of Barro Colorado Island, Panama. Using transcriptome sequences, we will target ˜300 genes from each of three species per lineage for capture and subsequent Illumina sequencing. Phylogenies will be inferred using Bayesian methods and will enable robust testing of phylogenetic congruence between figs and fig wasps. Further, they will guide population-level genotype by sequencing to test a priori predictions of potential cases of hybridization in the figs and host shifting and race formation in both pollinator and non-pollinator wasps. Combined with quantification of wasp-attracting fig volatiles and fruit-surface chemicals, this work will detect and resolve the genomic consequences of host introgression due to host-shifting pollinator wasps, and link them to the chemical basis of host-recognition.

This research will significantly clarify both the patterns and processes underlying the evolutionary ecology of fig and fig wasp interactions. Our standardized, genomic approach is essential for: 1) obtaining robust fig and fig wasp species trees, 2) delimiting fig species and discriminating cases of introgressive gene flow from shared ancestral polymorphism,

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London EvolutionarySystemsBiology

A postdoc position, supported by a generous career development fellowship, is available in my lab (see below). I'm happy to informally discuss potential projects (within my areas of interest and expertise) with candidates - just drop me an email.

Tobias Warnecke

Postdoctoral Research fellow (3 year fixed term)

>From Â£33712 to Â£37425 pa inclusive London, UK

We are looking for an enthusiastic, creative postdoctoral scientist to join a diverse computational/experimental research team that works at the intersection of molecular evolution, systems biology, and (more often than not) epigenetics. Recent questions we have tackled include:

- Can RNA chaperones buffer deleterious mutations (answer: yes! see Rudan et al. 2015 eLife 4:e04745) and how does buffering by chaperones affect the evolution and evolvability of their substrates? - How does chromatin architecture affect DNA sequence evolution? - Do different epigenetic marks all come with their own unique mutational burden? (Supek et al. 2014 PLoS Genet 10:e1004585) - What is the difference between prokaryotic and eukaryotic chromatin and how did complex epigenetic regulation evolve?

The ideal candidate will aim to make a major contribution to our ongoing research program and, in addition, develop and carry out his/her own line of research within the groupÂs areas of interest and expertise. Candidates keen to mix wet (E. coli, archaea) and dry lab work are particularly encouraged to apply. Candidates must have a strong publication record, excellent verbal and written communication skills, and a track record of addressing scientific problems in an innovative, thoughtful and systematic manner. Candidates with a mainly computational background should be proficient in at least one programming/scripting language (java, python, etc.) as well as R/matlab and, ideally, have experience in analysing data from high-throughput sequencing experiments (e.g. Chip-Seq, RNA-Seq). Candidates with an experimental background should have substantive experience in molecular techniques for the manipulation of prokaryotes and, ideally, experience with protein-DNA/RNA interaction assays (e.g. CLIP, ChIP). Whatever your background, a keen interest in evolutionary processes is a must.

The Clinical Sciences Centre is an Institute funded by the MRC and is a Division of the Faculty of Medicine, Imperial College. Based on the Hammersmith Hospital Campus in West London (W12), the CSC has first class facilities and provides investigators from clinical and basic science backgrounds with the opportunity to pursue innovative, multidisciplinary research within the established clinical base of Imperial College. For more information, visit www.csc.mrc.ac.uk . This post is a Career Development Fellowship to support postdoctoral scientists in early or changed career training and help establish them as successful research scientists in their chosen field. The Clinical Sciences Centre (CSC) is an institute funded by the Medical Research Council (MRC) and is a division of the Faculty of Medicine at Imperial College London, a thriving research environment with state-of-the-art facilities and equipment, including high-throughput sequencing and proteomics.

Please contact Dr Warnecke for further information about the post (tobias.warnecke@imperial.ac.uk) or apply here:

http://www.jobs.ac.uk/job/AMT203/mrc-postdoctoral-scientist/ Tobias Warnecke Group Leader Molecular Systems Group MRC Clinical Sciences Centre & Imperial College London http://csc.mrc.ac.uk/-research-group/molecular-systems/ “Warnecke, Tobias” <tobias.warnecke@csc.mrc.ac.uk>

MasseyU ComputationalFungalGenomics

Postdoctoral Fellow in Computational Fungal Genomics

I am looking for a motivated and productive postdoctoral fellow to explore the evolutionary implications of interactions between genome structure, epigenetic modification and gene expression, with a particular focus on the 3D arrangement of unraveled chromosomes in the nucleus. Using a fungal model system with direct agricultural applications (Epichloe festucae), the postdoc will validate genome assemblies using long-read data, build 3D models of genome packing in the nucleus, and explore statistical associations with gene expression using extensive transcriptome data. This position is primarily analytical with an emphasis on producing high-quality publications from existing and ongoing data collection efforts.

The position requires solid quantitative and computational skills in bioinformatics, with an emphasis on next generation sequencing and genome analysis. At minimum, a practical ability in basic scripting is required. Training in fungal biology and genomics can be provided as needed, and candidates from non-standard research backgrounds with a clear fit to the position are encouraged to apply.

Funding is guaranteed for two years. Salaries are extremely competitive, starting at NZ$68,000 (~US$46,000) per year.

The postdoc will be based in the Cox research group at Massey University, New Zealand. My research team is firmly embedded in the international scientific community, with extensive collaborative links to Australia, Europe and the United States. This position offers a rare opportunity to experience New Zealands unique natural and cultural environment, while undertaking world-leading research. Palmerston North, a university town with a large international community, offers a full range of social and cultural amenities. The city is located close to both mountains and the sea, and presents regular opportunities for hiking, skiing, surfing and adventure sports.

If you have any questions, please contact Prof Murray Cox (m.p.cox@massey.ac.nz). Information about the Cox research group (http://massey.genomicus.com) and the Bio-Protection Research Centre (http://bioprotection.org.nz) are available online.

To apply for this position, upload the following documents (in PDF format) at the official Massey University job website: http://massey-careers.massey.ac.nz/9147/postdoctoral-fellow-in-computational-fungal-genomics
1. A brief statement of research interests, qualifications and experience.

2. A curriculum vitae, including a list of scientific publications.

3. The names and contact details of three referees willing to provide a confidential letter of recommendation upon request.

Prof Murray Cox Statistics and Bioinformatics Group Institute of Fundamental Sciences Massey University Palmerston North NEW ZEALAND

http://massey.genomicus.com m.p.cox@massey.ac.nz

murray.p.cox@gmail.com

MaxPlanckEvolBiol GenomeAnalysisBioinformatics

A position for a postdoc in the field of genome analysis and bioinformatics is available in the group of Diethard Tautz (Max-Planck Institute for Evolutionary Biology, Department of Evolutionary Genetics, Ploen, Germany). The postdoc will join the sub-group working on de novo evolution of genes, funded by an ERC advanced grant. The insights into de novo evolution of genes shapes currently into a new paradigm of genome evolution (see Neme and Tautz 2014: CurrBiol 24:R38). A large genomic and transcriptomic dataset has been created for for a range of species representing the evolutionary lineage towards the house mouse (Mus musculus). Further population-level genome and transcriptome sequencing is ongoing. These data provide an excellent basis for studying in molecular detail the emergence of new genes from non-coding sequences. The postdoc will be part of a team of PhD students and postdocs who work on all aspects of de novo evolution, including functional testing in cell lines and mouse knockouts. The postdoc will also have the chance to initiate own experiments.

Qualification: PhD in genome data analysis, including programming and statistics; experience in protein structure analysis and/or population genetics would be of advantage.

Salary will be according to the TvoD 13-14 scale (depending on experience), including social benefits and pension scheme. The position is initially for two years, but can be extended.

The Max-Planck Institut for Evolutionary Biology in Ploen has developed in the past years into a major center for basic research on evolutionary topics, ranging from evolutionary genetics, evolutionary ecology, experimental evolution to evolutionary theory. It runs together with the nearby University of Kiel an international graduate program (IMPRS in Evolutionary Biology) and a Master program in Molecular Biology and Evolution. Scientists come from all over the world and the working language is english. Ploen is a small village in a beautiful postglacially shaped landscape with all the amenities of a touristically active area. Two major cities (Kiel and Luebeck) as well as the Baltic Sea are only 30-40min away, Hamburg is about 90min away (all well connected by train).

Applications should include a CV and a publication list (including papers in press or submitted), a statement of motivation, as well as two names for obtaining letters of reference. Applications should be sent by email with documents attached as pdf files to Diethard Tautz (tautz@evolbio.mpg.de).

Prof. Dr. Diethard Tautz Max-Planck-Institut fuer Evolutionsbiologie Abteilung Evolutionsgenetik August-Thienemannstrasse 2 24306 Ploen (Germany) Tel.: 04522 763 390 Fax: 04522 763 281 tautz@evolbio.mpg.de http://www.evolbio.mpg.de/15929/evolutionarygenetics Diethard Tautz <tautz@evolbio.mpg.de>

McGillU BioinformaticsEnvironmentalGenomics

Bioinformatics and Environmental Genomics Biology Department, McGill University, Canada

We invite applicants for a two-year postdoctoral position in Bioinformatics and Environmental Genomics at McGill University, Biology Department.

The position will be funded by the WSP and the Mitacs Accelerate program https://www.mitacs.ca/en/-programs/accelerate#postdoc. WSP is one of the world's leading engineering professional services consulting firms http://www.wspgroup.com. It provides services to transform the built environment and restore the natural environment, with expertise ranging from environmental remediation to urban planning, from engineering iconic buildings to designing sustainable transport networks, and from developing the energy sources of the future to enabling new ways of extracting essential resources. The Biology department offers a highly collaborative environment and excellent ecological-genomics facilities and experimental stations http://biology.mcgill.ca . The Postdoctoral Fellow will be involved in developing tools for assessing biodiversity and will use next-generation sequencing of environmental samples collected from a diversity of impacted aquatic habitats (ponds, streams, lakes, rivers). The candidate will have the opportunity to work closely with the WSP team of scientists and other industrial, governmental and academic partners. The candidate will compare results from traditional sampling techniques with biodiversity estimates based on refined metabarcoding approaches to describe the fish and invertebrate diversity within a diversity of impacted aquatic habitats. The candidate will be also involved in long-term, highly replicated laboratory and field experiments on the effect of multiple stressors on the structure and function of aquatic communities.

Experience with next generation sequencing or sequence data and related bioinformatics / computational / programming skills is strongly desired. Familiarity with one or more of the following would be an advantage: genomics, phylogenetic analyses, genome evolution / programming language (R/Unix/Python or Perl). Experience working with aquatic organisms is an asset. The candidate should have a good publication record and the ability to work well in a collaborative research environment. The position is for one year, but can be renewed for a second year and can begin as early as March 2016. Interested applicants should send their CV and a brief statement of research interest. For more information and inquiries about the position please contact Melania Cristescu at melania.cristescu@mcgill.ca.

Melania E. Cristescu Canada Research Chair in Ecological Genomics Co-Editor, Genome (http://-www.nrcresearchpress.com/journal/gen) Associate Professor Department of Biology (http://biology.mcgill.ca/-faculty/cristescu) McGill University 1205 Docteur Penfield Stewart Biology Building N6/1 Montreal, QC, Canada H3A 1B1 Ph: 514.398.1053; Fax: 514.398.5069

Melania Cristescu <melania.cristescu@mcgill.ca>

MonashU EvolutionaryEcol

Research Fellow Opportunity (Biological Sciences) at Monash University

Evolutionary Ecology

The Opportunity

Professor Dustin Marshall (www.meeg.org) is seeking an evolutionary ecologist to explore the dynamics of biological systems, specifically how size and shape affect the ways resources move through populations and communities.

As a postdoctoral researcher, you will explore how biological entities change their function as they change in size and shape, using empirical and/or theoretical approaches. The research will be conducted in collaboration with Marshall as part of the Centre for Geometric Biology at Monash University.

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.

If you believe you can fulfil these requirements, you are strongly encouraged to apply.

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

Your application must address the selection criteria.

Enquiries

Professor Dustin Marshall, +61 3 9902 4449 or dustin.marshall@monash.edu

More information can be found at;

http://www.jobs-monash.jxt.net.au/academic-jobs/research-fellow-biological-sciences-/534851 " – Henry Wootton Marine Evolutionary Ecology Group Marshall Lab Research Assistant Location: 17/104 School of Biological Sciences Monash University, Clayton Victoria 3800 Phone: +61 3 9905 5655 Email: henry.wootton@monash.edu Web: http://meeg.org/ Henry Wootton <henry.wootton@monash.edu>

OregonStateU SalmonEvolution

Post-Doctoral Research Associate

Oregon State University/Northwest Fisheries Science Center (NOAA Fisheries)

Responsibilities: We are seeking a post-doctoral associate to participate in our studies of the mechanisms and evolution of dispersal (i.e. olfactory imprinting, homing, and straying) in Pacific salmon. The post-doctoral associate will join a collaborative team of University, Federal, and State researchers working to develop tools for improving homing fidelity to salmon hatcheries. Specifically, the successful candidate will develop and conduct studies to (1) identify olfactory cues that may improve homing fidelity and, (2) identify critical periods for olfactory learning of homing cues by salmon using an interdisciplinary approach including behavioral experiments, electrophysiology, and cellular/molecular biology.

Qualifications:

Ph.D. in Zoology, Biology, Neuroscience, Fisheries Science, or a closely related field. Demonstrated research accomplishments and publications in the primary research literature. Knowledge of fish physiology, behavior, and ecology; a background in neurobiology and experience with molecular and/or electrophysiology techniques would be helpful. An ability to work independently and as part of multi-faceted research team is critical.

Salary: Competitive salary + Benefits

Start date: ASAP

Contact/Email:

Dr. David L. G. Noakes

Fisheries & Wildlife Department

Oregon Hatchery Research Center

104 Nash Hall, Oregon State University

Corvallis, Oregon

97331-3803 USA

david.noakes@oregonstate.edu

telephone: (01) (541) 737-1953 (OSU office)

(01) (541) 487-5513 (OHRC office)

Dr. Andrew Dittman

Environmental Physiology Program

Northwest Fisheries Science Center, NOAA Fisheries

2725 Montlake Boulevard East

Seattle, WA 98112 USA

andy.dittman@noaa.gov

telephone: (01) (206) 860-3392

"Johnson, Marc" <Marc.Johnson@oregonstate.edu>

OxfordU TuberculosisGenomics

We are seeking candidates with a PhD in genomics, evolutionary biology, statistics or a related subject to join our multidisciplinary team of researchers studying the evolution and genetic basis of antimicrobial drug resistance in tuberculosis (TB).

Working with TB experts from five continents we are aiming to uncover all genetic variants causing at least 1% of resistance to first-line TB drugs, building on existing approaches to genome-wide association studies in bacteria. The post is full-time and fixed-term for up to 3 years initially. This is a joint position with Prof. Derrick Crook's group and part of a larger international consortium.

For more details and how to apply, please visit http://www.ndm.ox.ac.uk/current-job-vacancies/vacancy/121787-Postdoctoral-Scientist-in-Microbial-Genomics Danny Wilson

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

PennsylvaniaStateU Archaeogenomics Paleogenomics

Postdoc Scholar in archaeogenomics and paleogenomics

The laboratory of George (PJ) Perry in the Department of Anthropology at The Pennsylvania State University is seeking applications for a postdoctoral scholar in archaeogenomics and paleogenomics. The postdoc scholar will manage the Penn State ancient DNA clean lab and will have opportunities to lead and participate in archaeogenomic and paleogenomic studies of extinct subfossil primates, prehistoric humans, human parasites, and other organisms having the potential to inform our understandings of human evolution and population history. For more information about our lab: www.anthgenomicslab.com Candidates for this position should be experienced in both ancient DNA laboratory techniques and genomics data analysis. The position will start between April and November 2016 and may be renewed annually. A qualified candidate must hold a Ph.D. degree or have completed all of the requirements for a Ph.D. by the time of appointment. To apply for this position, submit 1) a cover letter, 2) your CV, 3) the names and contact information of three people who can be contacted for letters of reference, and 4) up to three of your publications at https://psu.jobs/job/61355 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

RiceU BehaviourEvolution

Postdoctoral Research Position in Genetics of Social Behavior

A postdoctoral position is available in the Saltz lab at Rice University. Our lab is broadly interested in understanding the functional and evolutionary mechanisms that generate and maintain individual differences in social behavior, using fruit flies as a model system. More information about the lab and our work: saltzlab.wordpress.com

Position Details: The postdoc will collaborate on lab projects and pursue his or own independent research program on topics within the broad realm of individual differences in behavior. Scientists with experience in molecular and/or bioinformatics techniques, and from groups under-represented in biology, are especially encouraged to apply.

