
E v o l D i r

April 1, 2016

M o n t h i n R e v i e w

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.

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Almeria Spain Biodiversity Sep29-30

Dear all,

Nature and Oceans of Americas and Botanical Garden of University "Marta Abreu" de las Villas, Cuba in collaboration with Andalusian Center for the Assessment and Monitoring of Global Change (CAESCG), University of Almeria is also glad to announce the 1st Symposium on Biodiversity and Nature Conservation: Dissemination and transfer of knowledge among all society sectors.

The first annual Symposium will take place on September 29th-30th, 2016 at the University of Almeria, Spain.

This will become a great venue for a diversity of researchers, managers, conservationists, environmental journalists and general public, so we hope to attract a diverse group.

Information about our meeting: Our goal is to better integrate all society sectors focused on conservation. We

plan to continue annual workshops at Almería as this site is both beautiful and unique. This will be our 1st annual meeting and we have been attracting scientists from all over the country and overseas.

Registrations are now open.

Abstract and early bird registration are due on May 1st, 2016.

Symposium has a limited capacity of students.

Link to meeting information: <http://www.facebook.com/infoconserbio/> The registration form for the 2016 Symposium is active:

<https://mega.nz/#!QYIUQahD!R-AtI-kfIUbeyRz9WYyr3blTb1VX2TN-KU482tdwnKI>

For further information, please feel free to contact us:

infoconserbio@gmail.com

The organizing committee

marga lopez rivas <margaflor13@hotmail.com>

Ascona Switzerland EvolutionaryChange Jun5-9 2

Dear all,

This is the final call for applications for the conference on the 'Genomic basis of eco-evolutionary change' to be held from June 5th-9th 2016 at the Monte Verita conference centre in Ascona, Switzerland.

Conference costs (including registration, food and accommodation): 900 Swiss francs for PhD students 1200 Swiss francs for all other participants

Applications: Please email us by the 3rd of March if you are interested in attending the conference. However, we also ask you to send your CV (max 2 pages) and a poster abstract for the meeting, all in one PDF, by the 9th of March to monte-verita@env.ethz.ch.

Conference details: This conference is being organised in association with ETH Zurich's Center for Adaptation to a Changing Environment (ACE). The aim of this conference is to connect rapidly expanding information on the genomic basis of ecologically relevant traits to better understand and predict the dynamics of eco-evolutionary feedbacks. Through talks, breakout 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 Ben Kerr Hannah Kokko Tom Mitchel-Olds Patrik Nosil Ole Seehausen Victoria Sork Daniel Wegmann Yvonne Willi Noah Whiteman

More information on the conference and venue can be found at: <http://www.adaptation.ethz.ch/education/-monte-verita-conference2016.html> Best wishes,

The organising committee

James Buckley Katalin Csillery Robert D'Amico
Jonathan Levine Martin Turcotte Alex Widmer

Dr. James Buckley Adaptation to Changing Environments (ACE) postdoctoral fellow Institute of Integrative Biology, ETH Universitätstrasse 16 CHN G 35.2 8092 Zurich james.buckley@env.ethz.ch Tel: +41-44-633 8109 <http://www.adaptation.ethz.ch/-center.html> "james.buckley@env.ethz.ch" <james.buckley@env.ethz.ch>

Asilomar California LocalAdaptation Jul14-17

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

Awards will cover registration for graduate students who would like to attend and present posters. Six abstracts will be selected for oral presentations, and the students will receive \$500 awards. Details and registration are available at the AGA website: <http://www.theaga.org> APPLY BY APRIL 1ST

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

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

Sally Aitken University of British Columbia Jill Anderson University of Georgia Zach Cheviron University of Montana Emily Dittmar Michigan State University Suzanne Edmands University of Southern California David Field Inst. Science and Tech, Austria Lila Fishman University of Montana Jannice Freidman Syracuse University Steve Keller University of Vermont John Kelly University of Kansas Brian Langerhans North Carolina State University Curtis Lively Indiana University Robert Reed Cornell University Douglas Schemske Michigan State University Rena Schweizer UCLA Kerry Shaw Cornell University Peter Tiffin University of Minnesota

AGAJOH <AGAJOH@oregonstate.edu>

Austin Evolution Jun17-21 Spotlights 2

EVOLUTION2016 SPOTLIGHT SESSIONS Reminder- Application deadline is Apr. 30

This year we are introducing a new way to give an oral presentation at the annual 'Evolution meetings': SPOTLIGHT SESSIONS.

Each Spotlight Session will focus on an intellectually cohesive theme (see below), providing an excellent venue to present your research to a relevant and highly engaged audience. If your work falls within one of the themes, we strongly encourage you to apply to participate in the appropriate Spotlight session as it will include other speakers and audience members that are most interested in your work. Session organizers are now accepting applications. Session organizers are leaders in their field and have been asked to select presentations to create an intellectually stimulating session while ensuring speakers reflect diversity (including gender and career stage, i.e., grads + pdfs SHOULD APPLY). There is no cost/risk to applying as individuals can (and should) also register to give a standard talk in case they are not selected to participate in the Spotlight Session. Selection is competitive and for chosen speakers it will make a great addition to your CV.

The deadline for applications to all three Spotlight Sessions is Apr. 30 (coinciding with the end of early meeting registration). This year's Spotlight Sessions are:

1) The evolution of species interactions Organizers: M.C. Stoddard (Harvard), Marjorie Weber (UC Davis/Michigan State) and Jesse R. Lasky (Penn State) Applications to: jrl35@psu.edu

2) Next generation phylogenetic inference Organizers: Erick Matsen (Fred Hutchinson Cancer Research Center), Tracey Heath (Iowa State), and Felipe Zapata (San Francisco State) Applications to: matsen@fredhutch.org

3) Understanding history and process in rapid diversification with genomic data Organizer: Katie Wagner (U Wyoming) Applications to: cwagne22@uwyo.edu

Learn more about the themes of the Spotlight Sessions: <http://www.evolutionmeetings.org/special-talks.html>
APPLICATION INFORMATION A Spotlight Session consists of one 28 min, five 13 min, and twelve 5 min ('lightning') talks. If you are interested in speaking in a Spotlight Session please submit an application to the appropriate organizer (emails above). The application must include: (1) Name, (2) institution, (3) rank (e.g., student, pdf, faculty), (4) names & institutions of co-authors, (5) a short abstract (max: 300 words), and (6) which talk types you are willing to give (28, 13, or 5; the more flexible you are the more likely you are to be selected). Applications must be received by April 30, 2016. No financial support is provided to selected speakers (i.e., speakers must pay their own travel, accommodation, registration, etc.).

You may still register to give a standard or lightning talk in a regular 'open session' at the meetings even if you ap-

ply to participate in a Spotlight Session, and you should do so if you want to ensure that you can give a talk. However, if you are selected to speak in the spotlight session you will have to choose which talk slot to use as each attendee is allowed to give only one oral presentation. Spotlight sessions are committed to representing diversity. All interested individuals are encouraged to apply.

howard.rundle@uottawa.ca

Bloomington Indiana 2016 Galaxy Community Jun25-29

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

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

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

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

Abstract submission for oral presentations closes March 25. Abstract submission for posters and computer demonstrations closes May 20.

Early registration is now open. Registration starts at less than \$45/day for post-docs and students. Registering early assures you a place at the conference and also a spot in the training workshops you want to attend. You can also book conference housing when you register. Registration and lodging scholarships are available for attendees from underrepresented groups and developing countries.

Thanks, and we hope to see you in Bloomington!

The GCC2016 Exec

– <http://galaxyproject.org/> <http://getgalaxy.org/> <http://usegalaxy.org/> <https://wiki.galaxyproject.org/> Dave Clements <clements@galaxyproject.org>

Bloomington Indiana GalaxyCommunity Jun25-29 DeadlineExt

The oral presentation abstract deadline for GCC2016 has been extended to April 8 (<https://gcc2016.iu.edu/abstracts/>). Scholarship applications are still open as well.

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

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The GCC2016 Exec – <http://galaxyproject.org/> <http://getgalaxy.org/> <http://usegalaxy.org/> <https://wiki.galaxyproject.org/> Dave Clements <clements@galaxyproject.org>

Cambridge PlantEvolution Sep15-16

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

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

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

To register or submit an abstract see

<http://www.plantsci.cam.ac.uk/research/sambrockington/uk-plant-evolution-2016> or email bjg26@cam.ac.uk with any questions.

“bjg26@hermes.cam.ac.uk” <bjg26@hermes.cam.ac.uk>

**CornellU EEID EvolutionDisease
Jun3-5**

Dear Colleagues,

We are pleased to open Registration, Abstract Submission, and Reservations for On-campus Housing for the 14th annual Ecology and Evolution of Infectious Disease meeting, to be held at Cornell University June 3-5, with a welcome reception on the evening of June 2.

The registration fee is very modest this year, thanks to generous support from our Sponsors. Registration fees will be \$100 for Students and \$175 for Faculty/Staff. On-campus lodging is also modestly priced.

Link for Registration: <http://blogs.cornell.edu/eeid/eeid-2016-registration/> Link for Abstract Submission: <http://blogs.cornell.edu/eeid/eeid-2016-abstracts/> Link for Travel and Lodging: <http://blogs.cornell.edu/eeid/eeid-2016-travel-and-lodging/> Registration and Abstract Submission will remain open until May 2.

There will be four primary themes for the meeting, with both theoretical and empirical work in plant and animal systems included under all themes:

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

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

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

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

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

tel: 607-255-3254 fax: 607-255-0939 <http://www.lazzaro.entomology.cornell.edu> bplaz-zaro@gmail.com

**FayettevilleAR ICSB CaveBiology
Jun13-17**

23rd International Conference on Subterranean Biology
Fayetteville, Arkansas, United States

Abstracts due 13 March 2016.

>From the conference website (<http://www.speleobiology.com/icsb2016/>) :

“Welcome, on behalf of the Organizing Committee, to members of the International Society for Subterranean Biology, all speleobiologists, and anyone interested in subterranean life. The 23rd International Conference on Subterranean Biology, jointly sponsored by the Department of Biology at the University of Arkansas, will be held in Fayetteville, Arkansas, USA, from June 13 to June 17, 2016. This will be the first ICSB held in the United States, and we are eager to showcase the many caves and karst features in the area and to bring together scientists and students with an interest in subterranean biology from the U.S. and from around the globe. These meetings often have participants from more than 20 countries, and we hope to break that record in 2016. In addition to contributed papers and poster sessions, several special symposia on topics such as evolution and development as well as conservation are being planned. The meeting itself will be hosted on the campus of the University of Arkansas. A number of special events are also being planned, including a day long excursion and several receptions. As more information becomes available, we will post it on this website. Please stay tuned.

David Culver, Chair of the Organizing Committee

Committee Members: Daniel Fong, Matthew L. Niemiller, Megan L. Porter, Michael E. Slay, and Steven J. Taylor”

“czs0021@tigermail.auburn.edu”
<czs0021@tigermail.auburn.edu>

IST Austria SystemsBiol May18-20

The Information, Probability and Inference in Systems Biology Conference (IPISB2016) will be held from May 18-20, 2016 at IST Austria in Klosterneuburg, Austria.

<http://ist.ac.at/ipisb/> Conference organizers:

Peter Swain, University of Edinburgh Gasper Tkacik, IST Austria

The meeting will address the following key areas

- The links between control theory, decision-making, and information theory, as applied to systems, evolutionary, and synthetic biology
- New information-theoretic approaches to sensing and signal transduction by cells with an emphasis on dynamic problems, including the quantification and statistical estimation of information in molecular biology.
- Study of stochastic biochemical networks new developments in Monte Carlo simulation methods, approximate analytical techniques, and the need for a more developed theory of stochastic chemical reaction networks.
- Inferential methods for statistical modelling of time series data from single cells, including simulation-based methods, likelihood-free inference, particle filtering techniques and reversible jump MCMC.
- Cellular decision-making, both intracellular and inter-cellular how to apply mathematics of decision theory to the biological context.

“nick.barton@ist.ac.at” <nick.barton@ist.ac.at>

London Ontario CanadianSocietyZoologists May9-12

SECOND CALL

Just a reminder that the Early Bird Deadline for The Canadian Society of Zoologists / Société Canadienne de Zoologie Annual Conference is approaching. The conference will be held May 9-12th in 2016 at Western University in London Ontario. The Early Bird registration deadline is 15 March.

<http://www.csz-scz2016.com/> The meeting - including plenary talks, workshops, symposia, the ZET lecture, the Fry Award, and poster sessions - will showcase the latest advances in the study of animals and their environment. Social activities will include an opening reception, meet and greets, poster sessions, cocktails and a banquet.

This is shaping up to be a great meeting, on the beautiful campus of Western University, in spring! See the conference web page for full details.

<http://www.csz-scz2016.com/> Graham J. Thompson

Associate Professor Biology Department | Western University London | Ontario | Canada N6A 5B7 Tel: 1-519-661-2111 ext 86570 iPhone: 1-519-615-6066 e-mail: graham.thompson@uwo.ca Twitter: @termiteGT Web: www.uwo.ca/biology/faculty/thompson “graham.thompson@uwo.ca” <graham.thompson@uwo.ca>

Madison Wisconsin QuantGenetics Jun12-17

Dear Colleagues,

This is a quick reminder that the early-bird registration deadline for the 5th International Conferences in Quantitative Genetics (<http://www.icqg5.org/>) is March 25th, so less than a week away! ICQG 5 www.icqg5.org The ICQG5 will create a unique and vibrant forum for exchange of information on the latest advances in the development and application of quantitative methods to ...

The conference will take place in Madison, WI June 12 to 17, 2016 and includes an outstanding set of invited speakers, an opportunity for poster presentations and invited presentations from junior investigators to be selected from the poster abstracts (<http://www.icqg5.org/-#!schedule/cjg9>). Registration for the conference includes refreshment breaks, lunches and poster session receptions throughout the week, Sunday welcome reception, Wednesday happy hour and program book.

Fellowships are still available for students of US institutions working in quantitative genetics related to plant research. For more information please check - <http://www.icqg5.org/-#!register/mainPage> Four short courses will also be offered the week prior to the conference (June 6 to 10). More information about schedules and topics can be found at: <http://www.icqg5.org/-#!blank/rbgpy> We hope to see you all in Madison this coming June!

Sincerely,

ICQG5 co-chairs (Natalia de Leon and Guilherme Rosa)
& Organizing Committee

“bret.payseur@wisc.edu” <bret.payseur@wisc.edu>

**Minnesota TwinCities
AmericanSocMammalogists
Jun24-28**

Ninety-sixth meeting of the AMERICAN SOCIETY OF MAMMALOGISTS 24-28 June 2016 University of Minnesota ' Twin Cities

We have an exciting meeting planned for this year! The scientific program will include simultaneous technical sessions, poster sessions, as well as workshops, symposia, and plenary speakers. A full social agenda is planned with field trips, picnic, Run-for-Research, student pizza party, auction, and awards ceremony and social.

SAVE MONEY AND REGISTER NOW!!! Registration is now open for ASM 2016! Register online (<https://outreach.ksu.edu/etrakWebApp/-Registration.aspx?MeetingCode!1604>) now! Please keep in mind that your login password for conference registration is different than your society password used to access the ASM Business Office site. If you do not remember your password from previous years, simply select ³retrieve your forgotten password² and it will be sent to your e-mail quickly. Regular registration ends March 31st!!!