The start date is negotiable but ideally Summer or early Fall 2016. Initial appointment will be for one year with extension to a second year assuming satisfactory progress.

Community: The Saltz lab is a small and growing group of researchers that includes graduate students, a laboratory manager, and 9 undergraduate students. We value a collegial atmosphere with supportive mentoring and intellectual independence at all levels, which reinforces our shared obsession with behavior research. The Department of BioSciences at Rice University is home to a vibrant community of faculty, postdoctoral, graduate, and undergraduate researchers in Ecology and Evolution, Biochemistry, Cell Biology, Genetics and Neuroscience. We are located in Houston, Texas, an exciting, diverse, and affordable city with world-class opportunities for dining, arts, and entertainment and access to diverse terrestrial and aquatic environments. Rice is located beside one of the country's largest medical research centers, providing additional opportunities for genomics (and other omics) and bioinformatics collaborations.

Rice University is an Equal Opportunity/Affirmative Action Employer and values a diverse academic community. Women and minorities are encouraged to apply.

To apply: Please send a cover letter, a detailed CV, two letters of recommendation, and up to three relevant papers as a SINGLE PDF to Julia Saltz (julia.b.saltz@rice.edu). In the cover letter, please include a description of the independent projects you plan to pursue, how they will contribute to answering major questions in behavior or related fields, and how the work would fit into the overall goals of the lab; plus anything else you would like me to know. Review of applications will begin immediately, and continue until the position is filled.

Julia B. Saltz Assistant Professor of Ecology & Evolutionary Biology Department of Biosciences Rice University 6100 Main Street, MS-170 Houston, TX 77005 julia.b.saltz@rice.edu Saltzlab.wordpress.com

jbsaltz@gmail.com

Roscoff France MarineGenomics

Scientific project

This project is part of HAPAR ANR (Head L. Guillou), in collaboration with the ABiMS platform (Analysis and Bioinformatics for Marine Science) at the Station Biologique of Roscoff (France), the University of Ghent (S. Rombauts, Y. Van de Peer), and the Genoscope (P. Wincker, B. Porcel, France).

Microalgae can produce harmful and/or toxic blooms. These microalgae have many pathogens, especially roughly specialist eukaryotic microparasites. In cultures or in the field, these parasitoids are able to limit the growth of their host and thus to limit the impact of these blooms. These parasitoids, harmless to humans, are close to many human pathogens such as Plasmodium falciparum, the malaria agent. In the ANR project HAPAR (2014-2019), we focus on the molecular mechanisms related to the specialization of these parasites.

As part of this work a full analysis of the genomes of two parasitic dinoflagellates will be realized, one specific of a genus and one that can infect two different genera. The sequencing of these two genomes was performed and RNAseq data is already available for the annotation of these genomes, RADseq/MIG seq and proteomic data will also be available soon. These studies will highlight process (and products of metabolism) involved during host invasion.

Context The Marine Station provides to the scientific community a bioinformatics platform, ABiMS, in which the research will be conducted. The Ghent site on its side provides the ORCAE genome curation platform that will be used during the project. The postdoc will be under the responsibility of the head of the ABiMS platform with the co supervision of L. Guillou (UMR7144). He / she will interact with the different partners of the projects: the Ghent university and the Genoscope.

Missions The postdoc will be in charge of the genome, RADseq/MiGseq and RNAseq data analyses. From the first results of automatic annotation of these genomes produced by Genoscope, the postdoc will work on the improvement of the structural and functional annotation using NGS data. The study of the phylogenetic evolution of some gene families and species delineation will also be considered. Pipelines in place for the analysis will be deployed under the Galaxy platform for a valuation to the community.

Skills - Good experience of eukaryote genome annotation - Strong knowledge of NGS analysis tools and methods, and particularly in RNAseq and/or RADseq/MIGseq analysis - Good knowledge of phylogeny - Good knowledge of statistical analysis - Advanced knowledge of scripting languages (Perl, Python,$B!D(B) and/or in Linux and Unix - Global knowledge in genetics and molecular biology - Ability to work and integrate a team - Autonomy, rigor and openness

The salary is currently 1880 up to 2100 euros / month

Contract starting : as soon as possible

Location : Roscoff / France

Limited term contract with funding available for 15 months (could be extended to 24 months)

Send CV and cover letter to corre@sb-roscoff.fr and lguillou@sb-roscoff.fr before 15 of February 2016

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

RutgersU 2 EvolutionProteinTranslation

Two postdoctoral fellowships (2-3 years) and one research technician position (1-3 years) are available in the group of Dr. Premal Shah at Rutgers University at New Brunswick, NJ (http://www.theshahlab.org). The specific research project is flexible and can be tailored to the interests of the individual, but it will fall under the broad purview of evolution of coding sequences and regulation of protein translation.

1. Computational biology position:

Requirements for the position include a proven record of self-motivated research; a PhD in mathematics, statistics, physics, biology or related area; excellent communication skills. The ideal candidate should also be familiar with scientific programming and be able to handle high-throughput sequencing datasets.

2. RNA biology position:

Requirements for the position include a proven record of self-motivated research; a PhD in biochemistry, genetics, molecular biology or related area; excellent communication skills. The ideal candidate should have extensive experience in RNA biology, with an interest to work on ribosome profiling.

The postdoctoral fellows will have considerable freedom in developing their own research program, with the resources needed to distinguish themselves. In addition, the fellows will have several opportunities to interact and forge collaborations with research groups both at Rutgers as well as other institutions in the Philadelphia-New York corridor.

3. Lab Manager/Research technician position:

Requirements for the position include a bachelor's or master's degree in sciences with substantial laboratory research experience. The successful candidate will most importantly demonstrate a willingness to learn, have an ability to follow research protocols with attention to detail, and have strong organizational and record keeping skills.

The postdoctoral fellowship and technician positions provide a competitive annual stipend and health insurance. Start date and terms are negotiable. Applications are welcome from candidates of any nationality. Women and under-represented minorities are especially encouraged to apply.

Applicants should email a statement of research interests, CV, and contact details for references to premal.shah@rutgers.edu. Informal inquiries are also welcomed.

Premal Shah Assistant Professor Department of Genetics Rutgers University http://theshahlab.org Premal Shah <premal.shah@rutgers.edu>

StockholmU EvolutionaryGenomics

Post-doc position: Effects of linked selection on plant genomic variation

A two-year post-doc position in evolutionary genomics is currently available at Stockholm University/SciLifeLab, in the research group of Dr. Tanja Slotte.

Background Recent genomic studies have shown that the interaction between selection and recombination, or linked selection, can have a profound impact on genetic diversity. However, our understanding of the factors that determine variation in the type and strength of linked selection among organisms remains limited, especially in plants.

Project The post-doc will contribute to a project that aims to investigate the impact of plant mating systems on linked selection. This will involve analyses of population genomic data, coupled with simulations to assess the genomic signature of linked selection. Whole-genome sequence data sets of plant populations are already available, and more are currently being generated in the lab. The project therefore offers plenty of opportunities for the post-doc to devise analysis strategies using available genomic data.

Infrastructure and environment The Slotte lab (http://-tanjaslottelab.se) is part of the Dept. of Ecology, Environment and Plant Science, Stockholm University. We are located at Science for Life Laboratories in Stockholm (http://www.scilifelab.se), which holds considerable expertise in high-throughput sequencing technology and bioinformatics. The working atmosphere is international with English as the working language, and the position offers plenty of opportunities for scientific exchange with geneticists, evolutionary biologists and ecologists at SciLifeLab and Stockholm University. The city of Stockholm is known for its beauty, its buildings and architecture and its abundant clean and open water.

Qualifications We are looking for a post-doc with a strong background and interest in population genetics, with the prerequisite bioinformatic skills to carry out analyses of population genomic data sets. Candidates should have knowledge in at least one major programming or scripting language and be able to work in a Linux/Unix environment. A good understanding of statistics and proficiency in R is a plus. The candidate should have excellent writing skills, and be able to work both independently and as part of a team. Candidates should have a PhD in population genetics/evolutionary genetics, or a closely related field.

Application information Review of applications will begin on February 20th, 2016, and will continue until the position is filled. The position is available immediately, or as agreed upon with the successful candidate.

Applications should include: 1) a letter of interest / background (2 pages max), 2) a complete CV, including a list of publications, 3) the names and e-mail addresses of three referees, all in a single pdf file.

Applications should be sent by e-mail to Tanja.Slotte@su.se with the subject line <Postdoc application - linked selection >.

Please feel free to contact Tanja Slotte directly by email for more information about the position or questions about the project before submitting your application.

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

TexasAM PopulationGenomics

POSITION DESCRIPTION:

Postdoctoral fellowship in marine population genomics of Hawaiian 'opihi. Subthemes include but are not limited to connectivity, community managed areas, Bayesian modeling of fisheries.

PROJECT:

Assessing the efficacy of community managed areas, i.e. fine scale gene flow patterns, parentage analysis, . 2 yrs., funded by the NOAA Saltonstall-Kennedy program.

QUALIFICATIONS:

Ph.D. in a related field and experience in at least one of the following: population genetics, genomics, bioinformatics, statistical analysis, modelling, fishery ecology and management, unix/linux, computer programming

People skills are desirable

COMPENSATION:

Commensurate with skills and experience. Competitive.

OPPORTUNITIES:

Training in project management, mentoring graduate students, genomic laboratory techniques, population genomic analysis and modelling, community outreach, teaching bioinformatics for ecologists, manuscript writing, and grant writing.

RESOURCES:

HPC, high throughput genotyping laboratory, staffed Genomics Core Lab.

OTHER:

You will be expected to live in Corpus Christi, TX. There will be field work in Hawaii. I'll cover at least 1 conference per year. Two PhD and two Master's students and Dr. Rob Toonen (U Hawaii) are also involved in the project.

CONTACT:

chris.bird@tamucc.edu

Assistant Professor of Molecular Ecology

Director, Genomics Core Lab

Texas A&M University - Corpus Christi

Affiliate Faculty

Hawaii Institute of Marine Biology

"Bird, Chris" <Chris.Bird@tamucc.edu>

Toulouse GenomicClimateWarming

20 months Postdoctoral fellowship: Molecular basis of responses to climate warming in an ectotherm species

At the Department of Evolution & Biological Diversity, France (Toulouse, CNRS - UPS)

Project objectives

The position is offered within an ANR project, FRADISYN. This project aims at understanding the consequences of fragmentation and global warming on a lizard species, the common lizard (/Zootoca vivipara/). The major objective is to predict responses to global warming through plastic and evolutionary changes of dispersal behaviour and thermal physiology (heat absorption, thermal preferences).We created, in a semi-natural experimental system, several habitat patches connected by corridors and manipulated for their climatic conditions. In order to study how common lizards can adapt to global warming, we measured phenotypic variation (behaviour, melanism and thermal preferences) and life history traits (dispersal, survival, growth) through successive generations of populations maintained in different climatic conditions (e.g. Bestion et al. 2015, Plos Biol., Bestion et al. 2015 Eco. Lett.). Using this approach allows us to tease apart the influence of dispersal, selection and phenotypic plasticity into the response to climate change.

The post-doc fellow will primarily work on the molecular part of the project. Along with the monitoring of phenotypic traits, we collected DNA samples on all individuals and we recently obtained the transcriptome of few individuals characterized for their phenotype (dispersal, behaviour, melanism and thermal preferences) and from different climatic conditions. The main objective for the post-doc fellow is to detect genomic footprints of selection in response to climate change. The work will be performed in two steps: (i) thanks to this transcriptome and to the existing literature, we will select few candidate genes to be sequenced on a subset of individuals to study the selection processes which occurred during the past experiments on the basis of nucleotidic polymorphism. (ii) Furthermore, we started a long-term experiment manipulating climatic conditions and connectivity among patches in a full-crossed design. This experiment will provide the opportunity to monitor simultaneously the changes in nucleotidic polymorphism and in gene expression in response to warmer climates and fragmentation.

Task of the postdoctoral fellow

The recruited researcher will be in charge of 1) selecting candidate genes from the literature and the transcriptomic dataset, 2) performing the associated molecular biology work (extraction, PCR, sequencing), 3) collecting extra samples for gene expression analyses and performing these analyses (including qPCR) and 5) analyzing data (population genetic framework) and writing articles. This work will likely lead to, at least, two articles as a first author.

Required skills

Able to manage research and administrative activities

Knowledge in evolutionary ecology and the molecular basis of evolution.

Conceptual and technical knowledge in molecular biology

Able to actively participate as a member of a research team.

Good written and verbal communication skills

Experience with genomic data manipulation and statistical analysis

Closing of the applications: 15/02/2016Effective start date: April-May 2016

Gross monthly salary: ~1850 euro free of taxes

Applications to be sent to / Information to be taken with:

Thank you for sending CV, cover letter and contact details of at least two references.

Contact

Dr. Julien Cote

Email : julien.cote@univ-tlse3.fr <mailto:julien.cote@univ-tlse3.fr>

Website : http://www.juliencote.fr/ Dr. Delphine Legrand

Email : Delphine.LEGRAND@ecoex-moulis.cnrs.fr <mailto:Delphine.LEGRAND@ecoex-moulis.cnrs.fr>

Other people involved

Dr. Elvire Bestion, Dr. Simon Blanchet, Dr. Adam Richards, Dr. Murielle Richard, Félix Pellerin, Lucie Di Gesu.

– Dr Julien Cote 118 route de Narbonne 31062 Toulouse cedex 9 France laboratoire Evolution & Diversite Biologique UMR 5174 CNRS UPS phone: +33 (0) 5 61 55 61 97 Universite Toulouse 3 - Paul Sabatier email: julien.cote@univ-tlse3.fr

Julien Cote <julien.cote@univ-tlse3.fr>

TrinityC Dublin PopulationGenetics

Post-doc research position (18 months) in population/landscape genetics in Yvonne Buckley's population ecology research group, Trinity College Dublin.

A post-doctoral position in population/landscape genetics is available in Professor Yvonne BuckleyÂs ecology group http://www.tcd.ie/Zoology/research/research/-buckley/ in collaboration with Prof. Trevor Hodkinson's molecular systematics group https://www.tcd.ie/-Botany/staff/trevorhodkinson.php at Trinity College Dublin. The post-doc is for 18 months. You will be part of a team funded by a Science Foundation Ireland grant to develop general predictions of the ecological and evolutionary responses of plant populations to the environment.

You will work with data and samples from PLANTPOPNET, a coordinated distributed observational network for population ecology of Plantago lanceolata http://-plantago.plantpopnet.com/ . You will be co-supervised by Prof. Trevor Hodkinson (Botany, School of Natural

Sciences, Trinity College Dublin). You will develop microsatellite markers and/or use SNPs for P. lanceolata, design a sampling scheme, collect and analyse samples and analyse the resulting spatial and genetic data to determine how molecular diversity of Plantago lanceolata varies across its native and non-native ranges worldwide. There is scope to design landscape level sampling strategies in order to model population genetics at a finer scale. Additional data from PLANTPOPNET on trait distributions, population structure, density, management and environmental covariates will be available for testing hypotheses for how gene flow varies with the environment.

You will work with international networks of collaborators including, PLANTPOPNET ARC Centre of Excellence for Environmental Decisions http://ceed.edu.au/ and the COMPADRE plant matrix database http://-www.compadre-db.org/ . Yvonne Buckley is the coordinator of the PLANTPOPNET global observational network for Plantago lanceolata population biology.

Candidates will enjoy working in a collaborative team but must be highly self-motivated and work well independently. Candidates will be expected to undertake high quality research of international significance and produce peer-reviewed publications in high impact international journals. Candidates may be expected to mentor PhD students and undergraduate students undertaking projects closely related to their work. Candidates are expected (and will be supported) to present their results at an international conference during the course of their postdoc. Candidates will be expected to take part in collaborative workshops either in Ireland or overseas to lead and work with collaborators on multi-authored papers.

The closing date for application is 15/02/16 with the position to start on or after 04/04/16. This is an 18 month position.

Specific requirements for each position are given below, followed by details of the application process.

Essential criteria: 1. PhD in a relevant area in evolution, ecology, population biology, genetics, plant sciences or zoology. 2. Experience in laboratory and analytical population genetics with SSRs and/or SNPs.

Desirable criteria: 1. High quality publications in international peer reviewed journals 2. Experience with developing and using population models 4. Use of R for data manipulation and analysis 5. Experience with comparative analysis using modern phylogenetic and population genetic methods 6. Experience with population genetics and/or landscape genetics software 7. Experience working in multi-author collaborations/workshops 8. Experience with GIS 9. Experience with database design and/or use 10. Bioinformatics experience

Qualifications: For all positions the candidateÂs PhD must have been attained by 01/04/2016.

Salary range: Post-doctoral salary is based on the Irish Universities Association researcher salary scales for entry level postdoctoral researchers: The gross salary is Â37,750 (+ pension contributions). Applications for part-time positions will be considered (pro-rata salary).

Facilities The postdocs will be based in the Zoology Building, Trinity College Dublin and use resources in the Botany and Zoology buildings and with collaborators/co-supervisors. The post-doctoral researchers will have access to a newly renovated terrestrial ecology lab and a population genetics lab.

Application process Send an email to buckleyy@tcd.ie with an attached cv, the names of two referees, a full publication list, and cover letter addressing all of the essential criteria and giving evidence for the desirable criteria which you meet. Use one paragraph of the cover letter to outline your

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UArizona FungalEvolution

The Arnold lab at the University of Arizona (www.arnoldlab.net) seeks a postdoctoral researcher as part of a recently funded, collaborative project supported by the National Science Foundations Genealogy of Life (GoLife) program. The project centers on enriching phylogenetic knowledge of the Pezizomycotina through new collections of endophytic and endolichenic fungi, with special attention to the evolution of symbioses with photosynthetic prokaryotes and eukaryotes. The position will begin on or near April 15, 2016, with an expected duration of two years (potentially expandable to three).

The position will be based in Tucson, Arizona, in the School of Plant Sciences and in affiliation with the Department of Ecology and Evolutionary Biology, with opportunities for fieldwork in Panama, Chile, South Africa, and Borneo. The project represents a collaborative network with researchers at Duke University, North Carolina State University, the University of Connecticut, and the University of Mississippi, with ample opportunity for interactions among labs. The position also includes a meaningful outreach component to foster training in STEM for local high school students and opportunities to mentor undergraduate researchers from diverse backgrounds.

Minimum requirements: a PhD in ecology, evolutionary biology, microbiology, plant pathology, or a related discipline, and a strong background in molecular and/or fungal ecology (including next-generation sequencing), biodiversity informatics, computation, and/or mycology. Preferred candidates will have diverse research interests, excellent communication skills, high motivation, and a strong willingness to work independently and as part of an integrative team.

Home to the world-class University of Arizona, Tucson is a vibrant southwestern city with a rich and distinctive heritage, fabulous access to outdoor activities, and diverse opportunities for cultural engagement. The University of Arizona is currently in a dynamic phase of hiring new faculty, making the timing ideal for a candidate interested in engaging with a major initiative in ecosystem genomics.

At the University of Arizona, we value our inclusive climate because we know that diversity in experiences and perspectives is vital to advancing innovation, critical thinking, solving complex problems, and creating an inclusive academic community. We translate these values into action by seeking individuals who have experience and expertise working with diverse students, colleagues and constituencies. Because we seek a workforce with diverse perspectives and experiences, we encourage minorities, women, veterans, and individuals with disabilities to apply. As an Employer of National Service, we also welcome alumni of AmeriCorps, Peace Corps, and other national service programs.

Applicants should submit a cover letter, CV, copies of three recent publications, and a one-page lesson plan for a hands-on, one-day activity to teach a core concept in fungal biology, ecology, or evolutionary biology at the high school level. All application materials should be submitted in a single email to arnold@ag.arizona.edu (please put GoLife postdoc in the subject line) AND to the University of Arizona Human Resources website (https://uacareers.com, posting # P20132). Please also arrange for three letters of recommendation to be submitted as above.

Application review will begin on Jan. 20, 2016, and will continue until the position is filled.

A. Elizabeth (Betsy) Arnold School of Plant Sciences The University of Arizona Tucson, AZ 85721

http://arnoldlab.net barnoldaz@gmail.com

barnoldaz@gmail.com

UCalifornia Berkeley 3 EvolutionAntSociality

JPF00959

The Department of Environmental Science, Policy, and Management at UC-Berkeley is currently seeking one Postdoctoral Scholar in *Chemical Ecology *in the laboratory of Dr. Neil Tsutsui. We are seeking a Postdoctoral Scholar to study the chemical basis of ant social behaviors. Previous work has focused on the genetics, behavior, and chemical ecology of the invasive Argentine ant (*Linepithema humile*). The central focus of the Postdoctoral Scholar's research will be the chemical communication in social insects, including the production and perception of pheromones that Argentine ants use to regulate fundamental behaviors, including foraging, queen production, and colonymate recognition.

BASIC QUALIFICATIONS

Candidates must have completed all degree requirements except the dissertation or be enrolled in an accredited PhD or equivalent degree program in biology, chemistry, or related field at the time of application.

ADDITIONAL QUALIFICATIONS Candidates must have a PhD, MD, or equivalent degree in biology, chemistry, or related field by appointment start date.

PREFERRED QUALIFICATIONS Demonstrated expertise in chemical analysis using gas chromatography-mass spectrometry (GC-MS). Candidates fluent in chemical, genetic, and/or biochemical analysis of insect pheromones or experienced studying the mechanisms of chemoreception are desirable. Preferred candidates will demonstrate excellent communication skills and the ability to work both independently and as a member of a small team. Applicants must have fewer than five years of prior post-doctoral experience.

APPOINTMENT The targeted start date for this position is March 1, 2016. The initial appointment is for one year, with renewal based on performance and funding. This is a full-time appointment.

SALARY AND BENEFITS The salary range is between $42,840 - $50,112 commensurate with qualifications and experience and based on UC Berkeley salary scales. Generous benefits are included (http://vspa.berkeley.edu/-postdocs)

TO APPLY Visit: https://aprecruit.berkeley.edu/-apply/JPF00959 Interested individuals should include a 1-2 page cover letter describing their research experience, 1-3 relevant publications, a current CV, and the names and contact information of three references. Letters of reference may be requested for finalists. It is optional to include a statement addressing past and/or potential contributions to diversity through research, teaching, and/or service.

This position will remain open until filled.

Questions regarding this recruitment can be directed to Professor Neil Tsutsui (ntsutsui@berkeley.edu).

All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are provided via a third party (i.e. dossier service or career center) to the UC Berkeley Statement of Confidentiality (http://-apo.berkeley.edu/evalltr.html) prior to submitting their letters.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: http://policy.ucop.edu/doc/4000376/-NondiscrimAffirmAct The Department is interested in candidates who will contribute to diversity and equal opportunity in higher education through their research or teaching.

The University of California, Berkeley has an excellent benefits package as well as a number of policies and programs in place to support employees as they balance work and family.

JPF00958 < https://aprecruit.berkeley.edu/apply/-JPF00958 >

The Department of Environmental Science, Policy, and Management at UC Berkeley is currently seeking two Postdoctoral Scholars in *Genomics and Functional Genetics* in the laboratory of Dr. Neil Tsutsui. We are seeking two Postdoctoral Scholars to study the genetic basis of ant social behaviors. Previous work has focused on the genetics, behavior, and chemical ecology of the invasive Argentine ant (Linepithema humile). The central focus of the Postdoctoral ScholarsÂ research will be the genetic basis of chemical communication, including the production and perception of pheromones that Argentine ants use to regulate fundamental behaviors, including foraging, queen production, and colonymate recognition.

BASIC QUALIFICATIONS Candidates must have completed all degree requirements except the dissertation or be enrolled in an accredited PhD or equivalent degree

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UCalifornia Merced PlantAdaptation

A postdoc position in ecological/evolutionary modeling is available at UC Merced in the Moran lab (https://-sites.google.com/site/emilyvmoran/). Our research focuses on the ecological and evolutionary responses of plants to climate change. The aim of this postdoctoral project would be to develop an individual-based forest model incorporating both species differences and genetic differences in environmental responses, in order to investigate the importance of evolutionary responses relative to species range shifts under different scenarios of climate change and disturbance. We have already parameterized SORTIE with average growth, mortality, and dispersal parameters for Sierra Nevada tree species. The next steps will include fitting species-level climate response functions using a 30-year dataset, and incorporating heritability of climate responses. Our group will also be collecting field data with which will aid in further parameter refinement.

The initial appointment will be for one year and is renewable, depending on performance and availability of funding. The salary and benefits package associated with the position are based upon those established by the University of California.

Qualifications:

Candidates must have completed a Ph.D. in biology, ecology, modeling, or similar discipline, and have experience programming in C++. Experience with forest models would be particularly valuable. Experience with Bayesian modeling is also desirable. The candidate must also be creative, self-disciplined, and motivated. Additional desirable skills include experience with statistical methods and/or R programming.

Applications will be evaluated based on past research productivity, alignment of applicant experiences and interests with the goals of the lab group. The top-ranking applicants will be invited to interview by Skype, phone, or in person.

Salary:

Salary is based on the University of California Academic Salaries Scale.

To Apply:

Review of applications will begin February 2, 2016. To ensure full consideration please apply before February 8. Ideally, the start date will be in March.

To apply, please submit 1) a cover letter explaining your interest in and qualifications for the position, 2) academic CV, and 3) contact information for three references. Applications must be submitted via this website: https://aprecruit.ucmerced.edu/apply/JPF00286 . UC Merced, which opened in September 2005, is the newest school of the 10-campus University of California system (http://www.ucmerced.edu/). The university is still small (6,300 students, 270 faculty), but is diverse and rapidly growing. Merced is a town of 80 thousand people located in the central valley. It is conveniently located 1 hour north of Fresno (the closest airport), 2 hours east of Berkeley and San Francisco, 2 hours south of Davis and Sacramento, and 2 hours west of Yosemite National Park. Cost of living is relatively low.] - ecolog style. The University of California, Merced is an affirmative action/equal opportunity employer with a strong institutional commitment to the achievement of diversity among its faculty, staff, and students.

As of January 1, 2014 the University of California, Merced will be a smoke and tobacco free workplace. Information and the Smoke and Tobacco Free policy is available at http://smokefree.ucmerced.edu For more information: Please contact Emily Moran (emoran5@ucmerced.edu)

“emoran5@ucmerced.edu” <emoran5@ucmerced.edu>

UCapeTown AvianCoevolution

Post-doctoral research opportunity at the Percy FitzPatrick Institute of African Ornithology, Department of Biological Sciences, University of Cape Town

Project: Sociable Weaver nests as a resource to animal communities and the life history of the obligate associate African Pygmy Falcon

We invite applications for the above full-time research opportunity at the FitzPatrick Institute, a world-renowned, national Centre of Excellence (CoE) in ornithological research with a strong emphasis on postgraduate studies. The tenure of the Fellowship is for 2 years, with possible extension to a 3rd year considering satisfactory academic progress and availability of funds.

The successful applicant will focus on the interactions in animal communities associated with Sociable Weaver (Philetairus socius) nests, with particular focus on the role of the closely associated African Pygmy Falcon (Polihierax semitorquatus). The candidate will conduct research with Dr Robert Thomson. Applicants must have strong analytical skills, including a demonstrated expertise in programming with R. Supervision experience of post-graduates and a good publication record for the career stage are also desirable.

This project examines the importance of Sociable Weaver nests to a desert animal community and the role of African Pygmy Falcons in these communities. The exact research questions will be tailored to, and developed with, the successful candidate. The research could focus on the diet, behaviour, demography and physiology of the African Pygmy Falcon, investigating how the evolution of the species life history strategy is linked to its obligate association with Sociable Weaver nests (weaver nests provide the only nesting substrate used by the falcons in southern Africa). The research could also use the falcon-weaver system as a co-evolutionary model to understand the interplay between climate and biotic interactions in shaping the South African distribution of these two species. Areas of mismatch (where weavers are present but not falcons) could be identified and additional fieldwork would enable to collect environmental data aimed to explain the absence of Pygmy falcons in these areas. Ultimately, by integrating multi-species interactions into an ecological niche modelling framework, this project will offer a unique opportunity to predict the future range of this Kalahari falcon under different scenarios of climate change.

The researcher could also help supervise a recently initiated and closely linked PhD project investigating the diversity of species utilizing weaver nests and their interactions in an aridity gradient across the weaver range. Conditions of the award of a Postdoctoral Fellowship at UCT are: (i) postdoctoral fellowships are only available to individuals who have achieved a doctoral degree in a relevant subject within the past 5 years. (ii) applicants may not previously have held full-time professional or academic employment. (iii) the successful incumbent may, as part of their professional development, be required to participate in departmental activities including limited student supervision and duties incidental thereto. (iv) the successful incumbent will be required to comply with UCTs approved policies, procedures and practises for the postdoctoral sector.

It is expected that the candidate will submit papers to high quality peer-reviewed journals within the fellowship term.

The value of the Fellowship is R180 000 per annum. The Fellowship is compliant with the SARS guidelines and rules and is exempt from taxation. Adequate project running costs are available.

The successful incumbent should be available to commence with the Fellowship in the first half of 2016, although flexibility might be required if a non-South African resident is successful.

To apply, please send a CV (including your academic record, publication list & the names and contact details of two academic referees) plus a short motivation letter to Hilary Buchanan at hilary.buchanan@uct.ac.za. Informal enquires can be directed to Robert Thomson: robert.thomson@uct.ac.za.

For more information on the FitzPatrick Institute visit www.fitzpatrick.uct.ac.za Closing date: 15 January 2016 (possible interviews to be held in January) UCT is committed to the pursuit of excellence, diversity and redress. UCT reserves the right to disqualify ineligible, incomplete and/or inappropriate applications, and reserves the right to change the conditions of award or to make no awards at all.

UNIVERSITY OF CAPE TOWN

Robert Thomson <robert.thomson@uct.ac.za>

UExeter EvolutionInsectAntibiotic

New post-doctoral position available with Ben Raymond and Angus Buckling at the University of Exeter Penryn campus. This is an 18 month project looking at how best to use phage to combat the evolution of plasmid borne antibiotic resistance in insect/gut bacteria model systems. More details available at http://tinyurl.com/-gw6trjk < https://t.co/HnqeEibF1L > or contact b.raymond@exeter.ac.uk or A.J.Buckling@exeter.ac.uk

“Raymond, Ben” <B.Raymond@exeter.ac.uk>

UFlorida TropicsEvolution

The International Center at the University of Florida is pleased to invite applications for the John J. and Katherine C. Ewel Fellowship Program in Ecology and Environmental Science in the Tropics and Subtropics. This program will enable a recent doctorate recipient to study ecology and environmental sciences at the University of Florida (UF). The Fellow will work for two years with a University of Florida faculty member in any department to create new knowledge in any area of tropical and subtropical ecology. For complete details, criteria and application for, please visit http://ufic.ufl.edu/-OGRE/EwelFellowship.html Marta L. Wayne, Ph. D. Professor and Chair P.O. Box 118525 Department of Biology University of Florida Gainesville, FL 32611-8525 (courier: 876 Newell Drive) vox: 352-392-9925 fax: 352-392-3704 http://people.biology.ufl.edu/mlwayne/site/ mlwayne@ufl.edu

UHaifa Evolution

Biology, mathematics, computer science and bioinformatics students/researchers are needed

Dr. Livnat’s new lab for the study of evolution at the University of Haifa in Israel is seeking applications for Ph.D, postdoc, lab manager and other positions from individuals with a background in biology, mathematics, computer science or bioinformatics and a record of past excellence.