ABSTRACT SUBMISSION DEADLINE ' MARCH 31ST AT 5 PM (CDT)!!! Share your research with hundreds of mammalogists from around the world. Submit your abstract for an oral presentation or poster for ASM 2016! Abstract submissions will close on March 31, 2016 at 5:00 pm (Central Daylight Time).

All presenters must register and submit full payment for the conference prior to submitting their abstract. This MUST be done prior to 5:00 pm (Central Daylight Time) on March 31st to ensure timely processing. After registering for the conference, you will receive two auto reply confirmation receipts. After verifying your registration, you will receive a separate confirmation letter that will contain information about how to submit an abstract. An abstract will not be accepted for the program until the presenting author has registered and paid in full.

NEW THIS YEAR! Oral presenters interested in participating in a solicited Thematic Session can indicate such during abstract submission. These sessions are intended to highlight research in new and important areas. Thematic Sessions will occur alongside regular technical sessions but may use alternative formatting as necessary (e.g., 30-minute talks). Session topics this year include Climate Change and High-Latitude Mammals, Microbiome of Non-Model Organisms, Phylogenomics, and 5-Minute Lightning Talks. Abstracts will be vetted and selected for each Thematic Session by the Program Committee. Please contact John Hanson (j.delton.hanson@researchtesting.com) for more information!

RESERVE YOUR ROOM AND MAKE TRAVEL PLANS FOR ASM 2016 Housing: A variety of housing options are available this year, including campus dorm housing. Reservations should be made before the end of May for most housing options. Be sure to reference the American Society of Mammalogists to receive the conference group rate at the meeting hotels. Check out the meeting travel page (<http://conferences.k-state.edu/mammalogists/travel-and-lodging/>) for more information!

Transportation: Airlines servicing Minneapolis-St. Paul International Airport (<http://www.mspairport.com/>) include American, Delta, Frontier, Spirit, United, and Southwest. The airport also offers various car rental options. There are several options for travel from the airport to the hotels ranging from taxis and shuttles to public transportation. To research the method that best suits you, please see the options online (<https://www.mspairport.com/-GroundTransportation.aspx>). Minneapolis is also serviced by Greyhound (<http://www.greyhound.com/>) and Amtrak (<http://www.amtrak.com/home>).

For more information, visit the meeting website (<http://conferences.k-state.edu/mammalogists/>).

Contact: Tony Ballard K-State Conference Services
Phone: 785-532-2402 Email: tballard@k-state.edu

Cody Thompson <cwthomp@umich.edu>

MNHN Paris Morphometrics Jun1-2

Dear colleagues

It is my pleasure to inform (or remind) you that the 9th Symposium of Morphometrics and Evolution of

Forms (SMEF9) will take place in Paris Museum on June 1st and 2nd 2016. website (in french): <http://biogeosciences.u-bourgogne.fr/smef9/> This symposium aims at favouring exchanges among practitioners of morphometrics in various biological sciences, including evolutionary biology, developmental biology, bioarcheology, systematics, palaeontology and ecology. Beyond methodological aspects, it is aimed at all scientists interested in the quantification and study of biological forms.

Registration deadline is April 15 http://biogeosciences.u-bourgogne.fr/smef9/documents/-smef9_second_circular.doc This symposium is free of fees and open to all provided registration and in the limit of available places. Lunch are included for registered attendees.

Communications will be in the form of short talks (10' + 5' for questions) or posters. The main language has traditionally been French, but communications in English are also welcome.

Looking forward to seeing you in Paris

For the Scientific committee

Vincent Debat

– Vincent Debat UMR7205 ISyEB Museum National d’Histoire Naturelle 45 rue Buffon CP50 75005 Paris www.evomorpho.com 01 40 79 30 54

“debat@mnhn.fr” <debat@mnhn.fr>

NewHampshire GlobalChange Jul16-17

I am trying to attract evolutionary biologists to the GRS.

Thank you, Emily

Dear colleagues, We would like to attract evolutionary biologists to submit abstracts to our interdisciplinary Gordon Research Seminar associated with the Global Ocean Change Biology Gordon Research Conference. The seminar will be held on July 16-17 in Waterville Valley, NH and is open to graduate students, post-docs, and early career scientists.

Specifically, we are interested in presentations from evolutionary biologists studying local adaptation, rapid evolution, and transgenerational plasticity in the context of natural environmental variability and global ocean

change.

Understanding the Biological Consequences of Global Ocean Change: Insights from Environmental History The focus of this meeting is to bring together our understanding about how the environmental history of a population or individual influences tolerance or vulnerability to future environmental change and thus the ability for marine species to cope with the multi-stressor scenario of global ocean change. We are interested in studies that span a wide range of time scales (from carryover effects within an individual’s lifetime to trans-generational plasticity to population level timescales to pale oceanographic time scales), and we are also looking to highlight interdisciplinary tools for linking environmental exposure to organismal performance.

To submit an abstract for an oral or poster presentation and to find out more information, go to <https://www.grc.org/programs.aspx?id=17217> For full consideration, please *submit your abstracts by April 15.* Please contact Seminar chair Emily Rivest at ebrivest@ucdavis.edu with any questions.

Kind regards, Emily Rivest, chair Christopher Cornwall, co-chair

Emily Rivest <ebrivest@ucdavis.edu>

Orlando Florida GeneticsSocAm Jul13-17

HEADING: GSA-wide conf. on Population, Evolutionary, and Quantitative Genetics

We wish to call your attention to the Genetics Society of America’s society-wide meeting to be held in Orlando, Florida on 13-17 July 2016. Along with the traditional model-organism meetings, for the first time, the GSA will also sponsor a specific focal meeting on Population, Evolutionary, and Quantitative Genetics. The overall meeting is expected to attract a few thousand participants - one of the largest ever gatherings of geneticists from diverse areas, and will mark the 100th anniversary of the journal Genetics.

The PEQG venue will harbor about 85 slots for 15-minute individual talks, as well as a large number of poster positions. Plenary speakers include Dirk De Koning, John Willis, and Patricia Wittkopp. This meeting will also sponsor the inaugural James Crow Award for early-career investigators.

Key links:

Home page PEQG - <http://www.genetics2016.org/-communities/peqg> Abstract Submission Page - <http://www.genetics-gsa.org/genetics/2016/abstracts/-cgi-bin/index.pl?commu=peq> DEADLINE MARCH 23

Registration Page - <https://secure.genetics-gsa.org/-cgi-bin/tagc16r/index.pl?commu=peq> James F Crow Early Career Researcher Award - <http://www.genetics2016.org/awards-peq> DEADLINE MARCH 25

Home page TAGC - <http://www.genetics2016.org/-index.htm> Organizing Committee: Michael Lynch, Kirsten Bomblies, Lauren McIntyre, Bret Payseur, Dmitri Petrov

Suzy Brown, CMP Senior Director

Genetics Society of America 9650 Rockville Pike Bethesda, MD 20814

301/634-7341

301/634-7079 Fax sbrown@genetics-gsa.org

TAGC-Email-Signature

“Brown, Suzy” <sbrown@genetics-gsa.org>

Savannah Georgia PlantEvol Jul29-Aug3 UndergradTravel

We are pleased to announce the PLANTS program funded by the National Science Foundation and Botanical Society of America to bring talented and diverse undergraduates to the BOTANY 2016 meeting on July 29 - Aug 3, 2016 in Savannah, Georgia.

Why PLANTS? The PLANTS program (Preparing Leaders and Nurturing Tomorrow’s Scientists: Increasing the diversity of plant scientists) will fund up to 12 undergraduates from throughout the US and Puerto Rico to attend the meeting, receive mentoring from graduate students, postdocs and faculty, attend scientific sessions, and participate in networking events including the Diversity Luncheon and career-oriented activities. The program covers the normal costs of travel, registration, and food and accommodation at the meeting. An overview of the scientific conference is available at: www.botanyconference.org Why BOTANY 2016? The annual Botany Conference is a meeting of several scientific societies serving over 7,000 plant scientists and

students whose research and practice span the globe. The conference encompasses the diverse scope of botanical study, including areas such as systematics, ecology, evolution, physiology, genetics, development, paleobotany, and economic botany. Workshops cover topics as diverse as genomics, conservation assessments, teaching science, applying to grad school, and unconventional science and technology careers.

APPLICATIONS: Applications are accepted through MARCH 15, 2016 at http://www.botany.org/Awards/-F_PLANTS.php. Applications include completion of the online form providing your statement of interest, a letter of recommendation, and unofficial transcripts. Applications are welcome from all undergraduates who have an interest in the plant sciences; the admissions goal is to create a diverse pool of students. The application form is located online at http://www.botany.org/Awards/F_PLANTS.php. We encourage you to review the online form thoroughly before filling it out. Please have letters of recommendation and unofficial transcripts sent directly to Heather Cacanindin at HCacanindin@Botany.org. Students must be able to attend the entire Botanical Society of America meetings in Savannah, July 30- Aug 3, 2016.

Applicants must be domestic undergraduate students registered or very recently graduated (i.e., within the last 12 months). Students demonstrating a need for funds to attend BSA will be given preference, and will be selected so that as a group, they will help to diversify the pool of undergraduates attending the meetings. More information is available from Ann Sakai (aksakai@uci.edu), Anna Monfils (monf1ak@cmich.edu), or Heather Cacanindin (hcacanindin@botany.org).

“aksakai@uci.edu” <aksakai@uci.edu>

UBraunschweig Adaptation

Adaptation in nature “from ecology to genomes Environmental conditions change constantly and individuals have to adapt in order to persist. Adaptation therefore plays a central role in evolutionary processes. However, there are considerable gaps between ecological and genetic perspectives on adaptive evolution. Despite revolutionary changes in data acquisition in molecular biology, our current knowledge about trait evolution in natural systems is scarce. A holistic view on evolutionary processes is typically hampered by a lack of knowledge about the threads connecting molecular ge-

netic traits with higher-level phenotypes. Filling these gaps has been considered a key challenge for biologists of the 21st century.

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

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

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

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

Where: Technische Universität Braunschweig (Hauptgebäude).

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

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

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

Confirmed speakers:

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

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

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

UGoettingen Germany ConservationGenetics Oct5-7

We are pleased to announce the 2nd Annual Meeting in Conservation Genetics to take place October 5th to 7th, 2016 in Goettingen, Germany. Submission of abstracts is now open and possible until May 1st. Registration is also open and possible until July 31st.

Please find additional information on submission guidelines, registration etc. at

www.landscapegenetics.info/consgen16 You can also download the flyer to help spread the word:

www.landscapegenetics.info/consgen16/flyer.pdf We look forward to seeing you at the meeting!

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

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

UToronto OE3C Ontario Evolution May 5-7

Registration has now opened for the 2016 Ontario Ecology, Ethology, and Evolution Colloquium (OE3C), being held from May 5-7th at the University of Toronto St. George campus in downtown Toronto, ON.

OE3C is a broad and inexpensive conference covering many topics in the fields of ecology, evolution, and behaviour. This conference is an excellent opportunity for early and late career scientists alike to meet others in the field and present their work.

Early-bird registration is open from February 8th to March 21st. After this period, regular registration rates apply until registration closes on April 16th, 2016.

Register online for the conference at: <http://oe3c2016.org/register/> *OE3C REGISTRATION INFORMATION*

Before you register please read the following information.

COSTS: Early-bird registration for students and post-doctoral fellows is \$93, after March 21st registration fees increase to \$103.50. Registration for faculty and professionals costs \$119 for the entire registration period. These fees include breakfast, lunch, and coffee breaks for two days of the conference, alcoholic beverages at the Thursday night social, as well as the official OE3C '16 gift bag.

TALK FORMATS: We are excited to announce that this year we will be introducing a new talk format to OE3C Lightning Talks! Lightning talks will be 5-minute oral presentations with slides, followed by a 2-minute

question period. There is also the option of presenting a standard conference talk, a 12-minute oral presentation with a 3-minute question period, or a poster presentation during the Friday evening poster social.

ACCOMMODATIONS: We have arranged for lodging at U of T New College Residences. These rooms are on campus and less than a five-minute walk from the conference venue. If you require accommodation at New College Residences, you will have the option of a single (\$43/night) or a double room (\$30/person or \$60/room night). We recommend booking for three nights (Thursday May 5th to Saturday May 7th) so that you get the full OE3C experience and don't miss any sessions or social events. This offer ends on March 21st, so be sure to book before the early bird deadline. To register, visit www.torontores.com for a Reservation Form, then click on 'Book A Room'. Fill out the 2016 Summer Residence Reservation Form for Short Term Stays and email or fax it to the address indicated on the form. Be sure to enter special rate code `OE3C2016` on your Reservation Form.

SHIRTS: We will be selling T-shirts at OE3C. To secure your size, please purchase one during registration. They cost \$12 if purchased with registration and \$15 if purchased at the conference. The T-shirts feature the OE3C 2016 logo and can be viewed on the OE3C webpage.

ACCESSIBILITY: The lecture rooms that we will be using in the Bahen Centre are wheelchair-accessible. Please contact us at oe3c.uoft@gmail.com with any other accessibility-related questions or concerns and we will do our best to accommodate them.

Please write us at this address (oe3c.uoft@gmail.com) with further questions. We look forward to seeing you in Toronto from May 5-7!

Best regards,

OE3C 2016 Planning Committee

Amardeep Singh <amardeep.singh@mail.utoronto.ca>

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AarhusU EvolutionaryAdaptation

Applications are invited for a PhD fellowship/scholarship at Graduate School of Science and Technology, Aarhus University, Denmark, within the Bioscience programme. The position is available from 1 August 2016 or later.

<http://talent.au.dk/phd/scienceandtechnology/-opencalls/calls-on-specific-projects/may-2016/-environmental-stress-adaptation-in-invertebrates/>

Title: Environmental stress adaptation in invertebrates

Research area and project description: Evolutionary biology, ecophysiology and molecular biology

The successful applicant will participate in the Department's work on evolution, ecophysiology and molecular biology with emphasis on adaptation to thermal stress, responses to thermal stress (acclimation and hardening) and the molecular mechanisms underlying these adaptive responses. The work includes studies of membrane lipids, gene expression, protein expression and

sequence analysis, but also whole-organism studies of performance, mainly on the *Drosophila* model. Detailed studies of stress responses have shown that organisms have developed sophisticated physiological adaptations to combat environmental stress.

The project aims to identify and investigate candidate systems for studying thermal adaptation and responses. For example, several investigations point to a connection between thermal adaptation and genes associated with vision and phototransduction. To achieve the aim of the project a focus on molecular investigations combined with information from population level and physiology will be applied to achieve an integrated functional understanding.

The work will be done under the supervision of Assoc. Prof. Jesper Givskov Sørensen (AU), supported by a grant from Aarhus University Research Foundation.

Qualifications and specific competences: A Master's degree in Bioscience, Biotechnology or similar or a bachelor's degree in a relevant subject are possible backgrounds. A strong interest in experimental as well as analytical work and the ability to communicate scientific work is required. Experience with the model organism

Drosophila or alternatively other insect species is an advantage.

Place of Employment and Place of Work: The place of employment is Department of Bioscience, Aarhus University, Denmark, and the place of work is the section for Genetics, Ecology and Evolution, Ny Munkegade 114-116, 8000 Aarhus C, Denmark

Contacts: Applicants seeking further information are invited to contact:

Jesper Givskov Sørensen, phone: +45 3018 3160, e-mail: jesper.soerensen@bios.au.dk, for further information about the position.

“jesper.soerensen@bios.au.dk”
<jesper.soerensen@bios.au.dk>

BuenosAires AvianSpeciation

Ph.D. fellowship

Project title: Phylogenomic analysis of incipient Neotropical birds: studying the contribution of selection in the speciation process

Institution: Museo Argentino de Ciencias Naturales Bernardino Rivadavia, Buenos Aires, Argentina.