We study the deep principles of how evolution works both theoretically and experimentally. 1) Students with a background in theoretical computer science or other branches of mathematics may participate in work at the interface of evolutionary biology and theoretical computer science whose goal is to form a new mathematical framework for evolution. Our lab works in collaboration with leading computer scientists abroad and in Israel. 2) Students with a background in bioinformatics and students with molecular biology lab skills may participate in evolutionary research involving cutting-edge sequencing methods. 3) Students interested in the evolution of behavior are also encouraged to apply.

Applicants should send a cover letter and a CV to alivnat@univ.haifa.ac.il, including the names of 2-3 references. More info at http://sci3.haifa.ac.il/˜alivnat/
adi.livnat@gmail.com

UHalle Germany ViralBeeEvolution

3 year postdoc on viral evolution in bees

A postdoctoral researcher is sought for a newly funded project on the evolutionary ecology of viruses in bees within Robert Paxtons lab at the University of Halle, Germany. The overarching goal of the research is to understand the role of viral epidemiology and evolutionary change for pathogen emergence and host switching; the project is embedded within the DFGs priority program: Ecology and Species Barriers in Emerging Viral Diseases (SPP 1596). Research will involve lab and field-based experiments (in Germany and the UK V in very picturesque countryside) as well as molecular genetic analysis of viruses. We seek a highly motivated individual with experience in or knowledge of virology and bioinformatics, an interest in host-parasite interactions, and molecular genetic skills in the lab. Two pre-requisites are a valid driving licence and the ability or willingness to work with honey bees.

The working language of the lab is English. The neighboring group of Robin Mortiz makes for a strong profile in bee biology and genetics at the University of Halle. The position is available for 3 years and, though the start date is flexible, we seek a person to commence research during spring 2016. Halle is a delightful, historical city approximately 1.5 hours SW of Berlin. The salary is on the standard German postdoc scale E13, which translates to approximately Euro 51-57 K per annum (dependent on experience).

Further details of the position can be obtained from Robert Paxton (robert.paxton@zoologie-uni-halle.de), to whom applications should be sent by 23 February 2016 as a single pdf file to include: cover letter referring to 5-374/16-D, cv, list of publications, a statement of research interests and goals (maximum 1 page), and contact details of two referees. Interviews are planned for the first week of March 2016, with a start date in April or as soon as possible thereafter.

Robert Paxton <robert.paxton@zoologie.uni-halle.de>

UHelsinki EvolutionaryGenomics

A 2 YEAR POST DOCTORAL RESEARCHER POSITION is available in the research group of Assistant Professor Arild Husby. The successful applicant will be part of the Centre of Excellence in Metapopulation Research at the Department of Biosciences, University of Helsinki.

The main goal of the post doc project is to examine DNA methylation patterns in relation to timing of breeding using the great tit (Parus major) as a model species. Substantial genomic data is available for this species, including a high quality annotated whole genome sequence, transcriptome and methylome. The successful candidate will examine DNA methylation patterns using targeted bisulphite sequencing of previously identified candidate genes. DNA methylation levels will be compared among two experimental groups using blood samples already collected. In addition, the candidate will be involved in some field work to collect additional data to examine trans-generational DNA methylation patterns. The work will be performed in close collaboration with Prof. Marcel Visser and Dr Kees van Oers at the Netherlands Institute of Ecology (https://nioo.knaw.nl/en/-department-animal-ecology). Fieldwork will be carried out in the Hoge Veluwe national park near Wageningen, The Netherlands and in a recently established nestbox population close to Viikki campus, Helsinki, Finland.

The successful candidate should have PhD / postdoctoral experience within the fields of evolutionary genomics with previous experience in sequence based analysis of DNA methylation data and strong bioinformatic skills. Excellent written and verbal communication skills in English are required and you must also demonstrate ability to work as part of a team.

The position will have a probationary period of four months. The starting date is flexible but preferable before 15th April 2016.

The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal work performance.

To apply, please send, in a single pdf file, your CV with publication record included and a letter (max 2 pages) with a description of your research interests and, in particular, why you would be a suitable candidate for the project. The application letter should also contain possible starting dates and contact details of three references. The applications are to be addressed to Dr Arild Husby and submitted to biotiede-mrg@helsinki.fi by 10th February 2016 at 15.45 local Helsinki time.

The University of Helsinki, founded in 1640, is one of the world's leading universities for multidisciplinary research. The university has an international academic community of 40,000 students and staff members. The University of Helsinki offers comprehensive services to its employees, including occupational health care and health insurance, sports facilities, and opportunities for professional development. The International Staff Services < http://www.helsinki.fi/intstaff/ > office assists employees from abroad with their transition to work and life in Finland.

The Department of Biosciences situated at the Viikki science park belongs to the Faculty of Biological and Environmental Sciences of University of Helsinki and is the largest research and teaching unit in biosciences in Finland. The Department of Biosciences is one of the largest departments of Helsinki University with its c. 25 million euro budget and over 400 staff members. Cutting edge infrastructure is available at all levels, including high-performance computer clusters, a next-gen sequencing facility, as well as molecular labs.

For more information about this position, please contact Dr Arild Husby (arild.husby@helsinki.fi), see also our lab website: blogs.helsinki.fi/husby

Arild Husby, Assistant Professor Department of Biosciences (Biocenter 3, office 5415), University of Helsinki PO box 65, FI-00014 Helsinki, Finland

web: http://blogs.helsinki.fi/husby/ mail: arild.husby@helsinki.fi office phone: +358294157691

"Husby, Arild" <arild.husby@helsinki.fi>

UIllinois UrbanaChampaign GenomicBiology

Postdoctoral Fellowship

University of Illinois at Urbana-Champaign Urbana-Champaign, Illinois (USA) 50,000.00 Postdoctoral Fellowships in Genomic Biology at the University of Illinois at Urbana-Champaign

The Carl R. Woese Institute for Genomic Biology at the University of Illinois at Urbana- Champaign offers a number of fellowships for truly exceptional young scholars who have completed their Ph.D. within the last several years, and are looking for a stimulating and supportive interdisciplinary environment to carry out independent and collaborative research in the field of genomic biology. IGB Fellows will typically spend two years conducting research in one of several research themes in the Institute, and ideally this research will also overlap with two or more of these thematic areas. A personalized mentoring plan will be developed for each Fellow. Annual salary is $50,000. Applicants should submit their information and letter of intent to aweckle@illinois.edu. The closing date for all positions if January 29, 2016. Fellows will be announced on or about February 15, 2016.

Computing Genomes for Reproductive Health

We seek an individual with both a computational and clinical background to conduct research on the evolution of pregnancy and the development of human obstetrical syndromes. The Fellow will lead interactions between clinical service providers and basic scientists. They will conduct independent research while working with study coordinators, electronic medical records, and multi-omics high dimensional datasets. The ideal candidate will strengthen a multidisciplinary team working to drive advances in the field of reproductive medicine through the study of interactions among genes, their products, organisms, and environments. The theme takes a precision medicine-based approach to research obstetrical syndromes and the developmental origins of health and disease.

(Derek Wildman, Theme Leader). MD, PhD or MD/PhD required.

The University of Illinois is an Affirmative Action/Equal Opportunity Employer. The Carl R. Woese Institute of Genomic Biology is a pioneer in advancing life sciences research with program areas in systems biology, cellular and metabolic engineering, and genome technology. Visit www.igb.illinois.edu for additional information.

http://jobs.sciencecareers.org/job/390484/postdoctoral-fellowship/ Amy Weckle Senior Research Specialist Laboratory of Dr. Derek Wildman Computing Genomes for Reproductive Health Carl R. Woese Institute for Genomic Biology University of Illinois, Urbana-Champaign 1206 West Gregory Drive MC195 Urbana, IL 61801 ph (desk): 217-300-2101 Ph (lab): 217-333-2430

"Weckle, Amy Lorraine" <aweckle@illinois.edu>

forbes@uiowa.edu>

UIowa InsectEvolution

The Forbes Lab in the Department of Biology at the University of Iowa is seeking a highly motivated evolutionary ecologist with an interest in tropical insect diversity and expertise in population genomics for a 2-3 year postdoctoral position funded by NSF's Dimensions of Biodiversity Program.

Job Summary: The aim of the project is to examine patterns of present day and historical gene flow among species in the tephritid fruit fly genus Blepharoneura and the same for the Bellopius parasitoid wasps that attack Blepharoneura flies. These flies and wasps are highly host-specific, incredibly diverse, and many species often overlap in their apparent niche space. A major goal is to understand why these insects are so diverse. The postdoc will develop and score double-digest RAD markers for several existing fly and wasp collections from across Central and South America, use those data to model gene flow and migration within each fly and wasp species, and collaborate with other project participants to test hypotheses regarding species interactions and the origin of reproductive isolation in these hyper-diverse insect systems. More information about this system can be found in the following two publications:

http://www.sciencemag.org/content/320/5878/-928.short http://www.sciencemag.org/content/343/-6176/1240.short

Education required: * PhD in evolutionary biology or closely related field

Desirable Qualifications: * Experience developing and working with RAD-based marker system (or similar marker system) in non-model organisms * Strong background in population genetics / genomics * Interest in diversification, insect evolutionary ecology, insect population genomics, or related field * Interest in working as part of a collaborative research team

Preferred Starting date: September 2016 (negotiable)

Application Deadline: April 15th, 2016, or until position is filled

How to apply: send C.V., a letter of inquiry, two representative publications (if available), and contact information for three potential referees to: andrew-forbes@uiowa.edu

"andrew-forbes@uiowa.edu" <andrew-forbes@uiowa.edu>

UKentucky EvolutionaryGenomics

The Linnen Lab in the Biology Department at the University of Kentucky is seeking a full-time postdoctoral researcher to participate in a USDA-funded project that uses comparative genomics to investigate the genetic basis of ecological specialization in plant-feeding insects. The ultimate goal of the project is to test the hypothesis that changes in host use involve predictable genetic changes. To test this hypothesis, we are combining chemosensory gene annotations and host-use data from an experimentally tractable and well-studied group of pine-feeding insect pests in the genus *Neodiprion* (Hymenoptera: Diprionidae). This project dovetails with ongoing work in the lab that seeks to understand both the causes (molecular mechanisms) and consequences (population divergence and speciation) of phenotypic variation. For additional details about current research in the lab, please visit our website: http://www.linnenlab.com/ . The ideal candidate will be independent, organized, and motivated and have a keen interest in using genomic/transcriptomic data to address fundamental questions in evolutionary biology. Candidates should have a Ph.D. in evolutionary biology, genetics/genomics, or a related field. Interest/experience in developing functional approaches for non-model organisms is also desirable. Importantly, we are looking for someone who is personable and enthusiastic about working in a collaborative environment.

The preferred start date is Spring or Summer 2016 (negotiable) and funding is available for 2-3 years. Salary is commensurate with experience and includes benefits.

Interested candidates should submit a cover letter describing research interests/experience and a full CV with contact information for three references. Application materials and all queries should be sent to: catherine.linnen@uky.edu. Review of applications will begin immediately and will continue until the position is filled.

The University of Kentucky is an equal opportunity/affirmative action employer. Women, persons with disabilities, and members of other underrepresented groups are encouraged to apply.

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Catherine R. Linnen, Ph.D. Assistant Professor Department of Biology University of Kentucky 200A Thomas

Hunt Morgan Building Lexington, KY 40506 Email: catherine.linnen@uky.edu Website: www.linnenlab.com Phone: 859-323-3160

clinnen@gmail.com

UMichigan YeastEvolGenetics

A postdoctoral position is available immediately in the laboratory of Jianzhi "George" Zhang at University of Michigan, Ann Arbor, Michigan. The ideal candidate will use the budding yeast Saccharomyces cerevisiae and its relatives as model organisms to study evolutionary processes. Potential topics include but are not limited to (1) the fitness effects of various mutations including gene duplication, (2) genic/genomic basis of reproductive isolation, (3) evolution of dominance, (4) genetic mechanisms of heterosis, (5) evolution of gene essentiality, and (6) evolution of gene expression level and noise. The position requires a motivated individual with an interest in evolutionary genetics and wet lab experience in molecular genetics or genomics. Prior training in yeast genetics is a plus.

Applicants should email a short statement of research interests, CV, and contact information of three references to jianzhi@umich.edu. For further information about the Zhang lab, see http://www.umich.edu/~zhanglab/ . "jianzhi@umich.edu" <jianzhi@umich.edu>

UMinnesota HumanMicrobiomeGenomics

Two postdoctoral positions are available at the University of Minnesota - Twin Cities with Ran Blekhman (http://blekhmanlab.org)

The Blekhman Lab (http://blekhmanlab.org) is broadly interested in human genomics and host-microbiome interactions. The lab is based jointly in the Departments of Genetics, Cell Biology, and Development (http://gcd.umn.edu), and Ecology, Evolution, and Behavior (http://cbs.umn.edu/eeb). The successful candidates will work on a major research project is the lab, focused on understanding the mechanism and evolution of host-microbiome interactions and their implications for human health. The lab integrates human genomic and microbiome data to understand the genomic basis of host-microbiome interactions, how these interactions affect complex traits and disease, and how the symbiosis between us and our microbiome is affected by human ecological adaptations. The details of the specific project are flexible, and will depend on the expertise and interests of the successful candidate. Our recent relevant publications:

Host genetic variation impacts microbiome composition across human body sites. Blekhman et al., Genome Biology (2015)

Virulence genes are a signature of the microbiome in the colorectal tumor microenvironment. Burns et al., Genome Medicine (2015)

Variation in Rural African Gut Microbiota Is Strongly Correlated with Colonization by Entamoeba and Subsistence. Morton et al., PLOS Genetics (2015)

Temporal variation selects for diet-microbe co-metabolic traits in the gut of Gorilla spp. Gomez et al., ISME J (2015)

Social networks predict gut microbiome composition in wild baboons. Tung et al. eLife (2015)

Human genetics shape the gut microbiome. Goodrich et al., Cell (2014)

- Qualifications The ideal candidate would be highly motivated to conduct independent research, and hold a PhD in genetics, bioinformatics, evolutionary biology, computer science, statistics, microbiology, anthropology, or a related field, with a solid publication record. Candidates should have a strong analytical background, have experience with analysis of next-generation sequence data, and proficiency with computer and statistical programing languages. The successful candidates will enjoy a highly competitive salary and benefits package.

- Why The University of Minnesota? Founded in 1851, the University of Minnesota (http://umn.edu) is one of the largest, most comprehensive universities in the United States, and ranks among the most prestigious research universities in the world. The University provides a highly collaborative environment with cutting edge research institutions and facilities, including the Microbial and Plant Genomic Institute (www.mpgi.umn.edu), the Biotechnology Institute (http://bti.umn.edu), and the University of Minnesota Genomics Center (http://www.bmgc.umn.edu). Additionally, we are working with the Minnesota Supercomputer Institute (http://msi.umn.edu), which provides excellent infrastructure and support for high-performance computation.

- Why The Twin Cities? The Minneapolis-St. Paul metropolitan area is one of the most desirable places to live in North America. The Twin Cities are consistently ranked at the top in quality of life, personal safety, green spaces and parks, arts and culture, public schools, personal health, and are among the best cities to raise a family in the United States. For more information on living in the Twin Cities, see http://-umn.edu/wishyouwerehere/welcome .

- How to Apply Interested candidates are encouraged to contact Ran Blekhman by email (blekhman ˜ umn.edu), and provide a brief cover letter detailing research experience and interests, a CV, and contact information of three references. Informal enquires are welcome. Applications will be accepted starting immediately and until the positions are filled.