Director. Dr. Darío Lijtmaer (www.researchgate.net/profile/Dario.Lijtmaer).

Description of the Ph.D. project: The general project consists in the study of the speciation process in Neotropical birds and the role of selection. Within this general project, the Ph.D. project in particular is to analyze the recent radiation of the southern capuchinos, a group of 8 sympatric species of passerines belonging to the genus *Sporophila* that are still undergoing the speciation process. These species differ in their coloration and vocalizations, but do not show differences in their neutral DNA (due to their recent divergence and likely also hybridization). This suggests that selection (natural and/or sexual) is having a relevant role in the speciation process. Based on the study of the complete genome of some of these species we will identify areas that suggest the presence of speciation genes and they will be studied from a functional perspective. On the other hand, behavioral analyses will be performed to study homo- vs heterospecific recognition and the sexual characters used for mate choice, studying the possible role of sexual selection.

The Ph.D candidate should have a biology degree and should be motivated and interested in performing field work, lab work and bioinformatic analyses, including visits to Institutions outside Argentina. The capacity to work as part of a team is vital.

Deadline for applying: 01 April 2016

The fellowship will begin in May 2016

Contact: Send CV to dariolijtmaer@gmail.com (Spanish and English are preferred, Portuguese is also accepted).

dariolijtmaer@gmail.com

ETH Zurich PlantMicrobeCoevolution

Graduate position in Plant-Microbe Interactions:

In the Group of Plant Nutrition at ETH Zurich in Switzerland we combine basic research on mechanisms driving and mediating plant nutrition with field trials to solve topical problems in plant production. In the multidisciplinary team, we are recruiting a motivated PhD student for a project that combines community ecological analyses of microbial root symbionts with plant physiological ecological analyses to mechanistically elucidate microbe-plant-soil feedbacks. Specifically, the PhD student will address soil constraints to sustainable plant production, in a project entitled ‘Ecological intensification of organic rooibos cultivation in South Africa (EcoInt)’. Root-associated microbes are powerful mediators of plant nutrition and health and for this they are increasingly considered promising for farming on marginal land. The collaborative research project with Stellenbosch University and various stakeholders in South Africa has the goal to establish a knowledge base on suspected declines of beneficial and accumulation of antagonistic microbes, which are thought to be responsible for yield declines in monospecific and long-term cultivation of Rooibos tea, *Aspalathus linearis*, a legume bush endemic to South-Africa. The research will also engage producers to test promising methods of raising on-farm biological soil fertility. The PhD student will find out what aspects of root-associated microbial communities (composition, structure, or abundance) is determinant for the tea bushes’ growth, health, and tolerance against drought. This will be done by combining data of molecular barcoding analyses on rhizobia (R), arbuscular mycorrhizal fungi (AMF), and oomycetes (O)

and measurements on isotopic and total nutrient and water status indicators of leaf samples (12/13C, 14/15N, Mn, 16/18O, P). Based on i) a field survey in remaining wild stands, prospering and declining plantations, and ii) nursery-type common garden experiments with different soil origins and organic fertilizer amendments, as well as, iii) interviews with small- and large-scale farmers, the following main research questions are to be addressed: 1) Is plant performance related to consistent patterns of community composition, structure, and overall abundance of AMF, O, and/or R? 2) Are nursery seedlings healthier when raised in soil from remaining semi-natural vegetation patches, because of more balanced and mutualist-rich root-associated microbial communities? 3) Can natural nutrient flushes be replaced by application of mulch, dung and/or compost? Linking observations with data from experimental manipulation has good potential to reveal mechanistic linkages between complex interactions between microbes, physicochemical soil properties and plant performance. Such process-based knowledge is needed to identify opportunities for agronomic intervention to 'intensify' advantageous microbe-root interactions for sustaining yields with little use of external resources. Highly motivated students with an excellent academic track record are encouraged to apply. Applicants should be willing to travel internationally and work under remote and harsh environmental conditions. Preference will be given to candidates with demonstrated (international publications) and broad interests in ecology, evolutionary biology, microbial ecology and application of related knowledge. Desirable skills include experience in working with next generation DNA sequencing data (metagenomics), including associated bioinformatics analyses, and use of natural abundances of stable isotopes. The successful applicant will also be required to interview local farmers in a socio-economic component of the project. Requirements include an MSc in plant science (environmental or agricultural sciences) or (microbial) ecology, good spoken and written English, and a driver's license. Funding is guaranteed for three years by the collaboration between the Mercator Research Foundation and the World Food System Center at ETH, via the ETH Foundation. Salary follows the fixed salary rates for doctoral students at ETH. For further information please contact Dr. Hannes Gamper (no applications) by email: hannes.gamper@usys.ethz.ch, or Prof. Johannes J. Le Roux (no applications) by email: jlroux@sun.ac.za and/or visit the working group's websites: <http://www.plantnutrition.ethz.ch>, http://academic.sun.ac.za/cib/team_research.asp Please submit your application online with attention to: ETH Zurich, Olivier Meyrat, Human Resources, 8092 Zurich, adding a motivation letter describing your reasons for applying and quali-

fications for the position, a detailed CV, and contact details of three referees by April 15, 2016. Link to apply: <https://apply.refine.ch/845721/4483/pub/1/-index.html> Key words:

— / —

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>

Goettingen Quantitative Population Genetics

Dear colleagues,

The Centre for Statistics at the Georg-August-University Goettingen in Germany, is currently inviting applications for a

PhD Position in Genetic Modelling of Complex Traits (75 % E 13 TV-L)

within the Research Training Group (RTG) 1644 'Scaling Problems in Statistics', starting October 1, 2016. The position is funded by the German Research Foundation (DFG) for 3 years.

The remuneration is equivalent to 75 per cent of a post-doc position in the German system.

The highly interdisciplinary Research Training Group aims to solve current questions in the areas of agricultural economics, ecology, econometrics, genetics, and remote sensing by means of statistical methods, and at the development thereof. It distinguishes itself through joint supervision and a structured study program consisting of methodologically oriented lectures, interdisciplinary research seminars, and skills courses, as well as including a career enhancement program for female PhD students.

The Research Training Group involves working groups from agroecology, agricultural economics and rural development, animal breeding and genetics, ecosystem modelling, forest inventory and remote sensing, genetic epidemiology, statistics and econometrics. For more information, visit www.uni-goettingen.de/rtg1644. The advertised position is located at the Animal Breeding and Genetics Group with Prof. Dr. Henner Simianer.

The research project will be on 'Dissecting intraspecific variation in compound eye size in *Drosophila*

melanogaster via integration of genome, transcriptome and phenotype data'. While the evolution of simple morphological traits is well-understood, our knowledge about how the size and shape of complex organs evolve is still limited. The successful PhD candidate will address this question by analysing the genetic basis of eye size variation in various inbred strains of the *Drosophila melanogaster* Genetic Reference Panel (DGRP). For all DGRP lines genome sequences are available. For representative strains, developmental transcriptome data using RNAseq will be generated so that data across several scales (genome, transcriptome, phenotype) can be integrated. Similar data will be generated for artificial selection experiments based on a subset of the DGRP fly lines. The successful candidate will work in an interdisciplinary team at the Department of Animal Sciences (Prof. Dr. Henner Simianer) and the Department of Developmental Biology (Dr. Nico Posnien) as well as during an extended research stay in the group of one of the international collaborators overseas.

For more details, visit www.uni-goettingen.de/rtg1644/-jobs. By the time of appointment, the successful candidate will already have completed a M.Sc. degree or equivalent in biology, statistics, mathematics or bioinformatics. A solid background in statistics and quantitative genetics and a natural curiosity for basic biological questions is required. Prior experience with *Drosophila* genetics, population genetics and/ or basic programming skills is beneficial. You should show a high degree of independence in experimental planning and the structured analysis of large datasets. Very good knowledge of English is required.

The Georg-August-University is an equal opportunities employer and places particular emphasis on fostering career opportunities for women. Qualified women are therefore strongly encouraged to apply as they are underrepresented in this field.

The University firmly intends to raise the number of disabled persons in its employment. In the case of equally qualified applicants, disabled persons will be preferentially considered.

To apply for this position, please upload your application via the online application site <https://slotus.gwdg.de/uni/uwfb/grk.1644.nsf/enter>. Further application details are available on this webpage. The closing date for applications is May 15, 2016.

In case you have further questions, please don't hesitate to contact me

Best regards

Henner Simianer

Dr. Henner Simianer Professor of Animal Breeding and Genetics Department of Animal Sciences Georg-August-University Goettingen Albrecht-Thaer-Weg 3, 37075 Goettingen Tel.: +49-551-395604, Fax: +49-551-395587 Email: hsimian@gwdg.de <http://www.uni-goettingen.de/tierzucht> "Simianer, Henner" <hsimian@gwdg.de>

JagiellonianU EcologyEvolution

Master studies in Ecology and Evolution

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

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

Website: www.ecoevo.uj.edu.pl Facebook profile: <https://www.facebook.com/ecolevoluj/> Zofia Prokop <zofia.prokop@uj.edu.pl>

MaxPlanckResearchSchool 15 EvolutionaryBiology

The International Max Planck Research School for Evolutionary Biology is offering up to 15 PhD positions and fellowships.

The graduate school is dedicated to highest level of research and training in all areas of contemporary Evolutionary Biology. It is a joint initiative of the Max Planck Institute for Evolutionary Biology, the University of Kiel and the Helmholtz Center for Ocean Research Kiel (GEOMAR). The school offers an internationally

competitive research environment with state of art facilities. The participating groups are working on a broad variety of scientific topics including molecular, behavioral, theoretical and organismal approaches.

The graduate program starts with a rotation period of three months followed by a PhD project of three years including seminars, courses and workshops. The language of the graduate school is English. Financial support is provided throughout the program.

To obtain further information about our PhD program and application details please visit our website at <http://www.evolbio.mpg.de/imprs> . Well-motivated and highly-qualified students from all countries are welcome to apply. A Master of Science degree or a Diploma as well as a strong interest in Evolutionary Biology and flexibility in the research project are prerequisites for entering the program. We are looking forward to your online application for a PhD fellowship in the beautiful landscape of Northern Germany.

The deadline for applications is April 17, 2016.

The selection week will be held from June 27 - July 01 and

the program itself starts on September 19, 2016.

Contact: Dr. Kerstin Mehnert,

August-Thienemann-Str. 2, 24306 Pl????n, Germany

email: imprs@evolbio.mpg.de phone: +49(0)4522 763 233

The coordinator

Kerstin Mehnert

The steering committee

Tal Dagan, Diethard Tautz, Hinrich Schulenburg, Eva Stukenbrock and Thorsten Reusch

–

Dr. Kerstin Mehnert Scientific Coordinator IMPRS, Press and Public Relations, International Office

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www.evolbio.mpg.de, www.evolbio.mpg.de/imprs

Kerstin Mehnert <mehnert@evolbio.mpg.de>

McGillU QuantBiol

Quantitative Biology and Medical Genetics for the World Program Announcement The “Quantitative Biology and Medical Genetics for the World” program at McGill is offering a number of prestigious Queen Elizabeth II scholarships for Commonwealth citizens to pursue a PhD at McGill University.

The Program The Canadian Queen Elizabeth II Diamond Jubilee Scholarships (QEII) program is a new program established by the Association of Universities and Colleges of Canada to create a community of leading Canadian and Commonwealth scholars. For background see: <http://www.univcan.ca/programs-services/international-programs/canadian-queen-elizabeth-ii-diamond-jubilee-scholarships/> “Quantitative Biology and Medical Genetics for the World” at McGill is supported by the QEII program and coordinated by the McGill University and Génome Québec Innovation Centre (MUGQIC), one of Canada’s leading institutions for genome research. The goal is to provide interdisciplinary training at a PhD level interfacing between high-throughput biology and quantitative sciences. While applicants can be from any Commonwealth country, we will favour students with nationality from countries where similar training opportunities are not readily available. PhD students are admitted for studies at McGill commencing in January and September of each year.

Applications are presently open for an anticipated start date in September 2016. For the Department of Human Genetics, the deadline for applications for this start date is March 31, 2016.

More information can be found at: http://static1.squarespace.com/static/552e9d8be4b0e53cd8f7e76f/t/56d45c4cf699bb6f0beeb703/1456757837027/qe2_incoming_mcgill.pdf

Simon gravel <gravellab@gmail.com>

MNHN Paris Evolutionary Convergence

Funded PhD project : History of an evolutionary convergence : evolution of chemical defenses within mimetic butterflies communities.

The Labex BcDIV funds a PhD for 3 years on the evolution of chemical defenses in neo-tropical butterflies. This PhD project will be located in the Muséum National d'Histoire Naturelle in Paris (France) and jointly supervised by Violaine Llaurens (CNRS researcher, isyeb.mnhn.fr/annuaire-et-pages-personnelles/pages-personnelles/LLAURENS-Violaine) and Bastien Nay (CNRS research director, naygroup.wordpress.com), in collaboration with Marianne Elias (CNRS researcher, isyeb.mnhn.fr/annuaire-et-pages-personnelles/pages-personnelles/ELIAS-Marianne, 279). We are seeking a highly motivated student with a chemical ecology profile to work on this interdisciplinary project combining natural product chemistry and evolutionary biology.

Scientific context :

Many toxic butterflies display vivid wing colour pattern, used as a warning signal by predators. Evolutionary convergences in these wing colour patterns are frequently observed among distantly related species, creating 'mimicry rings' of butterfly species displaying similar colour patterns. The more individuals and/or species share the same warning signal, the more efficiently the signal is recognized by predators, which suffer from the effect of the chemical defenses carried by butterflies. The evolution of chemical defenses within Lepidoptera lineages therefore plays an important role in the evolutionary convergence of mimetic colour pattern. Chemical defenses can be sequestered from food or been neo-synthesized by butterflies, and may exhibit large variations within and among species. In turn, those variations have important consequences on predators' behaviour and on the dynamics of mimetic signal. This PhD project focuses on two highly divergent neo-tropical clades of mimetic butterflies (split circa. 90 million years ago), namely the sub-tribes Heliconiini and Ithomiini. In these two clades, chemical defenses are acquired through different routes, but some species display strikingly similar wing colour patterns. In Heliconiini, toxicity stems from cyanogenic glucosides stored at larval stage from Passiflora host plants, or can be neosynthesized by butterflies themselves. However, in

Ithomiini, toxicity relies on pyrrolizidic alkaloids, sequestered at adult stage from Asteraceae, Boraginaceae, and Apocynaceae flowers. The difference in plants from which toxins might be stored, together with the variations in the neosynthesis capabilities, and stage of acquisition suggests contrasted evolution of chemical defenses in the two clades. Furthermore, species within these two clades also differ in their behavior and ecology, e.g. can have gregarious or solitary larval stages, and various abundances of their mimicry rings and level of conspicuousness of the associated signal. These traits can also be influenced by other selective forces, therefore may intervene in the evolution of chemical defenses. This PhD project aims at qualitatively and quantitatively analysing variations in chemical compounds in different species of the two clades and characterizing their metabolic origin to understand the evolution of chemical defenses in those two mimetic clades.

Profile :

We are looking for a student with a Master degree in chemical ecology or natural product chemistry. A specific interest in macro-evolutionary questions would be appreciated. The student should be able to perform chemical analyses on biological material using various innovative analytical techniques. Together with those lab skills, the student should display a high motivation for fieldwork in tropical areas.

Schedule :

The PhD thesis will start in October 2016. Application files should contain: a CV, a cover letter, Master score sheets, and two recommendation letters. Complete application files must be sent to llaurens@mnhn.fr and bnay@mnhn.fr before March 30th. Selected candidates will then be interviewed by a selection committee in May. The PhD will start on October 1st, 2016.

Violaine Llaurens - CR1 CNRS

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

45 rue Buffon

75005 PARIS

01 71 21 46 96

Violaine Llaurens <violaine.llaurens@mnhn.fr>

MonashU EvolutionSexDifferences

PhD on the evolution of sex differences

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

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

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

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

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

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

Monash is located in Melbourne, a vibrant cultural and recreational centre, and is consistently rated one of the

world's most liveable cities (http://en.wikipedia.org/wiki/World's_most_livable_cities).

Application process

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

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

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

Damian Dowling

Email: damian.dowling@monash.edu

Website: damiandowlinglab.com

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

"damian.dowling@monash.edu"

<damian.dowling@monash.edu>

MonashU MitoNuclearEcol

PhD in mito-nuclear ecology

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

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

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

Successful applicants will be highly motivated, and pas-

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

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

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

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

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

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

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

Damian Dowling

Email: damian.dowling@monash.edu

Website: damiandowlinglab.com

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

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

MPI Cologne Computational Population Genomics

PhD position in Computational Population Genomics

Project Title: Modeling quantitative trait evolution during an episode of rapid adaptation

Location: Max Planck Institute for Plant Breeding Research (MIPZ), Cologne, Germany

We seek a highly motivated and curiosity-driven individual with a background in computational biology to join our Evolutionary Genomics research group.

Project Description:

Understanding the process of rapid adaptation to novel environments is imperative for successful prediction of future adaptive responses to both long- and short-term environmental change.

This project makes use of **Arabidopsis thaliana** population samples we collected from the Cape Verde Islands, which lie at the margin of the species range. Plants growing here experience a long and severe dry season, which places strong selective pressures on growth and reproductive timing. For example, key traits include drought tolerance, photosynthetic rate, and timing of germination and flowering.

The student will combine results of trait mapping studies with Illumina and PacBio sequence data to model the evolutionary history of *Arabidopsis* in the Cape Verde Islands.

Research Environment:

Research in the Hancock Lab is funded by the European Research Council (ERC) and Max Planck Institute (MPI) and focuses on understanding the molecular basis of evolutionary processes. For more information about work in the lab, see <http://www.mpipz.mpg.de/hancock> Our group is housed within the Max Planck Institute of Plant Breeding Research (MIPZ), a world-class research center, located in the Green Belt of Cologne, Germany. The Institute houses 25 research groups, its own Genome Center with cutting-edge PacBio and Illumina sequencing capabilities, Mass-Spec facility, Biomolecule Screening Center and Central Microscopy Center.

The MIPZ is part of a larger network of plant and

evolutionary biologists from the University of Cologne and Heinrich Heine University in Düsseldorf, and it is a member of (CEPLAS), a regional cluster of excellence in the area of molecular plant science.

The successful candidate for this position will be a member of the International Max Planck Research School (IMPRS) on Understanding Complex Traits using Computational and Evolutionary Approaches.

Application Instructions:

We encourage applications from candidates with backgrounds in population genetics, computer science, and/or bioinformatics. Experience programming and scripting (e.g., Python, R) is required. A Master's degree is preferred, but a highly qualified student with only a Bachelor's degree could be considered in an exceptional case.

English is the working language of the laboratory and the institute, so excellent communication skills in English are imperative.

To apply, please send a letter of motivation describing your reasons for applying to the position, CV, transcripts and contact details for at least two references. All materials should be sent in English and preferably in a single file to hancock@mpipz.mpg.de

Review of applications will begin immediately and will continue until a suitable candidate is found.

Angela Hancock <angela.m.hancock@gmail.com>

MPI Cologne MolecularBasisOfAdaptation

*PhD position - Mapping the Molecular Basis of Adaptation in *Arabidopsis thaliana**

Location: Max Planck Institute of Plant Breeding Research (MPIPZ), Cologne, Germany

We seek a highly motivated and curiosity-driven individual to join our Evolutionary Genomics research group.

Project Description:

Understanding how organisms adapt to their environments is a central goal of evolutionary biology. By focusing on the interplay between molecular and evolutionary change, we are working to elucidate the details of adaptive phenotypic shifts.

This project makes use of *Arabidopsis thaliana* popu-

lation samples we collected from the Cape Verde Islands, which lie at the margin of the species range. Plants growing here experience a long and severe dry season, which places strong selective pressures on growth and reproductive timing. For example, key traits include drought tolerance, photosynthetic rate, and timing of germination and flowering. The PhD student working on this project will dissect the molecular basis of adaptation to this extreme environment.

The project combines trait mapping in natural and recombinant populations, functional genetic analysis, including the application of CRISPR/Cas9 editing, bioinformatics, and population genetics. In addition, an interested student will have the opportunity to participate in ongoing fieldwork in the Cape Verde Islands.

Research Environment:

Research in the Hancock Lab is funded by the European Research Council (ERC) and Max Planck Institute (MPI) and focuses on understanding the molecular basis of evolutionary processes. For more information about work in the lab, see <http://www.mpipz.mpg.de/hancock>

Our group is housed within the Max Planck Institute of Plant Breeding Research (MPIPZ), a world-class research center, located in the 'Green Belt' of Cologne, Germany. The Institute houses 25 research groups, its own Genome Center with cutting-edge PacBio and Illumina sequencing capabilities, Mass-Spec facility, Biomolecule Screening Center and Central Microscopy Center.

The MPIPZ is part of a larger network of plant and evolutionary biologists from the University of Cologne and Heinrich Heine University in Düsseldorf, and it is a member of (CEPLAS), a regional cluster of excellence in the area of molecular plant science.

The successful candidate for this position will be a member of the International Max Planck Research School (IMPRS) on Understanding Complex Traits using Computational and Evolutionary Approaches.

Application Instructions:

We encourage applications from candidates with backgrounds in plant sciences, molecular genetics and/or population genetics. A Master's degree is preferred, but a highly qualified student with only a Bachelor's degree could be considered in an exceptional case.

English is the working language of the laboratory and the institute, so excellent communication skills in English are imperative.

To apply, please send a letter of motivation describing your reasons for applying to the position, CV, transcripts and contact details for at least two references.

All materials should be sent in English and in a single file to hancock@mpipz.mpg.de

Review of applications will begin April 1 and continue until a suitable candidate is found.

Angela Hancock <angela.m.hancock@gmail.com>

University Murray, KY 42071-0009 Phone: (270) 809 6054 (Office)

Oliver Beckers <obeckers@murraystate.edu>

MurrayStateU Kentucky EvolutionCommunication

Graduate position (M.S.) in evolution of animal communication at Murray State University (KY).

The Beckers' Lab at Murray State University accepts M.S. student who are interested in investigating the evolution of animal communication starting Fall of 2016. Our research focuses primarily on the proximate and ultimate causes of the physical environment on the evolution of male mating signals (i.e., phenotypic plasticity) and female preferences for these signals. We use crickets and katydids as model organisms to address our questions.

Qualifications: We seek driven, enthusiastic, and focused students to join our lab. Successful applicants have a B.S. in biology, ecology, or related discipline. Experience with insects and acoustics preferred, but not necessary. Teaching assistantship and housing at Hancock Biological Station on Kentucky lake are available. To Apply: Email a letter of application indicating your research interests and career goals, a curriculum vitae including undergraduate GPA and GRE scores to Dr. Oliver Beckers: obeckers@murraystate.edu

Deadline: review of applications starts immediately.

Please find more information on Dr. Beckers' research here:

<https://www.murraystate.edu/academics/CollegesDepartments/CollegeOfScienceEngineeringandTechnology/CollegeOfSciencePrograms/biologyDept/faculty/oliver-beckers/index.aspx>

Information on the Department of Biological Sciences at MSU:

<https://www.murraystate.edu/academics/CollegesDepartments/CollegeOfScienceEngineeringandTechnology/CollegeOfSciencePrograms/biologyDept/faculty/>

Oliver M. Beckers Assistant Professor Department of Biological Sciences 1112B Biology Building Murray State

NHM London DeepSeaSponge

PhD-candidate in deep-sea sponge biology Natural History Museum of London and the Uppsala University Life Sciences Department (NHM)- Medicinal Chemistry (UU)Salary per annum: £16,296

The position will be held during four years mainly at the Natural History Museum of London, which is one of top research institutes in Europe. The collective expertise of NHM staff represents a unique national and international resource. The scientific staff is one of the largest expertbodies of its kind in the world, with approximately 300 scientists working with an equivalent number of scientific associates, students, visitors and volunteers. Their activities span the earth and life sciences with fields of expertise that include planetary sciences, mineralogy, palaeontology, taxonomy, systematics, biodiversity, genomics, and informatics.

Project description PhD-project: Reproductive ecology and genetic connectivity in deep-sea sponges of the North Atlantic: assessment of dispersal and evolutionary patterns

As part of EU Horizon2020 project: SponGES - Deep-sea Sponge Grounds Ecosystems of the North Atlantic: an integrated approach towards their preservation and sustainable exploitation

Deep-sea sponge-dominated communities or sponge grounds of the North Atlantic are threatened by several anthropogenic activities, which could be affecting their abundance, structure, and, as a result, their reproductive and dispersal potential and ability to survive. Understanding the processes behind the maintenance and regeneration of populations is critical for predicting the magnitude of natural or anthropogenic impacts and estimating the capability of populations to recover. The main aim of this part of the project is to describe patterns of evolution, distribution and connectivity of deep-sea sponge populations and both the ecological and historical processes behind their maintenance and regeneration. Within this framework, we are looking for a highly motivated PhD candidate to work on the assessment of life cycles and dispersal abilities of deep-sea sponges and the development of a suite of tran-

scriptomic (RNAseq) and genomic (RADseq) resources to evaluate evolutionary patterns and genetic connectivity and diversity of deep-sea populations. Overall, the PhD student will have the opportunity to explore the evolution and impact of sexual reproduction in sponges.

Requirements The PhD candidate must have: - MSc in Marine Ecology/Biology and/or Cell Biology; - Proven skills in scientific writing and knowledge of statistics and R; - Experience in fieldwork on research vessels, and high motivation to work under greatly demanding conditions; - Experience working with molecular biology of marine invertebrates; - Ability to work combining multidisciplinary techniques; - Skills in bioinformatics or familiarity with Unix environment are appreciated;

Appointment The position will start preferably 1 May 2016 and will continue for a maximum period of 4 years, including an initial probation period of 6 months.

Job application Applications should include a detailed CV, transcripts for all subjects, the Master thesis, 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 24 March 2016 to: A.Riesgo@nhm.ac.uk and paco.cardenas@fkog.uu.se Interviews will be held by skype in the 1st week of April 2016.

Further information Dr. Ana Riesgo: A.Riesgo@nhm.ac.uk and Dr. Paco Cárdenas: paco.cardenas@fkog.uu.se

Research Leader at the Invertebrates Division Department of Life Sciences, Natural History Museum of London Cromwell Road London, SW7 5BDA. Riesgo@nhm.ac.uk anariesgogil@gmail.com <http://www.anariesgogil.com/> Ana Riesgo in ResearchGate

NHM UCopenhagen Beluga Whale Population Genomics

PhD fellowship in Population Genomics of Beluga Whales The Natural History Museum, Faculty of Science at University of Copenhagen is offering a PhD scholarship in the group of Associate Professor Eline Lorenzen, starting June 1, 2016 or as soon as possible thereafter.

The successful candidate is expected to use second-

generation sequencing methods to generate genome-wide data from beluga whale (white whale) populations from across the Holarctic. The candidate will apply population genomic approaches to characterize the evolutionary history of the species, including phylogeography, demographic history, and adaptation.

We are seeking a highly motivated, hard working student who is able to work in a multidisciplinary and international environment. The ideal candidate has strong expertise in bioinformatics and experimental genetics, and in the molecular tools used in next-generation sequencing and population genomics. She/he should have strong background in molecular and evolutionary biology, particularly in molecular methods for generating large-scale sequence/SNP datasets, and be familiar with basic concepts in computational science and optionally, with Bash or other programming languages such as R, Perl and/or Python. Experience in the analysis of population-level NGS data will be considered positively. The candidate should be equally comfortable working as part of a team and achieving assigned tasks autonomously, should care for details, have the inclination to provide constructive feedback, and the ability to keep physical objects and data archives well organized.

The Lorenzen lab is a recently started group at the Natural History Museum of Denmark. The group's main focus is molecular ecology of large mammals, with a broad interest in how climate and humans have impacted the past and present abundance, distribution and evolution of megafauna species and communities. The work is highly interdisciplinary and merges molecular biology with the palaeosciences, climate change research, and archaeology. Eline Lorenzen is one of five PIs in the Section for EvoGenomics, which spans all sorts of exciting, interdisciplinary research (<http://snm.ku.dk/english/research/sections/evolutionary-genomics/>).

For further information or to apply for the position (deadline is April 7, 2016), please check the full opening here:

<http://jobportal.ku.dk/alle-opslag/?show=3D812158>
Eline gmail <elinelorenzen@gmail.com>

NorthDakotaStateU ConservationGenomics

Conservation Genomics of the rare Californian endemic, Torrey Pine (*Pinus torreyana*)

A PhD position in conservation genomics is available to study the evolution and conservation of the rare Californian endemic, Torrey Pine with Jill Hamilton at North Dakota State University, Fargo, North Dakota in collaboration with Jessica Wright (USDA Forest Service, Research Geneticist, Pacific Southwest Research Station).

Torrey pine (*Pinus torreyana* Parry) is one of the rarest pine species in the world, restricted to two discrete populations, a mainland grove of approximately 3400 trees just north of San Diego and an island population of approximately 2000 trees approximately 280 km up the coast on Santa Rosa Island, one of the Channel Islands. This project will evaluate the genomic structure of natural populations and take advantage of a wealth of phenotypic data available from a common garden experiment of mainland, island and F1 individuals planted at the Santa Barbara Botanic Garden. The combination of a long-term common garden experiment coincident with large-scale genomic surveys in natural populations will provide a valuable resource to direct in situ and ex situ conservation guidelines for Torrey pine conservation. In addition, there will be plenty of room to pursue particular questions of interest depending on the interest and experience of the candidate. This interdisciplinary research will combine field work at both the common garden site and within the natural populations in California, collaboration with the Institute of Forest Genetics in Placerville, CA and lab work in the Hamilton Lab at North Dakota State University.

The ideal PhD student will be prepared to conduct field-based research as well as have some experience in molecular ecology/population genetics or bioinformatics for genomic data analyses.

For more information on the Hamilton Lab please visit the lab website at: <http://www.jillahamilton.com> and more information on the Department of Biological Sciences at NDSU at <https://www.ndsu.edu/biology/>. Fargo is the largest city in the northern Midwest and as Gateway to the West is a vibrant, growing community that has access to numerous outdoor opportunities for all seasons.

Interested students are encouraged to contact Dr. Hamilton (jill.hamilton@ndsu.edu). Please include a brief description of your research interests and a CV in your email. Funding options are available for both US students as well as international students.

Jill Hamilton <jill.hamilton@ndsu.edu>

NTNU Norway StatisticalQuantGenetics

As part of the research project Knowledge based Non-Stationary Modeling we announce a PhD position in statistical quantitative genetics available from August 1st, 2016. Application deadline is March 11th. The successful candidate will be offered a three-year position at the Norwegian University of Science and Technology (NTNU) in Trondheim, Norway. NTNU may offer a six to twelve month extension as a teaching assistant.