The University of Minnesota is an equal opportunity educator and employer

— Ran Blekhman, Ph.D. | Assistant Professor | University of Minnesota, Twin Cities Dept. of Genetics, Cell Biology, and Development | Dept. of Ecology, Evolution, and Behavior MCB 6-126, 420 Washington Avenue SE, Minneapolis, MN, 55455 Cargill 222, 1500 Gortner Ave., St. Paul, MN 55108 BlekhmanLab.org | Twitter: @blekhman < http://twitter.com/blekhman > | Phone: (612) 624-4092 | Fax: (612) 624-6264

“blekhman@umn.edu” <blekhman@umn.edu>

UMuenchen PDF 3PhD CancerEvolution

\f0\fs24 \cf0 \expnd0\expndtw0\kerning0 PostDoc: Single cell genomics for cancer evolution\ \ While the evolutionary nature of cancer is well established, it is challenging to generate and analyze data to quantify the dynamics of this Darwinian\'a0process. The clinical issue is for example when therapy-resistant cancer cells regrow after an initially successful treatment. Hence, patients die because\'a0the tumor is able to evolve. Hematologic neoplasms such as leukemia and lymphoma are well suited to study this process, because live cells can be\'a0sampled and studied in detail over the course of the disease. To better understand and eventually influence this process, it is necessary to measure the\'a0amount of genetic and epigenetic heterogeneity. New technologies to characterize genetic and phenotypic heterogeneity at the single cell level render it\'a0possible to tackle this issue.\ \ For further information please see\'a0www.sfb1243.bio.lmu.de/'a0and/-'a0Enard lab.\ \ Your Opportunities & Responsibilities\ \'95 Work on an exciting project that bridges genomics, evolutionary theory and oncology and will strengthen your profile in a field of great scientific\'a0and medical relevance.\ \'95 Investigate heterogeneity of hematologic neoplasms on the single cell level.\ \'95 Optimize established transcriptional single cell technologies (Fluidigm C1, SCRB-seq, Drop-seq) to elucidate new mechanisms in the evolution of\'a0AML in close collaboration with other CRC groups. This includes the molecular techniques as well as analyses.\ \'95 Make established single-cell technologies (Fluidigm, SCRB-seq, Drop-seq) available to collaborations within the SFB. This includes the molecular\'a0techniques as well as first analyses.\ \'95 Improve and extend the existing single cell technologies to combine RNA-seq, DNA-seq, and/ or ATAC-seq.\ Your Profile\ \'95 You should hold a doctoral degree or PhD in biology, molecular biomedicine, biotechnology or a related subject.\ \'95 You should have a strong background in molecular genomic wet-lab methods (e.g. RNA-seq) , ideally in a cancer-related field.\ \'95 You should enjoy working in collaborations.\ \'95 You should be open to learn and apply statistical and computational skills to analyze genomic data (R).\ \ Online applications are now being accepted until\'a0February 21, 2016. Please apply solely viahttp://portal.graduatecenter-lmu.de/-ocgc/sfb1243. Choose\'a0A14 as priority.\ The position should start as soon as possible and is for a period of up to 4 years. The LMU is an equal opportunity employer. Preference will be given to\'a0suitably qualified female applicants or handicapped people, all other considerations being equal.\ \ }

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\f0\fs24 \cf0 \expnd0\expndtw0\kerning0 PhD (SFB1243-A14): Clonal evolution\ \ While the evolutionary nature of cancer is well established, it is challenging to generate and analyze data to quantify the dynamics of this Darwinian\'a0process. This is a clinical problem, for example when therapy-resistant cancer cells regrow after an initially successful treatment. Hence, patients die\'a0because the tumor is able to evolve. Hematologic neoplasms such as leukemia and lymphoma are well suited to study this process, because intact cells\'a0can be sampled and studied in detail over the course of the disease. Within this project, genetic barcoding methods and analysis will be established to\'a0track clonal evolution of acute myeloid leukaemia (AML) in patient-derived xenograft mouse models in the presence and absence of therapeutic\'a0selection pressure (A05; Jeremias). Furthermore, single-cell genotyping and phenotyping (RNA-seq) will be done on AML patient samples before and\'a0after therapy to track clonal evolution and its associated phenotypes (A06; Klaus Metzeler). These technologies and their analysis will be implemented\'a0in the Enard lab (A14) in close collaboration with the other two groups.\ \ For further information please see\'a0www.sfb1243.bio.lmu.de,/-'a0Metzeler lab,\'a0Jeremias lab\'a0and\'a0Enard lab.\ \ Your Responsibilities\ \'95 Optimize genetic barcoding design, readout and analysis for tracking clonal composition of patient-derived AML xenografts.\

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UNC ChapelHill SpeciationGenomics Cerooncichlids pupfish

Title: Postdoctoral position in Cichlid and Pupfish Speciation Genomics

The Martin Fish Speciation Lab at the University of North Carolina at Chapel Hill seeks a postdoc for integrative studies of the evolutionary ecology of adaptive radiation. We are developing two study systems, Caribbean pupfishes and Cameroon crater lake cichlids, using a suite of evolutionary, ecological, and behavioral approaches. Pupfishes present an opportunity to measure complex fitness landscapes underlying the evolution of novel trophic specialists. Cameroon crater lake cichlids may be one of the best examples of sympatric speciation in nature, but more work is needed to examine whether secondary gene flow has facilitated their adaptive radiation. The postdoc will have substantial flexibility in pursuing ongoing projects in these promising systems, mainly focusing on analyses of whole genome resequencing data, quantitative genetics, or the genetic architecture of fitness landscapes. Alternative research directions will also be considered.

UNC Chapel Hill supports a vibrant community of evolutionary biologists interested in speciation, both within the department and the greater Triangle area. The postdoc will be integrated into departmental activities and will receive mentoring in professional skills. The quality of life in this area is consistently rated among the highest in the nation.

Basic qualifications:

Ph.D. or equivalent degree in biology, evolution, genetics, bioinformatics, or related field. Publications resulting from dissertation and broad interest in the evolution and ecology of adaptive radiation.

Preferred qualifications:

Demonstrated expertise in any area of speciation genomics. No pipetting experience necessary as this position is for downstream data analysis. There will be opportunities for fieldwork or live animal work in the fish room if desired, but this is not required for the position.

The position is for 12 months with the possibility of renewal dependent on performance. Start date is Summer or Fall 2016. Salary is $40,000 with benefits. The University of North Carolina at Chapel Hill is an equal opportunity employer with a strong institutional commitment to inclusiveness and diversity. Applicants from underrepresented backgrounds are especially encouraged to apply.

Interested candidates should submit a cover letter detailing their interest in the position, research statement, and CV to Chris Martin at chmartin@unc.edu.

Christopher Martin

Assistant Professor

Biology Department

University of North Carolina at Chapel Hill

Chapel Hill, NC 27599

labs.bio.unc.edu/martin/

“chmartin@unc.edu” <chmartin@unc.edu>

UNevada Reno CognitiveFitness

POSTDOC POSITION IN COGNITIVE ECOLOGY

I am looking for a postdoc to join my lab at the University of Nevada, Reno (http://wolfweb.unr.edu/homepage/vpravosu/; https://www.facebook.com/chickadeecognition/?ref=hl) to work on an NSF funded project investigating fitness consequences of individual variation in spatial memory. The project uses RFID technology to investigate whether individual variation in spatial learning abilities is associated with variation in fitness in free-living food-caching mountain chickadees in two environments (different elevations) hypothesized to be different in spatial memory demands associated with food caching.

All fieldwork is in the rugged mountain conditions ÂV in the beautiful Sierra Nevada along an elevation gradient from ca. 5,000 to 8,000 feet in the Lake Tahoe National Forest (about 40 min drive from Reno). The postdoc will be expected to work in the field throughout the year using a 4-wheel drive vehicle when there is no snow and a snowmobile during the winter.

The project generates large amount of data (more than 100,000 bird visits at just one spatial array with 8 feeders, per two weeks of testing), so experience with analyzing and manipulating large data sets using R and potentially other programming languages (e.g. Perl) is highly desirable. Experience working with birds and with mist-netting is also helpful.

The initial appointment will be for 1 year, which may be renewed based on performance up to 3 years. If interested, please email directly to me (Vladimir Pravosudov) at vpravosu@unr.edu.

Vladimir V Pravosudov <vpravosu@unr.edu>

UNewHampshire SoilMicrobialEvolution

Postdoctoral Position in Soil Microbial Evolution

Contact: Dr. Serita Frey, Department of Natural Resources & the Environment, University of New Hampshire, Durham, NH USA

(Questions can also be directed to Dr. Anne Pringle, University of Wisconsin-Madison: anne.pringle@wisc.edu)

Our laboratory aims to understand connections between microbial community structure and ecosystem function. We document the impacts of environmental change (climate warming, nitrogen deposition, biodiversity loss, invasive species) on the diversity, community composition, and function of the soil microbial community, and test whether shifts in the community subsequently influence ecosystem functions. A recent focus is on anthropogenic drivers of microbial evolution.

This two-year position will focus specifically on fungal evolution within global change contexts, with an emphasis on how fungi evolve in response to biotic invasions, soil warming, and nitrogen addition. The candidate will have the flexibility to explore questions that fall within this general topic area, while building on previous research conducted in the Frey and Pringle Laboratories. The candidate is expected to have strong interests and experience in evolution and ecology. Expertise in cultivation-based and genomic/metagenomic analyses is highly desirable. The candidate will be expected to work independently, but also cooperatively with other members of the lab and with the Pringle Laboratory at the University of Wisconsin, Madison. A Ph.D. degree in evolution, ecology, natural resources, microbiology, or related field, along with relevant research experience is required. Applications will be reviewed until the position is filled.

To apply please send the following items in a single PDF file to Serita Frey (serita.frey@unh.edu): letter of interest/experience, CV, and the names and contact information of three professional references.

Anne Pringle, Ph.D. Associate Professor Departments of Botany and Bacteriology University of Wisconsin, Madison new email: anne.pringle@wisc.edu http://www.botany.wisc.edu/Pringle.htm Anne Pringle <apringle2@wisc.edu>

UNorthCarolina Charlotte ComputationalMicrobialGenomics

The Department of Bioinformatics and Genomics at the University of North Carolina at Charlotte has multiple postdoctoral opportunities located at the North Carolina Research Campus in Kannapolis, NC (NCRC http://www.ncresearchcampus.net). The NCRC is a $1.5B, 350-acre biotechnology research park that is the home of research programs of several large private biotechnology companies, six other research universities from North Carolina and several health care organizations. We have multiple positions in computational microbial genomics focusing on human microbiome studies, host-pathogen evolution, and microbial communities associated with foods. Example projects include: (i) algorithm development for the analysis of large data sets generated from mixed microbial (metagenomic) communities from the external environment or associated with plants or animals; (ii) tracking development of antibiotic resistance or changes in microbial phenotype to the content of genes and genomes using next-generation sequencing; (iii) source tracking of pathogens across space and time in the external environment or within industrial, agricultural or hospital settings; (iv) utilizing microbial genomics for molecular epidemiological studies and precision medicine; (v) studies of microbial evolution and genomic structure; (vi) developing tools for visualization of microbial datasets; (vii) using computational tools to enhance agriculture and nutrition by manipulation of plant-associated microbes.

Candidates should have recently completed a doctorate in bioinformatics, computational biology, computer science, biology or a related field. Candidates should have substantial experience with next generation sequencing data analysis, scripting languages or other programming skills, and common analytical tools. In addition, candidates should have strong problem solving ability, be able to work collaboratively and have good communications skills.

Salary and benefits will be commensurate with experience. As an EOE/AA employer and an ADVANCE Institution that strives to create an academic climate in which the dignity of all individuals is respected and maintained, the University of North Carolina at Charlotte encourages applications from all underrepresented groups.

Interested candidates should apply by sending a cover letter expressing interest in our research, a curriculum vitae with publications, and the names of three references to international@uncc.edu

For informal inquiries about the positions please contact unccpostdoc@gmail.com

unccpostdoc@gmail.com

UNotreDame EvolutionBaboonGutMicrobiomes

NotreDame.Baboon.Microbiomes

Postdoc in the ecology and evolution of baboon gut microbiomes

A postdoctoral position applying ecological and evolutionary frameworks to understand the causes and consequences of gut microbial dynamics is available in the lab of Elizabeth Archie (University of Notre Dame, Department of Biological Sciences; http://blogs.nd.edu/archielab/). The postdoc will have access to an unprecedented data set of 20,000 microbiome samples, collected from 600+ individual baboons and spanning over 15 years. These samples are currently being sequenced at the 16S rRNA v4 region in collaboration with the Earth Microbiome Project (http://www.earthmicrobiome.org/); data will be available in the spring of 2016. Samples were collected from the well-studied Amboseli baboon population in Kenya (http://amboselibaboons.nd.edu/), which has long-term data on the baboons' ecology, social interactions, health, and fitness. Some relevant recent publications include Tung et al. (2015) in eLife and Archie & Tung (2015) in Current Opinions in Behavioral Sciences.

Postdoctoral applicants should have a strong background two or more of the following areas: microbial ecology, community ecology, evolution, behavior, bioinformatics, and genomics. Strong data analysis skills, including programming and statistical modeling experience, are preferred. Familiarity or experience with primates is a plus, but is not essential. Several projects are available; applicants will have the freedom to choose their own projects as long as they fit within the general interests of the collaborative research.

The Archie lab offers congenial research environments that foster strong interdisciplinary training and collaborative exchange. Collaborators on this project include Jenny Tung (http://www.tung-lab.org/), Ran Blekhman (http://blekhmanlab.org/) Luis Barreiro (http://luis-barreirolab.org/), Stuart Jones (http://www3.nd.edu/~sjones20/), and David Boone (IU School of Medicine), all of whom are available for advice and interaction. The postdoc is funded by the Eck Institute for Global Health, and the Environmental Change Initiative at Notre Dame.

To apply for the position please send an email to Elizabeth Archie (earchie@nd.edu), including a cover letter, current CV, and contact information for at least two references. The anticipated start date is in late spring or summer 2016. Applicants should submit their materials by March 1 to ensure full consideration.

Elizabeth Archie Associate Professor Department of Biological Sciences University of Notre Dame Notre Dame, IN Tel. (574) 631-0178 Office. 179 Galvin http://blogs.nd.edu/archielab/ Elizabeth Archie <Elizabeth.A.Archie.2@nd.edu>

UPotsdam 3 Biodiversity

TheUniversity of Potsdam (UP) together with the Freie UniversitÃÂt Berlin(FU) and the other partners in the Berlin-Brandenburg Institute forAdvanced Biodiversity Research (BBIB, www.bbib.org) have formed a consortiumto implement a major new interdisciplinary research initiative,the Bridging in Biodiversity Science (http://www.bbib.org/bridging-in-biodiversity-science.html)project fundedby the Federal Ministry of Research and Education (BMBF). The departmentof Plant Ecology and Conservation Biology at UP (http://www.uni-potsdam.de/en/ibb/-researchgroups/fullprofessors/plant-e cology.html)offers three PostDoc positions in two different work packagesof the project.

Withinthe work package ScapeLabs Experimental Platform, the UP seeksto fill the following two positions: 1PostDoc: Spatially-explicit modeling of rapid transitions in communitydynamics

Tasks:Theoretical concepts such as the meta-community or -ecosystem framework,spatial food web theory or the conceptual resilience frameworkare well-suited to address specific aspects of biodiversity andecosystem function dynamics under dynamic environmental conditions. However,there is still a need for developing and refining integrative modelsand concepts that address the mechanisms affecting rapid transitionsin biodiversity dynamics and ecosystem functioning at differentspatiotemporal scales or across different systems (e.g. aquaticand terrestrial) or multiple trophic levels.

Inclose linkage with ongoing experimental work at the experimental landScapeLaboratories (Agro-, City, - and Lake- ScapeLabs, http://www.bbib.org/experimental-platform.html),the PostDoc will test andrefine existing and develop new models and concepts of rapid communitychanges at the landscape scale. S/He will also be responsible forthe theory-driven, conceptual coordination of the cross-system, landscapescale experimental Ãâ¬ËScapeLabs′platforms.Theresearchwillstronglyimproveourabilitytopredicttheresponseofbiodiversitytoclimateorlandus

Requirements:The successful candidate will have a strong expertise in spatialbiodiversity concepts and the development of ecological models. Asound knowledge in programming (e.g., C++) is required. Applicants musthold a doctoral degree, have proven publication skills and should beable to work independently. Organisational skills, high motivation andthe willingness to work as part of a team within an interdisciplinaryproject are essential.

1PostDoc: Experimental design, meta-analyses and data management Tasks:The novel, landscape-level experimental ScapeLabs framework (http://www.bbib.org/-experimental-platform.html)requires new ideas and approachesto data generation through well-designed experiments, data (meta-)analyses,and data management. Together with experts from other BBIB-partners,the PostDoc will optimize and harmonize experimental designsat the different ScapeLabs, support and conduct overarching statistical(meta-)analyses, and contribute to an overall data infrastructureof the BIBS project, including developing and maintaininga Ãâ¬ËScapeLabs′database.Thespecificfocusoftheworkwithinthisra

Requirements:The successful candidate will have a strong expertise in atleast one of the following fields: (i) design of landscape-level experimentsand statistics, (ii) advanced statistics and meta-analyses, (iii)data and database management. Applicants must hold a doctoral degree,have proven publication skills and should be able to work independently.Organisational skills, high motivation and the willingnessto work as part of a team within an interdisciplinary projectare essential.