The starting point for this project is selected challenges in quantitative genetics that call for non-stationary modeling. Inspired by these challenges the primary objectives are to 1) develop non-stationary statistical models based on system knowledge, 2) gain knowledge about and develop methodology for studying and improving practical identifiability of parameters in such models, and 3) develop methodology for evaluating predictions, and investigate when predictions are improved in comparison to stationary models. The PhD-project' title is:

Non-stationary models in quantitative genetics for incorporating pedigree and SNP data.

Qualifications:

The applicants should have a MSc-degree in statistics, or quantitative genetics or comparable competence, have a strong background in multivariate statistics and have experience with programming. It is an advantage, but it is not required, to have experience with spatial statistics, integrated nested Laplace approximations (INLA), SPDE-models, genetics. Candidates completing their MSc-degree in the Spring 2016 are encouraged to apply. Applicants who do not master a Scandinavian language must document a thorough knowledge of English (equivalent to a TOEFL score of 600 or more).

The PhD fellow will be part of the Department of Mathematical Sciences at NTNU and will have her/his workplace there. See <http://www.ntnu.no/imf>. The Department currently has around 60 PhD fellows.

For further information, please contact Prof. Ingelin Steinsland by phone (+4773550239) or e-mail (ingelins@math.ntnu.no).

For more information about the PhD-position, and how to apply see: <https://www.jobbnorge.no/en/available-jobs/job/122167/2-phd-positions-in-statistics> Dr. Henrik Jensen Associate Professor and Head of Behaviour and Evolution Section Centre for Biodiversity Dynamics Department of Biology, NTNU NORWAY

henrik.jensen@ntnu.no

Roscoff EvolutionParasitism

PhD Fellowship

Project Title: The paradox of being a specialist for a parasite of marine blooming dinoflagellates

Institution: Station Biologique de Roscoff, France

Supervisor: Dr Laure Guillou https://www.researchgate.net/profile/Laure_Guillou To

see more details on the project: <http://www.sb-roscoff.fr/en/2016/03/17/open-phd-position-roscoff-france-dipo-team> Description: The parasitism is a

frequent lifestyle in nature and a major source of evolutionary pressure for both the host and the parasite. Given the ubiquity of host-parasite interactions, understanding the factors that generate, maintain, and constrain these associations is of primary interest with implications for a wide range of ecological issues, including dynamics of emerging infectious diseases and invasions (Daszak et al. 2000, Keane and Crawley 2002). Although little studied, many extremely virulent microeukaryotic parasites infecting microalgae have been detected in the marine plankton. Among them are Syndiniales, which constitute a diverse and highly widespread group (Guillou et al. 2008). Because of their virulence and abundant offspring, such parasites have the potential to control dinoflagellate populations, and therefore toxic microalgal blooms (Alves de Souza et al. 2015). These parasites usually exhibit a narrow host spectrum (Chambouvet et al. 2008). Such specialization strongly relies on the life-history traits and ecology of the host. However, coastal planktonic ecosystems are by nature characterized by strong environmental fluctuations and rapid turnovers, even at the population level (Dia et al. 2014). Considering the short generation time and the high dispersal capacity of microalgae, their parasites must adapt at a significantly

faster rate than for larger hosts (e.g. plants or animals). All of these considerations should theoretically lead to the natural selection of generalist parasites at the expense of specialists. The persistence and ecological success of specialists among marine planktonic parasites is thus an intriguing paradox.

We hypothesise that host specialization is constrained by evolutionary processes underlying key steps during the infection (such as penetration inside the host and the takeover of the host). We will explore this hypothesis at the cellular level, using molecular approaches

Deadline for applying: 15 April 2016

The fellowship will start in October 2016

Please send CV and cover letter to lguillou@sb-roscoff.fr

Laure Guillou, Directrice de recherche CNRS Station Biologique de Roscoff CNRS - UPMC Place Georges Teissier, CS 90074 29688 ROSCOFF CEDEX France Phone: +33 2 98 29 25 63

UMR7144, leader of the team Diversity and Interactions in the Oceanic Plankton

<http://www.sb-roscoff.fr/fr/dipo> Guillou Laure <laure.guillou@sb-roscoff.fr>

SGN Frankfurt AntEvolution

Job offer Ref. # 8.2.16

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member institution of the Leibniz Association. With almost 800 employees and its headquarters in Frankfurt am Main, Senckenberg conducts natural history research with research institutions in six federal states of Germany. As an interdisciplinary institute, the Senckenberg Biodiversity and Climate Research Centre (BiK-F) focuses on the interactions between biodiversity and climate.

A cooperative project conducted at the Senckenberg Biodiversity and Climate Research Centre (Frankfurt am Main), the University of Mainz and the University of Würzburg jointly invites applications for a

PhD position “Evolution, genetic basis and behavioural consequences of cuticular hydrocarbon profiles in parasitic ants” (65%)

Insect cuticles are covered with cuticular hydrocarbons (CHC), which serve two important functions: as desiccation barrier and as cues and signals for chemical

communication. Despite their high importance, the evolution of CHC profiles, the underlying genetic mechanisms and the role of specific CHC traits for intra- and interspecific recognition are still poorly understood. As a model system, we will use two parabiologically associated, tropical ant species, *Crematogaster levior* and *Camponotus femoratus*, which show unusually high chemical diversity.

In this project the PhD candidate will mainly focus on the genomic basis of CHC evolution. The candidate will assemble the genome, and investigate the population structure of different chemotypes of *Crematogaster levior* in French Guiana, using state-of-the-art population genomic tools (PoolSeq). In addition, the candidate will use the obtained information on the distribution and diversification of the chemotypes to test and verify the importance of specific CHC compounds and compound mixtures in intra- and interspecific behavioural essays in the field.

The project will be conducted in close collaboration with a second PhD student based at the Universities of Mainz and Würzburg, who will mainly focus on the CHC composition, the identification of candidate genes via transcriptome analyses and their functional verification using RNAi knockouts. Both students will conduct field work in French Guiana, some of the experiments and parts of the analyses together. Therefore, the candidate is expected to work independently within the project framework, but also be a good team worker.

Your profile:

- Master's/diploma in biology, environmental sciences or bioinformatics.
- Strong interest in evolutionary biology, ecology and genetics.
- High motivation to link field-, experimental- and lab work with bioinformatics.
- Excellent communication skills in English
- Programming skills or bioinformatics are important, but optional plus points
- The PhD position is funded for three years by the German Science Foundation. Within these three years the PhD student is expected to finish her/his degree. Salary and benefits are in accordance with a public service position in Germany (TV-H E 13, 65%). The contract shall start 01.06.2016 and will be initially limited until 31.12.2018. The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment will be Frankfurt, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please send your application before March, 24th preferably by e-mail with a single PDF containing a motivation letter that describes your scientific interests and

qualifications fitting this project (1 page), a detailed CV, a copy of the MSc certificate and contact details for 2 possible referees mentioning the reference of this position (Ref. # 8.2.16) to the address below:

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt am Main recruiting@senckenberg.de

For scientific enquiries please contact Dr. Barbara Feldmeyer (barbara.feldmeyer@senckenberg.de), Dr. Florian Menzel (menzef@uni-mainz.de), or Prof Thomas Schmitt (thomas.schmitt@uni-wuerzburg.de). In addition, please indicate in your application how our advertisement came to your attention.

Mit freundlichen Grüßen /Best Regards

Maria di Biase Personalsachbearbeiterin

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

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

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales - 1319 Elsen, Carina

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

Fax: 0049 (0)69 / 7542-1467 Mail: recruiting@senckenberg.de Homepage: www.senckenberg.de SENCKENBERG Gesellschaft für Naturforschung

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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>

SouthamptonU UK TheoreticalEvolBiol

Several fully-funded PhD scholarships are available in the Dept. of Computer Science (and affiliated with the Institute for Life Sciences) at the University of Southampton, U.K. - a top rated department in the UK with excellent international standing. Fees and stipend (for 3 year PhD) can be paid. Eligible for UK students (or EU students resident in the UK for past 3+ years) only. See details (1).

One scholarship is ring-fenced for theoretical evolutionary biology. This is part of 22 linked research projects by an international team of world-leading researchers, collectively designed to put the extended evolutionary synthesis (2) to the test. The sub-project at Southampton is led by Dr. Richard Watson (3), and will draw on recent developments unifying evolutionary theory with learning theory (4). Possible topics include the evolution of collective function and niche construction in ecosystems (5) - co-investigators: John Odling-Smee (Oxford), Michael Wade (Indiana), Andrew Gardner (St Andrews) - or the evolution of evolvability (6,7) - co-investigators: Gunter Wagner (Yale), Tobias Uller (Lund). The successful candidate will build mathematical/simulation models to develop our understanding of how these evo-eco or evo-eco feedbacks alter evolutionary dynamics and test the utility of learning theory to answer such questions. Applicants must have a first degree in a relevant numerate subject (e.g. maths, computer science, evolutionary/theoretical biology), strong mathematical skills and knowledge of evolutionary theory. Experience in simulation modelling/programming is desirable.

In total there are over 30 scholarships available in Electronics and Computer Science on any topic that members of the department can supervise (1) - including, machine learning, modelling, bioinformatics, computational biology, bio-inspired computation, multi-agent systems....

Open: now (March 2016). Closing: when suitable applicants identified. For further information contact: R.A.Watson@soton.ac.uk

(1) <https://jobs.soton.ac.uk/Vacancy.aspx?ref=3D3D700316FP> (2) Laland, K.N. et al. (2015). The extended evolutionary synthesis: its structure, assumptions and predictions. *Proc. R. Soc. B* (Vol. 282, No. 1813, p. 20151019). (3) <http://www.ecs.soton.ac.uk/people/raw> (4) Watson, R.A., & Szathmary, E. (2016). How Can Evolution Learn?. *Trends in ecology & evolution*, 31(2), 147-157. (5) Power, D.A., et al. (2015). What can ecosystems learn? Expanding evolutionary ecology with learning theory. *Biology direct*, 10(1), 1-24. (6) Watson, R.A. et al. (2014). The evolution of phenotypic correlations and “developmental memory”. *Evolution*, 68(4), 1124-1138.; (7) Kouvaris, K. et al. (2015). How Evolution Learns to Generalise: Principles of under-fitting, over-fitting and induction in the evolution of developmental organisation. preprint arXiv:1508.06854.

Dr. Richard A. Watson Associate Professor Institute for Life Sciences/Electronics and Computer Science, University of Southampton <http://www.ecs.soton.ac.uk/>-

people/raw R.A.Watson@soton.ac.uk

R.A.Watson@soton.ac.uk

SoutheasternLouisianaU FishSystematics

Southeastern Louisiana University, Hammond, Louisiana

MS position focusing on molecular systematics and diversification of cyprinodontiform fishes

Research focus: My lab is seeking a highly motivated student wishing to obtain a MS degree in biological sciences and participate on an NSF funded research project. The research focus of the Piller lab is the biodiversity of fishes. We address many different types of questions on the biodiversity of New World fishes. The available research assistantship will focus on generating a phylogeny for one or more groups of fishes within the Order Cyprinodontiformes. There is a fair amount of flexibility in the chosen project, but it must focus on generating a phylogeny and using it to address questions of diversification,

Qualifications: An undergraduate degree in Biology (or related field) and experience in molecular techniques (DNA extraction, PCR, DNA sequencing, etc) and sequence data analysis.

Application deadline: As soon as possible, although the position will remain open until filled. The start date will be Fall 2016.

Application materials: Please send a brief cover letter and a CV/resume to kyle.piller@selu.edu to be considered for the position. A candidate from the applicant pool will be encouraged to officially submit an application to the department.

Kyle R. Piller, PhD

Southeastern Louisiana University, Dept. of Biological Sciences,

Hammond, LA 70402

Phone: 985-549-2191

Email: kyle.piller@selu.edu

Websites: www.kylepiller.com – Kyle R. Piller, PhD Edward G. Schlieder Foundation Professor of Environmental Studies and Sustainability, Curator of Vertebrates, and Graduate Coordinator Southeastern

Louisiana University, Dept. of Biological Sciences Hammond, LA 70402 Kyle.Piller@selu.edu 985-549-2191 www.kylepiller.com kyle.piller@selu.edu

StockholmU BrainEvolution

PhD position in Brain Evolution at the Department of Zoology, Stockholm University. Closing date: 17 April 2016.

The Department of Zoology consists of five divisions: Ecology, Ethology, Functional Morphology, Population Genetics, and Systematics and Evolution. The advertised position will be part of the Division of Ethology. There is a long-standing tradition for researchers at the Division of Ethology to collaborate with researchers from other fields, such as evolutionary ecology, theoretical evolutionary biology, and the study of cultural evolution.

Project description We are seeking to recruit a PhD student who will work within a multidisciplinary project on brain evolution. The project uses the guppy (*Poecilia reticulata*) as a model to experimentally test the possibilities and consequences of evolving a more advanced brain. More specifically, the project addresses the evolutionary costs and benefits of intraspecific variation in the relative size of separate brain regions. As such, the project spans over multiple disciplines including artificial selection on brain anatomy, assays of individual and collective behaviour, assays on different aspects of cognitive ability, physiology, life histories, primary and secondary sexual traits and analyses of the genetic architecture that orchestrates changes in brain anatomy and cognitive ability. The already existing selection lines of large- and small-brained guppies will form the basis of the project but a new selection experiment on the relative size of a separate brain region will also be undertaken followed by relevant assays of behaviour and physiology. The overall aim of the project is thus to increase our understanding of the association between brain anatomy and behaviour, cognitive ability and physiology. The work will mostly be lab-oriented but includes also the possibility of temporary field work on Trinidad. The project will require hard work in the lab but at the same time provide excellent opportunities for personal initiatives and development towards a successful academic career. An important task will be to undertake laborious selection experiments followed by the collection and analysis of complex data in a way that controls for the setup of replicated artificial selection designs.

The project is undertaken in the brand new tropical freshwater fish labs in the Department of Zoology with room for over 6,000 aquaria and several separate experiment rooms with established assays of brain anatomy, several different aspects of cognitive abilities, swimming speed, personality, 2D and 3D analysis of individual and collective behaviour, respirometry etc. The successful candidate will be part of a dynamic team consisting of Ethologists (Niclas Kolm group, Stockholm University), Physicists and Mathematicians (David Sumpter group, Uppsala University), Information Technology researchers (Kristiaan Pelckmans group, Uppsala University), and Evolutionary Geneticists (Judith Mank group, University College London) in a multidisciplinary project that investigates the association between brain anatomy and behaviour through the development of new methods in behavioural assays, brain imaging and analysis of the genetic background to phenotypic variation.

Qualification requirements To be qualified for research studies in the program, the applicant must have completed a Master degree (or equivalent) or have passed at least 120 hp (2 years) of biological studies, including an approved independent project of at least 30 hp at advanced level within Ethology, Zoology, Behavioural Ecology, Evolutionary Biology or a related subject. Applicants who have in principle acquired the corresponding competence in Sweden or in another country are also qualified. We are looking in particular for candidates with a strong interest in brain evolution, with excellent analytical ability and experience from quantitative analyses of behaviour and other traits of interest.

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

Terms of employment 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 Professor Niclas Kolm, telephone:

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Tahiti Marine Genomics

PhD position in marine genomics

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

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

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

- Research environment: Ifremer (French Research Institute for Exploitation of the Sea) contributes to the knowledge of the ocean and their resources, through the monitoring of marine and coastal environments and the sustainable development of marine activities. Ifremer

performs targeted applied research to address the questions posed by society (climate change effects, marine biodiversity, pollution prevention, seafood quality...).

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

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

- Candidate's profile We encourage applications from candidates with solid knowledge in at least two of the following disciplines: population genetics, evolutionary genetics, bioinformatics, biostatistics, genomics, transcriptomics, epigenetics. Knowledge of the R language is strongly advised, and other scripting languages (for NGS pipelines implementation) are a plus.
- Application instructions: To apply, please send a motivation statement describing your interests in applying for the position, a resume, and contact details for at least two references to Celine.Reisser@ifremer.fr before the 1st June 2016. Interviews will be held mid-June.

Celine REISSER <Celine.Reisser@ifremer.fr>

U Aalborg Conservation Biology

Call for unsolicited Enquiries and Applications to the Doctoral School of Engineering and Science Aalborg University (AAU) (Denmark) in the field of Conservation Biology. The applicants is expected to work in the group of Professor Cino Pertoldi (https://www.researchgate.net/profile/Cino_Pertoldi), starting in September, 2016 or January 2017. The successful candidates are expected to conduct experimental works, use second-generation sequencing methods, apply modeling approaches, design breeding strategies with main focus on endangered mammals, reptiles, insects and amphibian. After that the candidates have proposed a research project and

have discussed it with Prof. Cino Pertoldi (e-mail: cp@bio.aau.dk) the students (in case that the project is judged relevant), are expected to submit their project proposal to the Doctoral School which is an independent unit organized under the Faculty of Engineering and Science, which is ranked amongst the top 100 engineering and science faculties in the world. The Doctoral School currently has more than 600 PhD students enrolled.

The following serves as a guideline in relation to the minimum requirements for all PhD applicants: You must hold a relevant Danish master degree or a master degree on a corresponding level (research based education including a 180 ECTS bachelor education followed by a 120 ECTS master education)

All international master educations are checked in relation to their academic level.

Your master degree must be characterized by a general high level of grades. This is particular relevant for your master thesis and courses relevant to the area in which you are pursuing a PhD

If you have been granted a scholarship from a governmental institution such as the Chinese Scholarship Council or the like please contact the Doctoral School. If you wish to finance your own PhD study the cost is approx. DKK 156.000 dkr annually in

tuition fee. You also need to finance your own living expenses.

In addition to this, it is required that a residence permit is granted prior to a foreigners entry into Denmark. A minimum of 50.000 DKK in savings is among the requirements to obtain such a permit.

For more information please consult the following website:

<http://www.nyidanmark.dk/en-us/frontpage.htm> for granting possibilities please go to the following link:

<http://studyindenmark.dk/study-options/tuition-fees-scholarships/tuition-fees-and-scholarships>

The conservation group of Prof. Cino Pertoldi focuses on empirical conservation and evolutionary genetics of animals, but also includes conceptual and theoretical studies in the interface between genetics, ecology and evolution. The group merge current efforts in evolutionary and ecological genetics, complementing molecular genetics and macroecology in order to understand how genetic measures can indicate causal processes.

For further informations please contact:

Professor Cino Pertoldi, e-mail: cp@bio.aau.dk

Deadline: 1 May 2016

Please specify in the mail which are your main interest and attach a short CV and if you are interested in a PhD fellowship grant or if you wish to finance your own PhD study or you have an external grant which can partially cover the tuition fee. Please consider the fact that new PhD students can be enrolled in all phases of the faculty's three-year PhD Programme. In connection with the enrolment, the PhD Board decides, upon recommendation by the Head of Department, the supervisor, and the PhD Board on the following issues:

Call for unsolicited Enquiries and Applications to the Doctoral School of Engineering and Science Aalborg University (AAU) (Denmark) in the field of Conservation Biology. The applicants is expected to work in the group of Professor Cino Pertoldi (<http://personprofil.aau.dk/-127902?lang=en#/minside>)(https://www.researchgate.net/profile/Cino_Pertoldi), starting in September, 2016 or January 2017. The successful candidates are expected to conduct experimental works, use second-generation sequencing methods, apply modeling approaches, design breeding strategies with special focus on endangered mammals, reptiles, insects and amphibian. After that the candidates have proposed a research project and have discussed it with Prof. Cino Pertoldi (e-mail: cp@bio.aau.dk) the students are expected to submit their project proposal to the Doctoral School which is an independent unit organized under the Faculty of Engineering and Science, which is ranked amongst the top 100 engineering and science faculties in the world. The Doctoral School currently has more than 600 PhD students enrolled.

The following serves as a guideline in relation to the minimum

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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>

UBasel CichlidSexDetermination

Graduate position Sex Determination in East African Cichlid Fish

A PhD position is available at the Zoological Institute, University of Basel, Switzerland and sciCORE, the center for scientific computing, University of Basel in collaboration with SIB, the Swiss Institute of Bioinformatics.

The scope of the project is to investigate the genomics of sex determination and evolution of sex chromosomes in Lake Tanganyika cichlid fish. The project is highly integrative combining bioinformatics analyses of genome and transcriptome data with wet lab experiments as well as some fieldwork.

The position is fully funded for three years by the Swiss National Science foundation as part of the Ambizione project “The role of sex determination in an adaptive radiation of cichlid fishes” and will involve working at the two institutes. Starting date is from July 2016. A master degree in Biology or Bioinformatics is required. The ideal candidate has a strong interest in evolutionary comparative genomics and data analysis. Experience in genomics and/or molecular biology are assets. Applicants should have high social skills allowing them to integrate into two working environments, the Zoological Institute and sciCORE. A good level of written and spoken English is necessary.

In order to apply, please email a single pdf containing a) a statement of research motivation (max 300 words), b) CV, c) copy of university degree, and d) names and contact information of 2 references, to astrid.boehne@unibas.ch by April 30, 2016. For further information see <http://www.salzbungerlab.org>, <http://scicore.unibas.ch/> and <https://www.unibas.ch> – Astrid Böhne Universität Basel Zoologisches Institut Evolutionsbiologie Vesalgasse 1 CH-4051 Basel Switzerland Phone +41 (0)61 267 03 05 Fax +41 (0) 61 267 03 01

astrid boehne <astrid.boehne@unibas.ch>

UBayreuth Germany SpermMicrobeInteractions

DISENTANGLING HOST-PARASITE AND MALE-FEMALE COEVOLUTIONARY EFFECTS ON HOST FITNESS

I am looking for an ambitious PhD-candidate interested evolutionary biology and reproductive physiology. The project aims to disentangle host-parasite and male-female coevolutionary effects on host fitness in the common bedbug, *Cimex lectularius*. The project is funded for 3 years by the German research foundation (DFG). It involves genomics, metagenomics, and amplicon sequencing of microbes associated with bedbug reproduction, including sexually transmitted microbes,

and experimental manipulation as well as immunoassays, molecular analysis of paternity and life-history trait analyses. The project aims to quantify sperm-microbe interactions and their consequences for male and female fitness. Therefore, I am looking for a candidate with an open mind to new research ideas, a solid background in experimental design and statistics. A plus would be if the candidate has some knowledge of either microbial ecology, bioinformatics (experience with a unix environment, the R programming language, especially the ‘vegan’ package) or skills in any of the above-mentioned areas. The starting date is 1st May 2016.

Within the Department of Animal Ecology I (<http://www.bayceer.uni-bayreuth.de/toek1/index.php?lang=3Den>) the successful candidate will join the group of Animal Population Ecology, which is working the fields of ecological immunology, host-parasite interactions, population ecology and biodiversity by studying various insect species in the lab and in the field.

If you are interested please send me an e-mail until Friday 18th March 2016 with your application consisting of one pdf containing a CV (incl. the names and phone numbers of two references and a list of publications) and a letter of motivation (max. one page DIN A4), in which you describe how your background and your personal interests will contribute to the project. Please submit the application without a picture of you and without your date of birth.

All the best, Oliver

Dr. Oliver Otti Animal Population Ecology Animal Ecology I University of Bayreuth Universitätsstrasse 30 95440 Bayreuth Germany

phone: +49921552646 e-mail: oliver.otti@uni-bayreuth.de

web: https://www.bayceer.uni-bayreuth.de/toek1/en/mitarbeiter/mit/mitarbeiter_detail.php?id_obj=106154
“oliver.otti@uni-bayreuth.de” <oliver.otti@uni-bayreuth.de>

UBristol SymbiosisGenomeEvolution

The principles of symbiosis in prokaryotes

A fully-funded, four-year Ph.D. studentship in computational evolutionary genetics is available in the lab of Dr. Tom Williams at the University of Bristol, UK.

Symbiosis “ evolutionary partnership between distinct life forms ” is one of the most important processes that shapes the evolution of life on Earth, from the nutritional endosymbionts of insects to the ancient origins of mitochondria and chloroplasts. The first steps towards genomic integration in those ancient lineages are no longer accessible to us, but there are contemporary symbioses between Archaea and Bacteria “ much studied for their ecological importance, but about whose evolution very little is known ” that promise to shed light on the principles of prokaryotic symbiosis, today and in the distant past.

In this project, the successful candidate will apply phylogenetic and comparative genomic methods to understand the genomic mechanisms and consequences of adaptation to symbiotic life among modern Archaea and Bacteria. As a model system, you will focus on modern methane-producing and methane-oxidising prokaryotic consortia, whose convergent evolution from multiple independent starting points will provide an excellent opportunity to distinguish general from lineage-specific features of symbiotic evolution. You will use the comparative method to identify the genes and metabolic pathways that change during transition to a symbiotic lifestyle, and to develop a general framework for the evolution of symbiosis between prokaryotes. The predictions of this framework will then be tested against genome data from novel consortia sequenced by our collaborators. The broader aims are not only to understand how modern prokaryotic symbioses evolve and function, but also to provide new insights into how they have co-evolved with earth system processes, including the carbon cycle, through deep evolutionary time. The project also offers scope for customization based on the successful candidate’s research interests “ for example, investigation of the deeper phylogenetic relationships among groups of distantly-related symbiotic bacteria could be an interesting secondary aim.

Requirements: We are looking for a highly motivated candidate with a passion for elucidating the fundamental principles of evolutionary biology through computational analysis. This is primarily a bioinformatics project, so experience with operating and programming computers (UNIX, bash, and/or a scripting language such as Python, Perl or R) is a plus. Both biologists with an interest in, and aptitude for, computational analysis, as well as computer scientists or statisticians with a demonstrated track record in evolutionary biology are encouraged to apply. To do so, send a CV and covering note explaining your interest in the project to Dr. Tom Williams (tom.a.williams@bristol.ac.uk).

Eligibility, application deadline and start date: The funding is available to citizens of the UK or any other

EU country. The application deadline is April 29th, 2016. The projected project start date is September 2016, although earlier dates are also possible.

Supervisory team at the University of Bristol: Dr. Tom Williams (primary supervisor), School of Earth Sciences; Prof. Richard Pancost (co-supervisor), School of Chemistry.

”tw15962@bristol.ac.uk“ <tw15962@bristol.ac.uk>

UGoettingen GeneticModelling ComplexTraits

Hi all,

We have PhD position available to start in October 2016 at the University Göttingen (3 yrs, 75% E 13 TV-L).

The main aim of the project will be to study intra-specific variation in compound eye size in *Drosophila melanogaster*. The successful PhD candidate will address this question by analyzing the genetic basis of eye size variation in various inbred strains of the *Drosophila melanogaster* Genetic Reference Panel (DGRP). For all DGRP lines genome sequences are available. For representative strains, developmental transcriptome data using RNAseq will be generated so that data across several scales (genome, transcriptome, phenotype) can be integrated. Similar data will be generated for artificial selection experiments based on a subset of the DGRP fly lines. The successful candidate will work in an interdisciplinary team at the Department of Animal Sciences (Prof. Dr. Henner Simianer) and the Department of Developmental Biology (Dr. Nico Posnien) as well as during an extended research stay in the group of one of the international collaborators overseas.

Please visit the website of the Research Training Group “Scaling Problems in Statistics” (<http://www.uni-goettingen.de/en/156579.html>) for more details about the general setting of this position.

A detailed description of the project, information about the application procedure and further requirements are available here: <http://tinyurl.com/gn3az25> Please forward this job ad to all your motivated future PhD students.

Thanks a lot!

Cheers,

Nico

Nico Posnie
 Georg-August-University Göttingen
 Johann-Friedrich-Blumenbach Institute for Zoology and
 Anthropology
 Department of Developmental Biology
 Ernst-Caspari-Haus (GZMB)
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 web: <http://www.evolution.uni-goettingen.de/-posnie/lab/index.html> web: <http://www.uni-goettingen.de/en/44993.html> Nico Posnie
 <nico.posnie@gmail.com>

UGuelph Theory

A PhD or MSc position is available in the area of evolutionary theory in the research group of Cortland Griswold (Department of Integrative Biology, University of Guelph, Guelph, Ontario, Canada).

Research topics in our group include

- Epistasis - Polyploidy - Gene transfer - Coalescent and ancestral graphs - Multivariate trait evolution - Evolutionary ecology

A student can also develop their own line of research.

For information on student funding see

MSc: http://www.uoguelph.ca/adr-cbs/-includes_content/pdf/CBS_MSc_Grad_Student_Stipends_W16.pdf PhD: http://www.uoguelph.ca/adr-cbs/includes_content/pdf/CBS_PhD_Grad_Student_Stipends_W16.pdf

Scholarships are available to eligible international students and on a first come, first serve basis that cover the difference between domestic and international tuition fees.

If you are interested in applying for the position, please send an email with a statement of interest, CV, university transcripts and the contact information for two references.

Dr. Cortland Griswold Associate Professor Department

of Integrative Biology University of Guelph
 cgriswol@uoguelph.ca <http://www.uoguelph.ca/ib/>

UIceland BrownTrout PopGenomics

The Institute of Life and environmental sciences at the University of Iceland invites applications for a PhD studentship.

The project is titled: Population genomics and ecology of brown trout in Iceland - genetic foot-prints of colonization and ecological diversification in novel habitats.

How flexible are the ecologically important traits of colonizing species? What is the role of isolation, adaptation and gene flow for diversification in novel habitats?

The principal objective of the research is to survey the phenotypic variation in Icelandic brown trout with respect to key ecological correlates and to employ population genomics to cast light on the processes of diversification.

The Ph.D. project builds on the fact that in Iceland brown trout (*Salmo trutta*) is found in widely varying habitats and situations; lakes v. streams; cold springs v. geothermally affected streams; with and without presence of other salmonids; small v. large populations. The project is designed to survey the phenotypic variation emerging from this recent and rapid diversification and to investigate the genetic foot-prints of these processes.

During the last ice age Iceland was covered with a thick ice cap that extended far out from the present shore line. As the ice retreated some 13 - 11.000 years ago physical conditions for the colonization of terrestrial and freshwater habitats were created. Three salmonids, Arctic charr (*Salvelinus alpinus*), brown trout and Atlantic salmon (*Salmo salar*), are all believed to have colonized Icelandic freshwaters as the ice retreated. The charr is the most diverse of these and is found in variable limnetic and benthic forms that in some cases coexist in sympatry. Although the brown trout is also known from a variety of habitats less is known of its phenotypic variation.

The Ph.D. project will focus on brown trout populations in one of the main watersheds in southern Iceland, including the River Sog and Lake Thingvallavatn, and streams in the mountainous Hengill geo-thermal area.