Withinthe work package Aboveground-belowground coupling, the UP seeksto fill the following position: 1PostDoc: Modelling the resilience of coupled plant-soil community dynamics

Tasks:Rapid transitions in ecosystems can be strongly mediated by plant-soilinteractions. Shifts in above- and belowground communities andtheir average trait values can be expected to impact the resilience andresistance of the system. In close collaboration with the departmentof Biodiversity Research/ Systematic Botany (Prof. Dr. JasminJoshi) at UP and partners at the FU Berlin the PostDoc will developnew or refine existing spatially-explicit, high-resolution simulationmodels that dynamically simulate feedbacks between above- (i.e.plant) and belowground (i.e. local root-inhabiting and rhizosphere-associatedbiota) community dynamics on the basis of trait

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UppsalaU PDF PhD FungalEvol

Genome organization of AM fungi

Post doc and PhD position in Evolutionary Biology

At the Department of Evolutionary Biology, Uppsala University, Sweden.

Description

Arbuscular mycorrhizal (AM) fungi form symbiotic interactions with almost all terrestrial plants and have done so since plants first colonized land. The postdoc and PhD position are both part of a newly funded ERC research program aimed at understanding the ecology and evolution of these widespread and important organisms. Using state-of-the art technology, e.g., PacBio long read sequencing and single nucleus genomics methods, the research program seeks to resolve the genome organization of AM fungi so that the evolutionary consequences of their genome organization can be studied. Specifically, the project aims at testing the hypothesis that genetically distinct nuclear genotypes coexist within AM fungi. The project involves culturing of AM fungi, sorting and genotyping of nuclei from individual fungal isolates, genome and meta-genome sequencing and assembly[INS: , :INS] as well as genome size estimation. Based on the outcome of this first part, the project will be developed to connect genotype and phenotype to mycorrhizal activity.

The postdoc and PhD student will work close together and be part of an expanding research team led by Anna Rosling (http://www.ieg.uu.se/evolutionary-biology/-rosling/research/) in collaboration with Hanna Johannesson (http://www.iob.uu.se/research/systematic-biology/johannesson/) at the Evolutionary Biology Centre (EBC), Uppsala University. EBC constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 300 scientists and graduate students. The scientific environment with numerous seminars, journal clubs and social activities offer excellent possibilities for contacts and collaborations. Local platforms for high-performance computational analyses (https://www.uppmax.uu.se/-uppnex), NGS, SNP genotyping and proteomic analyses (http://www.scilifelab.se) ensure immediate access to state-of-the-art technology. This project will utilize several of the technological platforms at SciLifeLab in Uppsala, in particular the Microbial Single Cell Genomics Platform (https://www.scilifelab.se/facilities/-single-cell/).

Qualifications

Experience in bioinformatics and genome analysis is necessary and experience in mycology is a merit. The ideal candidate is scientifically motivated and can work both independently and as part of a team. High standard of spoken and written English is required.

To apply for the PhD position you must have a Master Degree in Bioinformatics, Evolutionary Biology, Microbiology, Mycology or equivalent. Attach a copy of your diploma and your master thesis with the application.

To apply for the Post Doc position you must have acquired a PhD in Bioinformatics, Evolutionary Biology, Microbiology, Mycology or equivalent. Attach a copy of your PhD degree with the application.

Information about the position will be given by Anna Rosling tel +46 18-471 64 44, Anna.Rosling@ebc.uu.se.

Application: The application should include a letter with a short motivation of your interest in the position (one A4 page) and name and contact information to at least three reference persons and your CV. Use the link below to access the application form.

PhD candidates are welcome to submit their application using the link below no later than February 29, 2016. http://www.uu.se/en/about-uu/join-us/-details/?positionId=3D88336 Post Doc candidates are welcome to submit their application by email to Anna.Rosling@ebc.uu.se no later than February 15, 2016

Anna Rosling <anna.rosling@ebc.uu.se>

UTexas SexChromosomeGenomics

Dear colleagues,

We are seeking a postdoctoral fellow to join my lab at the University of Texas (Austin) on a study of the origin and evolution of young sex chromosomes. In an NIH-funded collaboration with Dr. Katie Peichel (Fred Hutchison Cancer Research Center), we are collecting genomic data from several species of stickleback fishes. My lab will be analyzing those data to study topics that include chromosome rearrangements, sexually-antagonistic selection, the evolution of recombination, and patterns of molecular evolution on recombining sex chromosomes.

The position can begin as early as May 1, and the starting date is negotiable. A requirements are a Ph.D. in evolutionary biology, genetics, modeling, statistics, bioinformatics, or related field. The postdoc should have experience in programming (e.g. in Python and/or C++) and/or bioinformatics.

The salary is $45,432 to $51,096 / year, depending on qualifications, and the position includes health and retirement benefits. The initial appointment is for one year, with possible extension up to three years depending on satisfactory performance.

If interested, please email Mark Kirkpatrick (kirkp@mail.utexas.edu) with a letter explaining your background and motivation, a C.V., and the email addresses of three people who have agreed to provide recommendations. The position will remain open until a suitable person is found.

Best wishes,

Mark Kirkpatrick

Mark Kirkpatrick <kirkp@austin.utexas.edu>

UWisconsin Madison YeastBiodiversity

A postdoctoral position is available in the Hittinger Lab in Yeast Biodiversity and Synthetic Biology.

The full ad can be viewed here: http://hittinger.genetics.wisc.edu/Images/postdocAd2016.pdf .

Please apply by 14th February 2016 for full consideration.

Chris Todd Hittinger, Assistant Professor of Genetics DOE Great Lakes Bioenergy Research Center University of Wisconsin-Madison 425-G Henry Mall, 4102 Genetics/Biotechnology Center Madison, WI 53706-1580 cthittinger@wisc.edu http://hittinger.genetics.wisc.edu

WashingtonU EvolutionaryEcol

Postdoctoral position in Evolutionary Ecology

Start date: 1 May 2016. Salary Range: $38X42K, depending on qualifications

The Botero Lab at Washington University in Saint Louis (https://pages.wustl.edu/botero) is searching for a driven and highly self-motivated postdoctoral colleague interested in applying the tools of evolutionary ecology to the study of human culture. This NSF funded position will involve highly collaborative, multi-institutional, and inter-disciplinary work on a range of topics with a strong emphasis on understanding the evolution of land tenure and natural resource management in traditional cultural groups. Ideal candidates will have a strong quantitative background, good programming background in R, and expertise in Structural Equation Modeling, spatial statistics, and/or spatially explicit simulation modelling (please comment on these skills in your cover letter). The successful candidate will be expected to develop synergistic projects with our research team at the University of Colorado Fort Collins, Yale University, the Max Planck Institute for the Science of Human History, and The Australian National University.

This is a two-year position but opportunities will exist for those interested to write grants that extend the scope and duration of our collaborative work.

Please apply directly at https://jobs.wustl.edu (job ID 32675). Additional inquiries should be addressed to Prof Carlos A. Botero (cbotero@wustl.edu).

"Botero, Carlos" <cbotero@wustl.edu>

WorkshopsCourses

ArnoldArboretum Boston PlantMorphology Jun13-24

microMORPH Summer Course 2016 - Plant Morphology: Linking Phenotype to Development

Due to overwhelming interest, plant developmental morphology has returned as the topic for the fourth annual microMORPH summer short course at the Arnold Arboretum. This short course will be taught by experts from around the world as an intense, two-week lecture, laboratory, and living collections learning experience. The course will be based at the Weld Hill Research Building at the Arnold Arboretum in Boston, which offers a state-of-the-art microscopy laboratory for teaching and sits amid the 15,000+ living specimens of more than 2,200 species at the Arnold Arboretum.

This course will provide a working knowledge of tools and concepts that are central to understanding the developmental basis for the remarkable structural and functional diversity of plants. Topics include developmental dynamics, evolutionary diversification, and ecological and physiological function. Ultimately, this course aims to provide the skills necessary to interpret the vast array of morphologies that exist among plants. Each day will consist of lecture and laboratory sessions, with ample opportunity to explore the Arnold Arboretum.

The microMORPH and Arnold Arboretum summer short courses are free for all participants, and funds are available to help defray costs of participant travel.

Application Deadline: Applications must be submitted by 11:30 pm March 15th, 2016.

Eligibility: microMORPH summer short courses are open to postdoctoral researchers, graduate students, and undergraduates in their final year of study (who have been admitted to a graduate or professional program for the fall of 2016). Non-US-citizens are welcome to apply.

How to Apply: For full application instructions and to submit applications, please visit the microMORPH website (http://projects.iq.harvard.edu/micromorph).

Pamela Diggle

Professor Department of Ecology and Evolutionary Biology University of Connecticut

860-486-4788<tel:860-486-4788>

"diggle@colorado.edu" <diggle@colorado.edu>

AveiroU Portugal AmphibianConservation May16-20

I am contacting asking for the divulgation of the Amphibian Husbandry and Conservation Course at the Biology Department of Aveiro University, Portugal. We invited, Amphibian Ark to give us the pleasure of their partnership.

The 1st Course on Amphibian Husbandry and Conservation (AHC) is an interesting and intensive course to researchers, technical staff working with amphibians or anyone looking for more complete basis on Amphibian

Husbandry and Conservation. The course will be held from 16th to 20th May 2016.

Registrations for this edition already available

https://amphibianhc.wordpress.com/ The course explores the principles of amphibians' husbandry, nutrition and dietary needs, captive reproduction, population management, veterinary aspects (diseases, pathology, and necropsy), biosecurity and quarantine, conservation, threats and global action. Hands on demonstrations, practical and group exercises are also included (enclosure demonstrations: tank drilling, false bottoms and plumbing, filters).

Speakers:

* Luis Carrillo, University of Mexico City, AArk * Michael Bungard, Wjitley Wildlife Conservation Trust (Paignton Zoo) * Arturo Munoz Saraiva, Coordinator of the Bolivian amphibian initiative and PhD in Ghent University * Isabel Lopes, University of Aveiro, CESAM

Important note: the course will not start if a minimum of 10 participants will not be reached; similarly the maximum number of participants is 15.

Inscription fees include: attending at the course and the use of all the materials provided by University of Aveiro and the AArk.

Fees:

AHC Course Early registration (29th February)

General: 280 euros

Student: 180 eurosÂ

AHC Course

General: 350 euros

Student: 250 euros

Applications should be sent to: amphibianhc@sapo.pt till the 31st of March 2016.

Instructions for payment will be notified to participants no later than 48h after. The payment proof must be sent to us for the registration to be valid.

I grateful for your help.

The organizing committe

"amphibianhc@sapo.pt" <amphibianhc@sapo.pt>

AveiroU Portugal AmphibianConservation May23-27 NewDate

New Date!!!! 23th to 27th May 2016

I am contacting asking for the divulgation of the Amphibian Husbandry and Conservation Course at the Biology Department of Aveiro University, Portugal. We invited, Amphibian Ark to give us the pleasure of their partnership.

The 1st Course on Amphibian Husbandry and Conservation (AHC) is an interesting and intensive course to researchers, technical staff working with amphibians or anyone looking for more complete basis on Amphibian Husbandry and Conservation. The course will be held from 23th to 27th May 2016.

Registrations for this edition already available

https://amphibianhc.wordpress.com/ The course explores the principles of amphibians$B!G(B husbandry, nutrition and dietary needs, captive reproduction, population management, veterinary aspects (diseases, pathology, and necropsy), biosecurity and quarantine, conservation, threats and global action. Hands on demonstrations, practical and group exercises are also included (enclosure demonstrations: tank drilling, false bottoms and plumbing, filters).

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I grateful for your help.

The organizing committe

"amphibianhc@sapo.pt" <amphibianhc@sapo.pt>

Barcelona InferenceInEvolBiogeography Nov28-Dec2

Course Announcement:

Nick Matzke and Dan Warren will be teaching a course entitled "Model-based Statistical Inference in Ecological and Evolutionary Biogeography" in Barcelona from November 28 to Dec 2, 2016.

This course will cover the theory and practice of widely used methods in evolutionary and ecological biogeography, namely ecological niche modelling / species distribution modelling, and ancestral range estimation on phylogenies.

The course will cover both the practical challenges to using these techniques (the basics of R, obtaining and processing geographical occurrence data from GBIF, setting up and using the models), and the assumptions that various models and methods make.

R packages we will use include rgbif, dismo, ENMTools, and BioGeoBEARS.

Finally, this course will introduce several new approaches being developed by the instructors for linking ecological and evolutionary models.

For more details or to enroll, please see the Transmitting Science web site

http://www.transmittingscience.org/courses/biog/statistical-biogeography/ dan.l.warren@gmail.com

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Barcelona PhylogeniesMacroevolution Sep19-23

Dear colleagues,

Registration is open for the course "THE USE OF PHYLOGENIES IN THE STUDY OF MACROEVOLUTION 4th edition", September 19th 23rd, 2016.

INSTRUCTOR: Dr. Juan López Cantalapiedra (Museum für Naturkunde, Germany).

FOR WHOM?: This course is aimed at postgraduate students, postdoctoral researchers and established academics.

First, this course will introduce participants to the use, modification and representation of phylogenetic trees. Then, we will focus on the use of phylogenetic information to reconstruct ancestral characters and biogeographic histories, learning how to apply Phylogenetic Comparative Methods.

This course will also tackle trait evolution modeling and the assessment of phylogenetic signal. Finally, we will learn about the shape of phylogenetic trees and its evolutionary causes and how to estimate the rates of diversification throughout the evolutionary history of groups.

Participants are encouraged to bring their data sets to use in the practical class.

Important note: Please bear in mind that this course is not about reconstructing (building) phylogenetic trees.

Software: Mesquite, FigTree, BayesTraits (using BayesTraits Wrapper in R), RASP and R (ape, TreeSim, TreePar, Geiger, OUwie, BioGeoBEARS).

More information: http://www.transmittingscience.org/courses/evol/phylogeny-and-macroevolution/

PLACE: Facilities of the CRIP at Els Hostalets de Pierola, Barcelona (Spain).

Organized by: Transmitting Science, the Centre de Restauració i Interpretació Paleontologica and the Institut Catalá de Paleontologia Miquel Crusafont.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Soledad De Esteban-Trivigno, PhD. soledad.esteban@transmittingscience.org Transmitting Science www.transmittingscience.org

soledad.esteban@transmittingscience.org

Finland StructuredPops Aug21-28

Reminder (application deadline 31 January) Summer school: Structured populations (21-28 August 2016, Finland)

Dear Colleagues,

We are pleased to announce the 2016 edition of The Helsinki Summer School on Mathematical Ecology and Evolution, an EMS-ESMTB School in Applied Mathematics, which will focus on structured populations. The school will be held between 21 and 28 August 2016 in Turku, Finland. The core program consists of five series of lectures:

Mats Gyllenberg (University of Helsinki): Dynamics of structured populations Hans Metz (University of Leiden): Adaptive dynamics in structured populations Reinhard Bürger (University of Vienna): Population genetics of spatially structured populations Hisashi Inaba (University of Tokyo): Infectious diseases in structured populations André de Roos (University of Amsterdam): Population and community ecology of ontogenetic development

All young researchers working in mathematical ecology can apply from all countries, especially from Europe and the Mediterranean. The school is aimed at graduate students of mathematics, but we also welcome students of biology with sufficient background in mathematics, as well as advanced undergraduates and postdocs.