The specific aims are to:

I) To survey phenotypic variation (e.g. in morphology, life history characteristics) in populations from a wide variety habitats and communities II) To employ next generation sequencing techniques (RAD-seq) to survey genetic variation within and among populations which will enable the student to: a) assess the genetic connectedness among populations and probe the history of colonization b) implicate loci that associate with morphological and ecological characteristics and assess if and how variation at these loci correlates with ecological specializations across multiple populations.

We are seeking a student with dedication, drive and good theoretical background in population genetics and evolutionary biology and an interest in the ecology and genetics of divergence. Good laboratory skills and knowledge of computer programming, data analysis and statistics is preferred. The work involves planning and executing sampling in the field, acquisition and analysis of high-throughput sequencing data and numerical analyses.

The position will be at the University of Iceland, within the Arctic charr and salmonid group. The student would be a part of this group and receive theoretical and technical support from its specialists and students that are conducting comparable work on the Arctic charr in Iceland. The project involves collaboration with experts at the Icelandic freshwater institute, with input from collaborators at the University of Guelph, Canada, the University of Aarhus, Denmark, and the Hólár University College, Iceland.

The applicant must have completed a M.Sc. degree in Biology or related fields from a University approved by the University of Iceland's Graduate School. Those with an advanced degree including at least a 60 ECTS credits thesis project will be given precedence. Startdate: summer/fall 2016.

Applications should be sent before the 9th of April 2016, to sigsnor@hi.is, with scanned documentation of University degrees, a CV and names of 2 references.

Further information on the Arctic charr and salmonid group at the University of Iceland: http://luvs.hi.is/-arctic_charr_development_evolution_and_genetics Best regards, Arnar Pálsson

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

Arnar Pálsson <apalsson@hi.is>

ULausanne PopulationGenetics

Available:

PhD position, 3-4 years

Department of Ecology and Evolution, University of Lausanne, Switzerland

Start: September 2016 or earlier

Our group studies the selective forces that act on freshwater fish, i.e. the effects of human activities in interaction with natural and sexual selection. Our current research focuses on salmonid fish (brown trout, grayling, whitefish) and combines different types fieldwork, labwork, and modeling. See <http://www.unil.ch/dee/home/menuinst/research/group-wedekind.html> We are seeking candidates with an interest in population genetics, life history, evolutionary ecology, and population management. The candidate would start her/his thesis with experimental field and lab work on a whitefish population in a Swiss lake.

Send your application by email to claus.wedekind@unil.ch. Please include your Curriculum vitae, a short description of your research interests and research experience, and contact details of one or two references. Review of applications will begin end of March 2016, but applications will be considered until the position is filled.

Claus Wedekind Department of Ecology and Evolution, Biophore, University of Lausanne, 1015 Lausanne, Switzerland. Tel. +41 21 692 42 50, Fax +41 21 692 42 65 <http://www.unil.ch/dee/home/menuinst/people/group-leaders/prof-claus-wedekind.html> Claus Wedekind <claus.wedekind@unil.ch>

ULeeds UK AgeingInBadgers

A funded PhD studentship on "Early-life environment effects on ageing in European badgers" is available at the University of Leeds, UK, supervised by Dr Hannah Dugdale and co-supervised by Dr Amanda Bretman. The PhD is in collaboration with Prof David Macdonald and Dr Chris Newman at the University of Oxford.

This PhD will address why individuals differ in the point and rate at which they senesce - senescence being the loss of function with age, from the cellular to the organism level. Our understanding of the factors that affect senescence is limited: Within a species, are some individuals better able to buffer against senescence due to physiological adaptations (such as greater oxidative damage resistance and longer protective chromosome caps - termed telomeres), environmental effects (e.g. born in years with high food availability), or social conditions (e.g. low levels of intra-sexual competition)? This PhD will investigate these key questions, using data from a natural population of European badgers subject to variable environmental and social conditions. This will generate critical knowledge that will improve our understanding of how and why some individuals live longer, healthier lives than others, improving our understanding of animal health and informing conservation management decisions. Further information is available here: <https://hannahdugdale.wordpress.com/opportunities> Why you should apply: The University of Leeds is in the world top 100 universities, globally recognised for its quality of teaching and research, and is in the leading group of UK universities, creating an excellent environment for a PhD. Dr Hannah Dugdale and Dr Amanda Bretman will provide expertise in evolutionary biology. In particular, we will provide supervision in the evolution of senescence, social evolution and conservation biology, and we will encourage you to develop your own research ideas. You will gain specialist training in molecular ecology techniques to conduct laboratory work, and you will have the opportunity to gain fieldwork skills - fieldwork takes place in Oxford over two weeks in June, August and November. You can develop your networking and team skills through collaborations with researchers on the long-term Wytham badger project. You will also benefit from a wide-range of training courses, such as: <http://www.emeskillstraining.leeds.ac.uk> and <http://www.fbs.leeds.ac.uk/postgraduate/professionaldev.php>. Funding: The studentship covers UK/EU tuition fees and a stipend at RCUK rates (~£14,296 pa) for 3 years full-time. Applicants from the UK/EU are eligible; international tuition fee payers are not eligible. Deadline: Friday, April 29, 2016. To apply: <http://www.fbs.leeds.ac.uk/postgraduate/researchdegree.php> Requirements: An Honours or Masters degree in a related subject are essential. You should be passionate about evolutionary biology and molecular ecology with a keen interest in learning laboratory skills, such as qPCR. Previous laboratory, database, statistical and fieldwork experience would be beneficial.

Hannah Dugdale <H.Dugdale@leeds.ac.uk>

ULincoln UK AntipredatorBehaviour

Fully-funded PhD studentship: Using virtual reality to investigate 'protean' anti-predator behaviour

School of Life Sciences, University of Lincoln, UK

We are seeking to recruit a graduate with an MSc or a good BSc degree (or equivalent) for a project on the evolution of 'protean' anti-predator behaviour, starting in October 2016. This is a fully-funded position covering fees and stipend for three years, and will be supervised by an interdisciplinary team with expertise spanning behavioural ecology and computer science.

Protean anti-predator behaviour is broadly defined as behaviour that is sufficiently unpredictable to prevent a predator anticipating in detail the future position or actions of its prey, and anecdotal examples (including zigzagging, spinning, looping and bouncing) are extremely common across the animal kingdom. However, compared to other anti-predator behaviours, protean movement has received almost no experimental investigation. The overarching aim of this project is therefore to elucidate the mechanisms that allow protean behaviour to be an effective anti-predatory strategy. It will do this through (a) the three-dimensional tracking of protean movement in live animals evading simulated predation events, combined with (b) the use of virtual reality to allow human 'predators' to attack and chase virtual prey in three-dimensions. This will enable us to not only test the efficacy of natural protean behaviours, but also virtually 'evolve' protean behavioural strategies in order to explore the specific underlying mechanisms. There is considerable scope for the student to input into the direction this project will take, but general questions that could be investigated include: (1) How random does protean behaviour need to be in order to be effective as an anti-predator strategy? (2) How does predator learning impact on the evolution of protean escape strategies? (3) And how does prey morphology (such as the presence of strongly contrasting body patterns) interact with protean behaviour? Addressing these, and related, questions will give the student an exciting opportunity to work at the interface between behavioural ecology and computer science, and develop a highly transferable skillset.

To apply, please send a CV and cover letter to Tom Pike

(tpike@lincoln.ac.uk) by 1 April 2016. You may also contact Tom Pike for informal enquiries. Shortlisted applicants will be invited for interview.

The University of Lincoln, located in the heart of the city of Lincoln, has established an international reputation based on high student satisfaction, excellent graduate employment and world-class research.

“TPike@lincoln.ac.uk” <TPike@lincoln.ac.uk>

UNice MolEvolGeneticsAllometry

Graduate position: Molecular and evolutionary genetics of cell/organ size relationships

A PhD fellowship jointly supervised by Christian Braendle & Pierre Léopold is available at the Institute of Biology Valrose in Nice (starting data 01/10/2016).

Project summary: Molecular mechanisms that coordinate size relationships among different cell types and organs are fundamental for organismal growth and fitness, yet still poorly understood. Moreover, it remains unclear how mechanisms governing such allometry evolve within and between species. This project addresses these questions using an integrative - molecular and quantitative genetic - approach and taking advantage of two genetic model organisms, the nematode (*C. elegans*) and the fruit fly (*Drosophila melanogaster*).

The principal objectives of the project are:

1. Mapping of natural genetic variation in cell/organ size relationships and their plasticity in *C. elegans* using Genome-Wide Association Study, QTL mapping using F2 RILs and/or experimental evolution/selection lines.
2. Molecular characterization of uncovered candidate gene variants affecting cell/organ size relationships using complementation analysis, RNAi, transgenesis and targeted genome editing.
3. Molecular-developmental analysis of select candidate genes in *Drosophila* growth and organ size regulation.

This PhD fellowship is available in the context of the Signallife PhD program of the University of Nice Sophia Antipolis. This 3-4 year position is open to all nationalities and interested candidates should apply directly through the Signallife website: <http://signallife.unice.fr> For more information, please visit: <http://ibv.unice.fr/> <http://www.braendlelab.net> <http://ibv.unice.fr/EN/-equipe/leopold.php> or contact: braendle@unice.fr or leopold@unice.fr

Relevant publications

Colombani, J., Andersen, D.S., Boulan, L., Boone, E., Romero, N., Viole, V., Texada, M., and Leopold, P. (2015). *Drosophila* Lgr3 Couples Organ Growth with Maturation and Ensures Developmental Stability. *Curr.Biol.* 25, 2723-2729.

Poullet N, Vielle A, Gimond C, Ferrari C & Braendle C 2015 Evolutionarily divergent thermal sensitivity of germline development and fertility in hermaphroditic *Caenorhabditis* nematodes. *Evolution & Development* 17: 380-397.

Colombani, J., D. S. Andersen, and P. Leopold. 2012. Secreted peptide Dilp8 coordinates *Drosophila* tissue growth with developmental timing. *Science* 336:582-585.

“Christian.BRAENDLE@unice.fr”
<Christian.BRAENDLE@unice.fr>

UOslo Genomics

See below:

Department of Biosciences, University of Oslo PhD Research Fellowship in Genomics Position as PhD Research fellow available at the Department of Biosciences.

Online:

<http://uio.easycruit.com/vacancy/1597275/96323?iso=-3D3Dgb> 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 01.10.2016.

No one can be appointed for more than one fixed-term period at the same institution.

Job/ project description:

The PhD fellow will be appointed on the project entitled “Evolutionary and functional importance of simple repeats in the genome” funded by the Research council of Norway through the FRIPRO program and lead by Professor Kjetill S Jakobsen. The candidate will be working in an internationally leading research group recently awarded Frontier Research status.

The project focuses on the functional modulation of regulatory mechanisms affecting the phenotype by variations in simple trinucleotide repeats residing inside (coding) and in the vicinity (or in introns) of genes.

Specifically, we would like to test the hypothesis that hypervariable coding/regulatory repeats are promoting the ability of a species or population to adapt to a changing environment. To address this we will use Atlantic cod and Arabidopsis as model systems. The project is cross-disciplinary and will utilize genomic, bioinformatics, statistics and experimental approaches and the appointed PhD candidate will work in a larger team and in close connection with an additional PhD that will be hired concurrent with this position.

The PhD candidate will investigate the genomic architecture of repeats and repeat-length variation in individuals of Atlantic cod and Arabidopsis using PacBio long read technology. A particular focus will be on simple repeats within or in the vicinity of genes. Data from the Aqua Genome Project and the 1001 Arabidopsis genome project will also be investigated. Further, trans-generational variation in repeat length will be addressed. A goal will be to obtain a number of candidate genes containing repeat length variation as a response to selection regimes. Another goal will be to build models for how repeat length variation within the protein affects structural properties.

The project as a whole consists of three interconnected work packages. The successful candidate will work on the work package entitled "Genomic repeat architecture in Arabidopsis and Atlantic cod and length variation in simple repeats" led by professor Kjetill S Jakobsen. The project has international collaborators and research visits to collaborating partners will be encouraged.

Requirements/qualifications:

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 biology, molecular biology or bioinformatics/biostatistics and have experience with bioinformatics methods for analysis of high throughput sequencing genome data. The applicant must be qualified for the doctoral program within these disciplines. The successful applicant should preferably have experience in using bioinformatics and computational methods in a comparative or evolutionary setting. Experience with programs for analyses of genomic repeats will be particularly useful.

Candidates without a Master's degree have until 30 June, 2016 to complete the final exam.

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

The fellowship requires admission to the PhD program at the Faculty of Mathematics and Natural Sciences. The application to the PhD program 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/phd/> <http://www.mn.uio.no/english/research/doctoral-degree-and-career/phd-programme/index.html> A good command of English is required.

Salary:

Position code 1017, Pay grade: 50 - 57 (NOK 430 500 - 483 700 per year)

The application must include:

Application letter CV (summarizing education, positions and academic work - scientific publications) Copies of educational certificates, and transcript of records Documentation of English proficiency List of publications and academic work that the applicant wishes to be considered

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UPoitiers Metagenomics

Dear all,

I seek a motivated candidate for a 3-year PhD position (from October, 2016) on:

Metagenomics of the association between Wolbachia and woodlice: evolution and organization of interaction networks

Project description: Most of the arthropods are hosting symbionts which play a major role in the fitness of their hosts. It is well known that the resulting interactions between hosts and symbionts, ranging from mutualism to parasitism, are a source of genetic novelty [1]. In this context, we have to consider the host as a complex ecosystem including all the symbiotic microbiota [2]. The aim of the PhD project is to analyze the genomic interactions of the terrestrial isopods microbiota. Terrestrial isopods are unconventional models as i) they constitute the only group of crustaceans that are mainly adapted to terrestrial environment and ii) they are prone

to sex manipulation by the *Wolbachia* proteobacteria [3]. In a recent study [4], we determined the bacterial communities in the pill-bug *Armadillidium vulgare*. A high level of bacterial diversity is recorded in all tissues from the host. A quantitative analysis demonstrated that the *Wolbachia* strains that have been identified in *A. vulgare* exhibited specific distribution patterns in tissues [5]. When present, *Wolbachia* dominate the microbial community even if other major bacteria are found. Finally the structure of the bacterial communities is influenced by two major triggers: the type of the *Wolbachia* strain and the origin of the environmental bacteria for which the host is highly permissive [6]. Some hypotheses have been proposed on the implication of these interactions on the functional level. New high throughput sequencing data recently obtained allow us to test these hypotheses. Transcriptomic data were obtained by whole transcriptome shotgun sequencing (RNA-seq) on different host tissues. Differentially expressed genes involved in extended phenotypes (immunity, nutrition, sex determination, symbiotic interactions or regulation etc) were identified from the comparative analysis of the resulting transcriptomes. Metagenomics data (HiSeq Illumina) obtained from *A. vulgare* confirm the results on bacterial diversity and also reveal a huge viral diversity. This approach identifies some microbial effectors.

The first steps of the project involve bioinformatics tools in order to construct a de novo metagenomic assembly, to identify the taxonomic and the functional profiles of the resulting assembly and to analyze their potential interactions. In a second step, the host-microbiota interactome will be studied using network analysis of the metagenomic assembly and the transcriptome of the host. A particular focus will be put on the impact of *Wolbachia* on such an interactome. In vivo (and/or in vitro) approaches will be developed in order to test the potential effectors of the interactome.