The deadline for applications is 31 January 2016. For more details and application, see the school's website at

https://wiki.helsinki.fi/display/BioMath/The+Helsinki+Summer+School+on+Mathematical+Ecology+and+Evolution+2016%3A+Structured+Populations
Eva Kisdi, Mats Gyllenberg and Francesca Scarabel

"eva.kisdi@helsinki.fi" <eva.kisdi@helsinki.fi>

Glasgow ViralBioinformaticsAndGenomics Aug1-5

Training course on Viral Bioinformatics and Genomics Glasgow, United Kingdom

Monday 1st - Friday 5th August 2016 Application deadline 18th March 2016 Cost Â£450

For full information and details on how to apply see: http://www.bioinformatics.cvr.ac.uk/Downloads/Joseph/OIE_announcements_2016.pdf After the successful training course in 2015, the Viral Genomics & Bioinformatics team at the Centre for Virus Research will be repeating the course this year.

We will be giving a 5-day course, which will consist of a series of lectures and practical exercises that directly address bioinformatic challenges posed by the current deluge of sequence data. We will enable participants to understand and deal with high-throughput sequence datasets and encourage the exchange of ideas among diagnosticians, virologists, bioinformaticians and evolutionary biologists.

The 2016 course will introduce the participants to the power of the UNIX command-line and bash scripts, as well as a suite of bioinformatics tools covering the following topics:

- HTS sequencing technologies: overview of the different HTS platforms and sample preparations. - The power of Unix: essential bash scripting. - Reference assembly: aligning sequence reads to a known reference and visualizing the alignment; (e.g., bowtie2, BWA, Tanoti, Tablet, UGENE). - Variant calling: consensus sequence generation, low frequency variant calling and error correction; (e.g., LoFreq, VPhaser). - De-novo assembly: overlap layout and De Bruijn graphs approaches for sequence assembly; (e.g., Velvet, IDBA-UD). - Metagenomic analyses: sanitizing sequence datasets, assembling, annotating, visualizing; (e.g., MetAMOS, Krona, MEGAN). - Genomics: scaffolding, improving the assembly, finishing the assembly, gene annotation; (e.g., ICORN, Artemis). - Phylogenetic analysis: introduction to multiple sequence alignment and phylogenetic reconstruction; (e.g., clustal, PhyML).

The course will be held at the Centre for Virus Research, Garscube Campus, University of Glasgow, Glasgow, UK.

The CVR has been designated an World Organisation for Animal Health (OIE) Collaborating Centre for Viral Genomics and Bioinformatics at the 82nd OIE General Session.

Richard Orton <Richard.Orton@glasgow.ac.uk>

GreifswaldU GeneticAdaptation Mar15-18

07-01-2016

International Summer School on Genetic Adaptation

Date: 15^th -18^th March 2016

Venue: Greifswald University, Zoology Lab Building, Soldmannstraße 14

The DFG funded Research Training Group RESPONSE (Biological Responses to Novel and Changing Environments; www.uni-greifswald.de/RESPONSE/) organizes a summer school on genetic adaptation. We are broadly interested in responses to environmental change, for which genetic adaptation may play an important role. The summer school aims at deepening the knowledge of the prospects and limitations of different genetic approaches in understanding adaptation to environmental change.

We will cover the following topics: Adaptive genetic variation and its detection, Omics technologies in ecological research, heritability and quantitative genetics, dynamics of rapid adaptation and niche evolution. The programme will include lectures given by renowned experts in the field and a young investigators' day providing the opportunity to present the own research project. There will also be computer courses including exercises on estimating heritabilities and on eco-evolutionary population modelling (for details please visit www.uni-greifswald.de/RESPONSE/).

The summer school is open to a limited number of external graduate / PhD students. If you would like to participate, please send an email including a short CV and a letter of motivation (no more than half a page) to Michael Schöner (schoenerm@uni-greifswald.de) before 15^th February 2016. Participation is free of charge, though we cannot cover travel expenses and accommodation.

Prof. Dr. Klaus Fischer Zoological Institute & Museum Greifswald University J.-S.-Bach-Str. 11/12 D-17489 Greifswald Phone: +49-3834-864266 Fax: +49-3834-864252

"kfischer@uni-greifswald.de" <kfischer@uni-greifswald.de>

Guarda Switzerland Evolution Jun18-25

Guarda summer school in evolutionary biology 2016

It my pleasure to announce this year's Guarda summer school in Evolutionary Biology for master and PhD students. The main aim of the course is to develop the skills to produce an independent research project in evolutionary biology.

The summer school takes place 18. - 25. June 2016 in the Swiss mountain village Guarda. Faculty includes Hopi Hoeckstra (Harvard University, USA), Spencer Barrett (University of Toronto, Canada), Sebastian Bonhoeffer (ETH-Zurich, Switzerland) and Dieter Ebert (University of Basel, Switzerland)(organizer).

The course is intended for master students and early PhD students with a keen interest in evolutionary biology.

The web page with all details can be found under: http://www.evolution.unibas.ch/teaching/guarda/index.htm Application is open now. Deadline is 12. February 2016.

Please communicate this information to interested students.

If you receive this email multiple times, please excuse me.

With best wishes,

dieter ebert

Dieter Ebert University of Basel, Zoological Institute, Vesalgasse 1, 4051 Basel, Switzerland Tel. +41 (0)61 267 03 60 Email: dieter.ebert@unibas.ch

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Leicester NGSAssemblyVariantCalling Feb1-3

Deadline for applications is approaching for the BBASH training course "DNA-Seq Next Generation Sequencing".

Applications are welcome until Friday 15/01/2016!

BBASH at University of Leicester is pleased to announce that applications for the upcoming Next Generation Sequencing training course are now open.

Deadline for applications: 15th January 2016 Notification of acceptance: 18th January 2016 Course dates: 1st-3rd February 2016

Venue: University of Leicester - College Court Conference Centre, Leicester, UK (http://collegecourt.co.uk/)

Instructors: Richard Badge (BBASH, University of Leicester, UK) Chiara Batini (University of Leicester, UK) Matthew Blades (BBASH, University of Leicester, UK)

Course description

This course will provide an introduction to next generation sequencing (NGS) platforms, data analysis and tools for data quality control, genome assembly and variant calling. The course will be delivered using a mixture of lectures and computer based hands on practical sessions using real data.

This course is aimed at wet-lab biologists who are involved in research projects that will require the handling and analysis of NGS data. A significant proportion of the course will be computer-based using command line tools in the Unix environment, therefore, in order to gain maximum benefit from the course all attendees will be required to have basic Unix skills.

For additional information: https://www2.le.ac.uk/colleges/medbiopsych/facilities-and-services/cbs/bbash/training/workshop-webpages/copy_of_ngs-workshop-2016 The Organisers Chiara Batini (University of Leicester, UK) Matthew Blades (BBASH, University of Leicester, UK)

"cb334@leicester.ac.uk" <cb334@leicester.ac.uk>

LundU GeometricMorphometrics May9-13

Subject heading: PhD course: "Geometric Morphometrics Using R". Lund University, 9-13 May 2016. We are happy to announce a PhD course entitled: "Geometric Morphometrics Using R" that is about to take place at Lund University, 9-13 May 2016.

Info @: http://www.biology.lu.se/education/phd-studies/phd-courses/phenomics -geometric-morphometrics-using-r Description: The analysis of organismal shape is central to many questions in ecology and evolution. This course aims at providing an introduction to the theory and methods of geometric morphometrics for analyzing variation in shape and its covariation with other variables. It will provide an overview of the theory underlying the quantification of shape using landmark methods, and a practical guide to data acquisition, standardization for obtaining shape variables, statistical treatment of shape variation and visualization of the results in the R language for statistical programming.

Content: The course will include both theoretical and practical sessions. During the theoretical session we will provide a comprehensive introduction to the methods of landmark-based geometric morphometrics, which aims at providing the participants with a solid theoretical background for understanding the procedures used in shape data analysis. Practical sessions will include worked examples of data acquisition, standardization and statistical analysis, giving the participants the opportunity to gain practical experience in the treatment of shape data using the R package geomorphic and other statistical routines in R. We will provide an example dataset, but we encourage the participants to bring their own data for treatment.

The course is organised by: Dean Adams Mike Collyer Antigone Kaliontzopoulou GENECO Course host: Johan Hollander, Lund University Application Please apply by email to: Johan.Hollander@biol.lu.se Deadline: 4 March. A first come, first serve, principle applies.

Many thanks, Johan Hollander

Dr. Johan Hollander (Docent) Associate Professor Aquatic Ecology, Department of Biology Lund University Ecology Building 223 62 Lund, Sweden Office phone: +46 (0) 46 22 234 73 Cell phone: +46 (0) 70 17 49 660 Fax: +46 (0) 46 222 45 36 Home page: www.lu.se/aquaticecology GENECO: www.geneco.se Johan Hollander <johan.hollander@biol.lu.se>

MichiganStateU Avida-ED Jun

2^nd Active LENS Workshop: June 2016

The 2^nd annual Avida-ED Active LENS Workshop will be held at Michigan State UniversityJune 9-11, 2016 in East Lansing, MI.The purpose of this workshop is to train instructors in the use of the Avida-ED software package, developed to help students learn about evolution and the nature of science, so that workshop participants can both implement classroom interventions using this software and also train other educators./Teams of two/ will learn to use Avida-ED and how to best incorporate it into courses that they teach.Travel and expenses related to the workshop will be covered for the 20 workshop participants as part of an NSF-funded IUSE grant.

Avida is a digital evolution software platform used to study evolutionary processes, and harness evolution to solve engineering problems.Avida-ED is a free, user-friendly version of Avida developed specifically for educational purposes, with a graphical user interface and visualizations that allow the user to observe evolution in action. (See http://avida-ed.msu.edu/for more information and to download a copy of the software.)Organisms within this software (Avidians) are self-replicating computer programs, competing for computational resources supplied by the environment.Their replication is imperfect, resulting in mutations in some of their offspring, which may alter the ability of those organisms to make use of their environmental resources.Populations studied over the course of generations therefore display all of the elements necessary for evolution by natural selection: variation, inheritance, selection, and time.Avida-ED thus provides not a simulation of evolution, but an actual instance of it.

Avida-ED has been developed for undergraduates and advanced placement high school students to learn about the nature of science and evolution in particular.Users have significant control of the environment, and are able to change parameters such as the world size, the mutation rate, and what resources are available.Individual organisms can be saved in a virtual freezer, analyzed individually to watch how they perform tasks and replicate themselves, and used to start new evolutionary runs.Because digital organisms grow and divide much faster than even the fastest microbes, Avida-ED allows users to test evolutionary hypotheses over the course of hours or minutes.By generating hypotheses, collecting data, and analyzing results, users gain experience not just with concepts in evolution, but with the nature and practice of science as a whole.

Workshop participants will join a growing community of educators using digital evolution to let their students directly observe evolutionary processes through inquiry-based exercises that advance reform-oriented active learning.Participants will develop new lesson plans and will help collect assessment data from their classroom implementations.They will help disseminate materials and train other science educators; financial support is available for this.At least one member of each pair will attend a 1-day follow up meeting at MSU in early summer 2017 to report on their experience.

The team application form for the Active LENS Workshop must be completed online on the following page: http://avida-ed.beacon-center.org/. Applications should be submitted no later than March 7, 2015.If you have any questions or difficulties with the application, contact Michael Wiser (mwiser@msu.edu).

“mwiser@msu.edu” <mwiser@msu.edu>

MichiganStateU Avida-EDTraining Jun9-11

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The team application form for the Active LENS Workshop must be completed online on the following page: http://avida-ed.beacon-center.org/. Applications should be submitted no later than March 7, 2015. If you have any questions or difficulties with the application, contact Michael Wiser (mwiser@msu.edu).

– Louise S. Mead, PhD Education Director BEACON Center for the Study of Evolution in Action 567 Wilson Ave, BPS 1441 East Lansing, MI 517-884-2560

Louise Mead <lsmead@msu.edu>

OxfordBrookesU EvoDevo Aug8-12

Dear all,

We are delighted to offer our 3rd Eco-Evo-Devo Summer School from August 8th to 12th 2016 at Oxford Brookes University. For full details please see the Summer School website:

http://bms.brookes.ac.uk/ceec/courses/eco-evo-devo-summer Thanks and best wishes,

Alistair, Sebastian, Dani and Casper.

Professor Alistair P. McGregor

Department of Biological and Medical Sciences Oxford Brookes University Gipsy Lane Oxford OX3 0BP United Kingdom

Tel: +44 (0)1865484191 Fax: +44 (0)1865483242

www.mcgregor-evo-devo-lab.net twitter: @McGregorLab

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Dr. M. Daniela S. Nunes

Department of Biological and Medical Sciences Oxford Brookes University Gipsy Lane Oxford, OX3 0BP UK Tel. +44 (0)1865 484191

Dr Casper J. Breuker

Department of Biological and Medical Sciences, Oxford Brookes University Gipsy Lane, Headington,Oxford, OX3 0BP, UK tel: +44(0)1865483244; fax: +44(0)1865483242

"p0076379@brookes.ac.uk" <p0076379@brookes.ac.uk>

Ploen Germany BridgingTheoryExperiments Apr18-22

Dear Colleagues

We would like to announce a workshop: Bridging Theory and Experiments Location: Max Planck Institiute for Evolutionary biology in Plön Germany.

Dates: April 18-22 2016 This workshop will help dissolve the division between theoretical and empirical biology. We hope to establish solutions on the issues that prevent fruitful collaboration between these sides. The workshop will focus on evolving communities, i.e., evolution of complex species interactions, which might result from the species interactions as well as from abiotic changes.

Confirmed Speakers: Thomas Bell (Imperial College) Tal Dagan (CAU Kiel University) Arjan deVisser (Wageningen University) Ursula Gaedke (University Potsdam) Ivana Gudelj (University Exeter) Hanna Kokko (University Zürich) Anna-Liisa Laine (University of Helsinki) Joachim Hermisson (University Vienna) Arne Traulsen (Max Planck for Evolutionary Biology) Deadline for registration and abstract submission is January 31 2016.

Costs: 180 Euros (including all meals, events, *accommodation) Travelling awards: There is limited funding available to support travelling cost.

For more information please visit http://web.evolbio.mpg.de/brite/ Maria Abou Chakra Max Planck Institute Evolutionary Biology: theory group Plön Germany

http://web.evolbio.mpg.de/~abouchakra Maria Abou Chakra <abouchakra@evolbio.mpg.de>

Portugal cE3c Evolution

Subject: Portugal-cE3c-Course : three advanced courses with deadlines January2016

cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the three with closer deadlines.

Additional informations at: http://ce3c.ciencias.ulisboa.pt/training/?cat=1 cE3c - Centre for Ecology, Evolution and Environmental Changes Advanced Course Island Biogeography by Ana Margarida Santos - February 22-26 2016 @ Lisbon, Portugal

OBJECTIVES: This five-days intensive course covers the main aspects of island biogeography, and on completion of the course the students shall have acquired knowledge and understanding on: 1) Ecological/evolutionary theories developed from studies on islands, and its applications in other research areas; 2) Processes that occur during and after island colonization, that shape island communities; 3) Island evolutionary processes; 4) Applications of island biogeography to conservation biology

See the PROGRAMME at: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id Course INSTRUCTOR (coordinator): Ana M.C. Santos (Marie Curie Research Fellow, Museo Nacional de Ciencias Naturales - CSIC; http://guidasanto1.wix.com/anamcsantos2)

INTENDED AUDIENCE This five days intensive course will be open to a maximum number of 20 participants, being directed to PhD and master students as well as post-docs and professionals with a bachelor in Biology, Geography or related areas.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL, UP) and Biology and Ecology of Global Changes (BEAG UL, UA). For information of fees for other participants see the programme details.

Deadline for applications: January 25th, 2016

For additional details about the course and to know how to register, click here: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id For more information about the course, please contact: ana.margarida.c.santos@googlemail.com

Bioinformatics analysis of biological sequences by Teresa Nogueira & Rita Ponce - February 15-19 2016 @ Lisbon, Portugal

OBJECTIVES: This five-days intensive course has as main objective provide the participants with knowledge about the biological sequences from reliable databases, as well as with autonomy and critical attitude in the use of bioinformatics software freely available in the Internet.

See the PROGRAMME at: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id=9 Course INSTRUCTORS: Teresa Nogueira (cE3c collaborator http://ce3c.ciencias.ulisboa.pt/teams/user/?id=285), Rita Ponce (https://www.linkedin.com/in/rita-ponce-7189283b)

INTENDED AUDIENCE

The course will be open to a maximum of 20 students, being directed to PhD or MSc students, postdocs, clinical analysts and other professionals working in Biology, Biochemistry and related topics. The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL, UP) and Biology and Ecology of Global Changes (BEAG UL, UA). For information of fees for other participants see the programme details.

Deadline for applications: January 22nd 2016

For additional details about the course and to know how to register, click here: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id=9 For more information about the course, please contact: teresainogueira@gmail.com

Nature-Based Design Frameworks by Gil Penha-Lopes, Hugo Oliveira & Luísa Nunes - March 14-18 2016 @ Lisbon, Portugal

OBJECTIVES: This five-days intensive course will introduce participants to different Nature-based bodies of knowledge and experience, such as the Biomimicry, Permaculture and Resilience topics. With almost 2 days per topic, the students will get a good feeling of how these topics see, do research and implement effective and sustainable solutions targeting a wide variety of societal, ecological and economic challenges.

See the PROGRAMME at: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id=7 Course INSTRUCTORS: Gil Penha-Lopes (CCIAM, cE3c), Hugo Oliveira (CCIAM, cE3c), Luísa Nunes (Escola Superior Agraria de Castelo Branco -IPCB, CEABN)

INTENDED AUDIENCE The course will be open to a maximum number of 25 participants, being directed to PhD or MSc students in Biology,

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SCENE Glasgow PythonForBiologists May23-27

INTRODUCTION TO PYTHON FOR BIOLOGISTS REPEAT COURSE!!

This course is being delivered by Dr Martin Jones, an expert in Python and author of two text books, Python for Biologists [http://www.amazon.com/Python-Biologists-complete-programming-beginners /dp/1492346136/] Advanced Python for Biologists [http://www.amazon.com/Advanced-Python-Biologists-Martin-Jones/dp/14952 44377/].

Due to high demand a repeat of this course will run from 23rd - 27th May 2016 at SCENE (the Scottish Centre for Ecology and the Natural Environment), Loch Lomond National Park, Glasgow.

Course overview: 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. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackle problems in their own research and (2) continue their Python education in a self-directed way.

Intended audience: This workshop is aimed at all 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.

Teaching format: The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizer's discretion. There will also be plenty of time for students to discuss their own problems and data.

Assumed background: 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.

Curriculum: Day 1: Module 1 - Introduction Module 2 - Output and text manipulation Day 2: Module 3 - File IO and user interfaces Module 4 - Flow control 1: loops Day 3: Module 5 - Flow control 2: conditionals Module 6 - Organizing and structuring code Day 4: Module 7 - Regular expressions Module 8 - Dictionaries Day 5: Module 9 - Interaction with the file system Module 10 - Optional free afternoon to cover previous modules and discuss data

The cost is Â£500 including lunches and course materials. An all-inclusive option is also available at Â£710; this includes breakfast, lunch, dinner, refreshments, accommodation and course materials. Participants will need a laptop with a recent version of Python installed.

Please send inquiries to oliverhooker@prstatistics.co.uk or visit the website www.prstatistics.com Please fee free to distribute this information anywhere you think suitable Other upcoming courses - TIME SERIES MODELS FOR ECOLOGISTS AND CLIMATOLOGISTS; GENETIC DATA ANALYSIS USING SIAR; ; APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS; SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R; ADVANCING IN STATISTICAL MODELLING USING R; INTRODUCTION TO STATISTICS AND R FOR BIOLOGISTS; DNA TAXONOMY; ; BIOINFORMATICS FOR GENETICISTS AND BIOLOGISTS; MULTIVARIATE ANALYSIS OF SPATIAL DATA; ADVANCES IN DNA TAXONOMY USING R;

Oliver Hooker PR˜Statistics

"oliverhooker@prstatistics.co.uk"
<oliverhooker@prstatistics.co.uk>

Switzerland Evolutionary Biology in the Alps June21-27

Application deadline: 14 February

Dear Colleagues

The 2016 edition of the Evolutionary Biology Workshop in the Alps will take place on 21-27June 2016 in Arolla, Switzerland.

Target participants are PhD students in early stages of PhD and advanced Master students - please pass the info to potential participants.

The main goals of this annual workshop, based on a concept developed by Stephen Stearns and John Maynard Smith, are to develop the following skills: - developing your scientific ideas through discussions in groups; - thinking critically and expressing oneself clearly; - turning a general idea into a research project; - writing a research proposal and defending it.

Faculty: William Rice (University of California Santa Barbara) Dolph Schluter (University of British Columbia) Tanja Schwander (University of Lausanne) John Pannell (University of Lausanne) Tad Kawecki (University of Lausanne)

It is you, the students, who will be in charge in this course. You will be divided in groups of 4-5 students. In those groups, you will work on your ideas. You, as a group, will decide what the important open questions in broadly defined evolutionary biology are, you will choose one, and attempt to develop a proposal for a research project that will address it. The faculty will visit the groups during the discussions to answer your questions, provide coaching and give you feedback on your projects, but they will generally take the back seat. Additionally, the faculty will give talks about their research and be available for informal discussion with individual students. At the end you will present your projects to other participants, and we will party.

The workshop will take place in the 100-year old hotel Kurhaus http://www.hotel-kurhaus.arolla.com/, located in a small alpine village at an altitude of 2000 m, which will help you to concentrate on the course while giving you also the chance to enjoy the views, small hikes, marmots and the alpine flora.

Fee: CHF 450.- (this covers part of the cost for room and board, the rest being subsidized by the Herbette Foundation).

Participants will receive a course certificate for 3 ETCS credits.

To apply, send a single file (pdf or rtf) containing a short motivation letter including a brief summary of your research interest, a cv, and the name of your scientific advisor to Caroline Betto-Colliard <ecologie-evolution@cuso.ch>, with Cc to tadeusz.kawecki@unil.ch . Please put “Evolutionary workshop” in the subject. Application Deadline: February 14, 2016.

– Tadeusz J. Kawecki Associate Professor Department of Ecology and Evolution University of Lausanne Biophore, office 3111 CH 1015 Lausanne, Switzerland

“tadeusz.kawecki@unil.ch” <tadeusz.kawecki@unil.ch>

UBirmingham EnvGenomics Mar6-11

NERC-MDIBL Environmental Genomics and Metabolomics Course, 2016

Online Registration Site: www.birmingham.ac.uk/-EnGen Date: March 6-11, 2016

Location:The University of Birmingham, UK

Number of Places:up to 50

Participation:Open to everyone.

Priority is given to NERC-funded PhD students and early-career scientists. Confirmation for attendance will be announced February 12, 2016.

Bursaries: Twelve (12) bursaries are available for the metabolomics track and 18 for the genomics track, covering registration, travel and accommodations.

Costs for Non-NERC Funded Researchers: Early bird £2105, standard £2340.

Course Leaders:John Colbourne, Joseph Shaw,Xin Zhou and Ben Brown (for genomics). Mark Viant and Warwick Dunn plus staff from the NERC Biomolecular Analysis Facility and Birmingham Metabolomics Training Facility (for metabolomics).

Research Organisations Involved: University of Birmingham (UK), BGI China National GeneBank (Shenzhen, China), Mount Desert Island Biological Laboratory (USA)

Online Registration Site: www.birmingham.ac.uk/-EnGen DESCRIPTION This training opportunity is the third European/UK installment of a successful annual course originating from Mount Desert Island Biological Laboratory. The curriculum is expanded to highlight a multi-omics (system biology) approach to research in environmental sciences. It trains PhD students and early career postdoctoral scientists to investigate how gene function and metabolism are influenced by environmental conditions while accounting for variation that exists within and among natural populations. The course is built on the paradigm that this multidisciplinary research field encompassing ecology, evolution, toxicology, biostatistics and informatics will most effectively grow by training early career environmental scientists to properly design comprehensive, large-scale, Next Generation Sequencing and Metabolomics experiments enabled by drastically increased sample-throughput and lower costs. Most importantly, the challenges of manipulating and analysing population-level omics (big) data must be addressed.

The course provides a significant introduction and much hands-on training experience so that participants can initiate their own environmental omics study and network with others in the field to launch Environmental Scientist careers in academia and industry. Case studies using multi-omics data sets collected at the University of Birmingham will be provided so that you can gain practical experience of analysing and integrating multi-omics data.

Course Details The course will include ~1.5 days of generic environmental omics training and ~3.5 days of specialised genomics or metabolomics training (parallel tracks).

The combined sessions will include: * Overviews of environmental genomics and metabolomics * Practical experience of analysing and integrating multi-omics data * Synthesis sessions to obtaining grant funding * Question and answer sessions with a panel of experts

The genomics track includes: * Library construction methods and QC * Introduction to automation systems and sequence data workflow * Software solutions for sequence workflows and their application in environmental research * RNA-seq alignment * Statistical considerations for analysing genome-scale data * Practical experience in applying open-source analysis tools to visualise complex sequence data and explore genome sequence variation, analyse Tuxedo output and perform gene set enrichment analysis * Synthesis sessions to explore using the most appropriate model organism and maximising outputs from your sequence data

The metabolomics track includes: * Experimental design * Quality assurance and quality control in metabolomics * Hands-on sample preparation * Analytical technologies including mass spectrometry and NMR spectroscopy * Data processing, including LC-MS and SIMS stitching procedures * Univariate and multivariate data analysis approaches * Metabolite identification

Evening Lecture Series Distinguished visiting academics will provide keynote lectures on each day of the course to highlight environmental omic applications that draw on the expertise of our guest faculty.

Daphnia is used for training because of its growing use as a model system in the environmental sciences and for improving environmental health protection, yet the skills learned during the course will be applicable to all study systems with maturing genomics and metabolomics resources.

j.k.colbourne@bham.ac.uk

UCalifornia LosAngeles ConservationGenomics Mar20-24

UCalifornia_LosAngeles.ConservationGenomics.Mar20-24 Reply-To: Mario Colon <mario.colon@ucla.edu> x-mailer: Apple Mail (2.3112)

UCLA/La Kretz Workshop in Conservation Genomics, 20-24 March, 2016

Conservation biology, genetics, and evolutionary biology have had a long and intimate relationship, and conservation constitutes one of the key applications of evolutionary analysis to real-world biological problems. The impacts of population and landscape genetics and gene expression studies have been particularly striking, and are helping to solve some of the most pressing problems in biological conservation.

As the field of conservation genetics continues to grow and mature, the availability of genome-scale data stand to make profound new contributions to our ability to identify and protect at-risk populations and recover those that are most endangered. However, genomic analyses also carry a heavy burdenÂXdata sets are enormous, often requiring diverse computational approaches for assembly, quality control and analysis.

The La Kretz annual workshop provides a comfortable, rigorous, but informal training environment for a small group of motivated graduate students to explore how conservation problems can best be addressed with genomic-level data. Our goal is to provide hands-on experience in the efficient collection, troubleshooting, and analysis of large data sets for conservation-relevant problems. One of the highlights of our workshop is active participation from members of several governmental agencies who are at the forefront of endangered species protection and management, providing a forum for exploring the most relevant aspects of conservation genomics to managers.

The UCLA/La Kretz workshop is held at the La Kretz Field Station (http://www.environment.ucla.edu/lakretz/fieldstation/) and Stunt Ranch Reserve (http://stuntranch.ucnrs.org) in the heart of the Santa Monica Mountains. Only 30 miles from UCLA and the LAX airport, but nestled in the relatively undeveloped 160,000 acre Santa Monica Mountains National Recreation Area, the Field Station/Stunt Reserve provides an ideal location to explore new developments in genomic science and pressing needs in conservation and management together in a single setting.

Our current instructor list, drawn from UCLA faculty and several other partner institutions, includes:

Ben Fitzpatrick (U. Tennessee Knoxville)

Kirk Lohmueller

Evan McCartney-Melstad

Gideon Bradburd (UC Berkeley)

Brad Shaffer

Victoria Sork

Bob Wayne

Ying Zhen

Plus a soon-to-be-disclosed RNA-seq teamÂK

Agency partners represented include: USGS

BLM

USFWS

CDFW

Topics covered include:

Overview of traditional conservation genetics

Next generation platforms: the best tool for the job

Data management pipelines:

Quality Control

Data storage

Data organization

Data types and analyses:

SNPs

Sequences

Exploring very large data sets

Functional genomic data

RNA-seq

Genomic data and GIS

Visualizing geographic structure and demographic history

Admixture, clines, and hybridization

Detecting adaptive variation

RNA-seq and the analysis of genes that matter

Prerequisites

Available housing limits course enrollment to ~20 students. Preference is given to doctoral candidates who are in the early to middle stages of their thesis research, and who have some familiarity with using a command line interface or programming languages (i.e. Perl, python etc.). Postdocs, faculty, and government researchers may also apply, but preference will be given to graduate students. We encourage applications from women, minorities, and individuals from under-represented demographics in the sciences.

Admission and Fees

Applicants will be admitted based on academic qualifications and appropriateness of research interests. The course fee is $425. This includes food and lodging at the La Kretz Field Station, as well as any incidental fees, for the duration of the course (arriving Sunday March 20, departing Friday March 25). In addition, course participants who would like to extend their stay at the field station for the remainder of the weekend may do so for no extra charge. For those opting to stay the weekend, departure time will be by 5:00 pm on Sunday March 27.

This year, the workshop is co-sponsored by a UC Catalyst program grant that will provide some support for faculty and student support and staffing needs. University of California students may apply for partial support (up to $225) from the newly awarded Conservation Genomics Consortium (https://sites.lifesci.ucla.edu/eeb-conservationgenomics/) funded under the UC Catalyst program.

UCLA students are encouraged to take the La Kretz Workshop for graduate credit. Other

— / —

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

UMichigan NextProf May10-13

NextProf Science - Future Faculty Workshop

The University of Michigan will host NextProf Science, May 10-13, 2016, to encourage talented scientists with a demonstrated commitment to diversity to consider academia as a career. Targeted at postdoctoral fellows and advanced doctoral students, the workshop is aimed at helping participants develop strategies that will strengthen their ability to pursue academic careers.

Underrepresented minorities and women are especially encouraged to apply. Travel, lodging, and meals will be provided for those selected to participate. Deadline for submission of all application materials is February 21, 2016. Learn more at: sites.lsa.umich.edu/nextprof-science.

– 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

"knowlesl@umich.edu" <knowlesl@umich.edu>

UWashington SummerInstituteGenetics RegistratonsOpen

Registrations for the 2016 Summer Institute in Statistical Genetics are now being accepted. Scholarship applications are processed as they are received.

Information is available at:

< http://washington.us3.list-manage1.com/track/click?u=6909f79868b4fbd3c79e21516&id=78d1d879d5&e=e1777cab14 >

Bruce Weir Department of Biostatistics University of Washington Box 359461 Seattle, WA 98195-9461 Phone: (206) 221-7947

Bruce Weir <bsweir@uw.edu>

YosemiteNatlPark Symbiosis May6-8

Dear Colleagues,

The Sixth annual Symbiosis Workshop will take place on May 6th-8th, 2016 at the Sierra Nevada Research Station, Yosemite National Park. This has become a great venue for a diversity of symbiosis researchers, so we hope to continue to attract a diverse group:

Keynote speaker 2016: Dr. Betsy Arnold from the University of Arizona.

Information about our meeting:

Why: Our goal is to better integrate scientists that focus on symbiosis research. We plan to continue annual workshops at Yosemite as this site is both beautiful and secluded. This will be our 6th annual meeting and we have been attracting scientists from all over the country and overseas.

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

When: The talks and formal meeting will be held May 7-8, 2016, though we make accommodation arrangements available for attendees to arrive on Friday the 6th to provide opportunities to enjoy the park. Since time at the conference is limited, we ask attendees to submit an abstract and a preference (talk versus poster). Priority will be given to those presenting. Abstract and early bird registration are due on February 15, 2016.

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

Link to meeting information: http://www.sachslab.com/symbiosis-2015.php The registration form for the 2016 Symbiosis Workshop is active: http://snri.ucmerced.edu/symbiosis Payments should be made at: https://intelforms.ucmerced.edu/Form/Symbiosis Please direct any questions to the organizers: Joel Sachs joels@ucr.edu A. Carolin Frank cfrank3@ucmerced.edu

Joel Lawrence Sachs <joel.sachs@ucr.edu>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.