References: [1] MORAN N.A., MCCUTCHEON JP AND NAKABACHI A. 2008 Genomics and Evolution of Heritable Bacterial Symbionts. *Annu. Rev. Genet.* 42:165-90. [2] SICARD M., DITTMER J., GREVE P., BOUCHON D. AND BRAQUART-VARNIER C., 2014. A host as an ecosystem: *Wolbachia* coping with environmental CONSTRAINTS. *Env. Microbiol.* DOI: 10.1111/1462-2920.12573 [3] BOUCHON D., CORDAUX R. AND GREVE P. 2008. Feminizing *Wolbachia* and evolution of sex determination in isopods. In *Insect Symbiosis Volume 3* (Eds K. Bourtzis & T.A Miller), pp. 273-294, CRC Press, Boca Raton. [4] DITTMER J., 2013. Host-associated MICROBIOTA in *Armadillidium vulgare*: feminizing *Wolbachia* and other major players. Thèse d'Université [5] DITTMER J., BELTRAN-BECH

S., LESOBRE J., RAIMOND M., JOHNSON M. and BOUCHON D. 2014. Host tissues as microhabitats for *Wolbachia* and quantitative insights into the bacterial community in terrestrial isopods. *Mol. Ecol.* 23 :2619- 2635. [6] DITTMER J., LESOBRE J., MOUMEN B. and BOUCHON D. 2015. Host origin and tissue-microhabitat shaping the microbiota of the terrestrial isopod *Armadillidium vulgare*. *FEMS Microbiol.Ecol.* (in revision)

Requirements for applicant: - Master's degree in Evolutionary Ecology or Evolutionary Biology - Strong experience in Evolutionary Ecology focusing on host-parasite or host-symbiont interactions and interest in numerical analyses (bioinformatics, statistics) - Excellent writing skills

Application: - Please send your CV and motivation letter to: didier.bouchon@univ-poitiers.fr - Deadline: 15 April 2016

- Pr. D. Bouchon

Universite de Poitiers UFR Sciences Fondamentales et Appliquées Laboratoire Ecologie et Biologie des Interactions - UMR CNRS 7267 Equipe Ecologie Evolution Symbiose - Batiment B8-B35 5 rue Albert Turpain TSA 51106 F-86073 POITIERS Cedex 9 tel : +33 (0)5 49 45 38 95 fax : +33 (0)5 49 45 40 15

<http://ebi.labo.univ-poitiers.fr/>

<http://-ecoevol.labo.univ-poitiers.fr/>

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UppsalaU PlantGeneticsGenomics

Position for one PhD student in Ecological Plant Genetics/Genomics in the program of Plant Ecology and Evolution at Uppsala University, Sweden

Adaptive differentiation among natural populations is often attributed to fitness trade-offs, i.e., that adaptation to one environment reduces performance in other environments. However, the prevalence of fitness trade-offs, and the traits and genes underlying fitness tradeoffs are poorly known. You will work in a project studying the genetic and ecological mechanisms underlying adaptive differentiation among natural populations of the plant

model organism *Arabidopsis thaliana*. The goals are (1) to determine the functional and adaptive significance of differences in plant phenology (timing of germination, and flowering time) between populations close to the northern and southern margins of the native range, (2) to explore the molecular basis and geographic distribution of QTL (quantitative trait loci) for seed dormancy and flowering time identified in previous experiments, (3) to quantify the individual and combined effects of these QTL on fitness, and (4) to determine their contribution to fitness trade-offs across environments. The project is conducted within the framework of an international research collaboration. The successful candidate will settle the exact profile of her/his PhD project together with the supervisor Jon Ågren.

The position requires a MSc degree (or equivalent) in evolutionary biology, ecology, genetics or a related field. Proficiency in English is a requirement. Strong motivation, and ability to work independently and as part of a team are important qualities. The successful candidate should have a keen interest in population biology, and ideally experience from previous work in evolutionary biology, ecology or genetics.

The postgraduate training comprises four years of full time studies within the postgraduate school at the Department of Ecology and Genetics, at the Evolutionary Biology Centre (<http://www.ieg.uu.se/>). The position can be combined with up to 20 % of teaching assistantship, which will then prolong the position accordingly.

Deadline for application is 31 March 2016

Please find the announcement, with all information about how to apply, at:

<http://uu.se/en/about-uu/join-us/details/-?positionId=90943> For informal enquiries, please contact prof Jon Ågren, jon.agren@ebc.uu.se, +46-18-471 2860.

Jon Ågren Plant Ecology and Evolution Dept of Ecology and Genetics, EBC Uppsala University Norbyvägen 18 D SE-736 52 Uppsala Sweden

Jon Ågren <jon.agren@ebc.uu.se>

UStAndrews ComparativeGenomics

PhD St Andrews, comparative genomics

A PhD is available at the University of St Andrews, Scotland, on “Comparative genomics of the virilis group of *Drosophila*”. Lead supervisor Prof Mike Ritchie, co-supervisor Dr Konrad Lohse at the University of Edinburgh. The project is also collaborative with colleagues in Finland and Oxford.

The deadline for applications is April 10th 2016 and full details, including application procedure are available at <http://master.findaphd.com/search/-ProjectDetails.aspx?PJID=3D67228> . Informal enquiries to Mike Ritchie at mgr@st-andrews.ac.uk. UK and European candidates have to be prioritised due to the nature of the funding.

Mike Ritchie

Centre for Biological Diversity, School of Biology,
University of St Andrews, Fife. Scotland KY16 9TH
UK

Phone: 0 (44 outside UK) 1334 463495

Some websites:

Lab: <http://biology.st-andrews.ac.uk/ritchielab/>
Uni: <http://www.st-andrews.ac.uk/profile/mgr>
Google: <http://scholar.google.co.uk/citations?user=3DJSkvwMsAAAAJ&hl> CBD: <http://biodiversity.st-andrews.ac.uk/> Michael Ritchie <mgr@st-andrews.ac.uk>

USunshineCoast Adaptation

UniversitySunshineCoast_Adaptation_to_Urbanisation

I have a scholarship available in my lab (celinfrerelab.com) to work on adaptation to urbanisation using the eastern water dragon as a study system. Follow this link for more information: <http://www.usc.edu.au/learn/what-will-i-pay/scholarships/research-scholarships/adaptation-to-urbanisation-phd-scholarship>

Thanks

Celine
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 Celine Frere <cfre@usc.edu.au>

UUlm Germany 2 EvolutionaryGenetics

The Institute of Evolutionary Ecology and Conservation Genomics invites applications for a
 2 PhD positions in Evolutionary Genetics
 The project aims to disentangle the impact of the adaptive immune system (MHC class I) and habitat disturbance on viral infections in tropical A) bats and B) rodents. It will employ novel next generation sequencing approaches and bioinformatics data processing. The position A is primarily lab-based, the position B involves 6 months of highly demanding field work in Panama per year. Both PhD projects are embedded in an ongoing multi-disciplinary project in the Panama Canal area that aims to discriminate the effects of ecological and genetic disturbance on wildlife health on a landscape level. Landscapes differ in their extent of anthropogenic disturbance, isolation of natural habitat and contact probability to humans and livestock.
 Applicants should have a M.Sc. degree in Biology. We

expect candidates to have a strong background in evolutionary ecology and population genetics, and interest in bioinformatic data processing and statistics. We seek highly motivated and scientifically creative graduate students with experience in molecular lab techniques, a good literature overview in the field, ability to work independently and in a team, as well as social and organisational skills. A high standard of spoken and written English is required. Preference will be given to candidates with next generation sequencing experience and/or demanding field work under tropical conditions. A background in statistics, R programming language and bioinformatics data processing would be advantageous. The applicants assessed as the best qualified will be called to an interview, which might be carried out online.

Remuneration is in accordance with TV-L 13 (65%). The positions funded for 3 years by the German research foundation (DFG). Applicants should submit a letter explaining their interests and particular skills for position A or B, a CV including candidate's photo, a summary of their Master thesis, two letters of recommendation and a publication list. The position is open until filled, and applications will be reviewed continuously, but for full consideration please apply by April 01, 2016. Please send your application per email to Prof. Dr. Simone Sommer (simone.sommer@uni-ulm.de).

Severely disabled applicants with adequate qualification are given preference. The University is an equal opportunity employer that tries to increase the number of women in research. Hiring is done by the Central University Administration.

Prof. Dr. Simone Sommer

University of Ulm

Head Evolutionary Ecology and Conservation Genomics (BIO III)

Helmholtzstr. 10/1 (Containerstadt)

D-89081 Ulm

Tel.: 0049-731-5022660

Tel.: 0049-731-5022661 (Secretary)

Fax: 0049-731-5022683

Simone.Sommer@uni-ulm.de

"Prof. Dr. Simone Sommer" <simone.sommer@uni-ulm.de>

UVictoria BC 2 InsectParasiteInteractions

I am looking to fill two fully funded MSc or PhD positions in evolution and ecology of insect-parasite associations, in my lab in the Dept. of Biology, University of Victoria, Victoria, British Columbia, Canada. One position focuses on interactions between *Drosophila* and their parasites (nematodes, trypanosomatids) and/or inherited symbionts (protective *Spiroplasma*, *Wolbachia*). The second position focuses on an extreme sex ratio distortion in booklice (close relatives of parasitic lice). For more information about research in my lab, please visit <http://web.uvic.ca/~stevep/> The ideal candidates have a strong background in evolutionary biology, demonstrated strength in data analysis, and excellent oral and written communication. Experience working with insects and/or microbes, and with transcriptome and/or genome data are also assets. The minimum GPA to be admitted to UVic Biology is B+/A- (or equivalent) in the last two years/second half of your undergraduate degree. In order to apply, please email a single pdf containing a) a statement of research interests, b) CV, c) unofficial transcript, and d) names and contact information of 2 references, to stevep@uvic.ca by April 18, 2016. Please also indicate which of the two positions you would like to be considered for.

Steve Perlman Associate Professor Department of Biology University of Victoria

“stevep@uvic.ca” <stevep@uvic.ca>

Vienna PopulationGenetics

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

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

We invite applications from highly motivated and out-

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

Topics include:

- Convergent and adaptive evolution during ecotype formation
- *Wolbachia* infection dynamics in evolving *Drosophila* populations
- Optimizing novel, NGS-based, approaches for dissecting the genetic basis of complex traits
- Evolution of the transposable element landscape in *Drosophila*
- Selfish mutations
- Inferring evolutionary trajectories from time series data
- Functional characterization of beneficial alleles in *Drosophila*
- Modified evolve and re-sequence design
- Statistical inference for experimental evolution using pooled NGS data

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

Monthly salary of a successful candidate will be according to the regulations of the Austrian Science Fund FWF. All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at <https://twitter.com/PopGenViennaPhD> c/o Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1, 1210 Wien

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

<http://www.vetmeduni.ac.at/en/population-genetics/> <https://twitter.com/PopGenVienna>
julia.hosp@gmail.com julia.hosp@gmail.com

WageningenU AnimalGenomics

We are looking for talented and enthusiastic PhD candidates to join a multi-disciplinary team at the interface of molecular and quantitative genetics, at the Animal Breeding and Genomics Centre (ABGC) and the Centre for Genetic Resources, the Netherlands (CGN) of Wageningen University and Research Centre.

Project: Using Whole Genome Sequence information for demographic and functional evaluation of managed populations.

Summary of research objectives: As sequencing entire genomes is becoming a standard practice in population studies, a wealth of information on variation in species is becoming available that can ignite novel applications for population management. The overall aim of the project is to use entire genome data of managed populations (in situ and ex situ) and evaluate how best to use that data to reduce inbreeding risk and loss of diversity in the species.

The main objectives of the project are: a. To identify extent and nature of key demographic events in managed populations, such as inbreeding, hybridization, or changes in selection, based on genomic data. b. To use in-silico predictions of the function of genomic variation that may underlie unique phenotypes or inbreeding risk. c. To quantify demographic discontinuities and functional variation in relation to variation in the entire species, with the aim to develop a rational, genomics-based, appraisal of managed genetic resources as reservoirs of variation. d. To apply methods at the interface of population genetics and machine learning to develop classifiers that can be used for automated evaluation of key population processes, including inbreeding risk.

Case studies will be used to advance the concepts central to the project. By analysing whole genome data of thousands of individuals, demographic discontinuities and inbreeding risk can be quantified. This is vitally important for sustainable population management, especially in relation to the value of recognized in situ (live populations) or ex situ (genebank) resources. While the project focuses on domesticated populations, the concepts are universally applicable to any managed species since predictors and classifiers will be derived from generic whole genome data sources.

Profile of candidate: Enthusiastic PhD candidate, either biologist (or related field) with a background in population/conservation genetics and/or functional genomics, with affinity for bioinformatics, or bioinformatician or computational biologist with affinity for biodiversity and population genetics.

We offer a challenging position in an inspiring multidisciplinary and international environment, in one of the leading groups on animal breeding and genomics in the world. You will be part of a research team involving multiple partner organisations. The proposed start is June 2016.

A fulltime position as a PhD candidate for 4 years, after after which you should have completed your PhD thesis and individual training plan. The salary for a PhD candidate starts at euro 2.147,- gross per month in the first year and extends to a maximum of euro 2.745,- gross per month in the fourth year (in accordance with the Collective Labour Agreement for Dutch Universities).

Participation in the training program of the Graduate School 'Wageningen Institute of Animal Sciences' (WIAS), see www.wias.nl. An excellent opportunity to develop an international scientific network.

Additional information about this vacancie can be obtained from:

Dr. Hendrik Jan Megens (hendrik-jan.megens@wur.nl)

To apply go to this website: <https://www.wageningenur.nl/en/Jobs/Vacancies/Show/-Phd-Genomics-and-biodiversity-two-fulltime-positions-project-2.htm> Partners involved: The project is part of the Horizon2020 funded IMAGE consortium. IMAGE is a unique European collaborative project of 28 partners, including 3 non-European partners. A variety of stakeholders (gene banks, breeding organisations, science, NGOs) participate in IMAGE. The IMAGE project is important for strengthening the gene bank infrastructure in Europe (EUGENA) and for the conservation and sustainable use of farm animal breeds (animal genetic resources) at the European level.

"hendrik-jan.megens@wur.nl"

<hendrik-

jan.megens@wur.nl>

ZFMK Bonn Barcoding

The Center for Molecular Biodiversity Research at the Zoological Research Museum Alexander Koenig in Bonn (ZFMK, Germany) invites applications for a PhD studentship. The studentship will be part of a project within the German Barcode of Life (GBOL). Starting date: not later than 1st May 2016, preferentially earlier. Duration: until 31st December 2018 Salary: German salary scale (TV-L E13, 55 %).

We seek an enthusiastic and highly motivated candidate to work on a project on metabarcoding and biodiversity at ZFMK in Bonn. The main objective of the studentship is to create a biodiversity map of invertebrate communities using environmental DNA samples derived from the Eifel National Park and to monitor species/ecosystems over time. This will be a timely project since there is no comprehensive biodiversity study German National Parks, such as the Eifel NP, using HTP (high-throughput) sequencing approaches. This will move towards establishing an efficient biodiversity-monitoring approach providing critical insights into biodiversity assessment on a temporal scale. The project will involve handling environmental samples (Malaise insect traps and soil samples) in the lab and in the field, as well as using next generation 'metagenetics/ metabarcoding' approaches to tracking mainly meio- and macrofauna communities. There will be opportunity to develop a preliminary pipeline as a tool for biomonitoring and best-practice guidelines for environmental barcoding (sampling protocols, preservation and downstream data analysis). The student will join a multi-disciplinary supervisory team led by Dr Vera Fonseca (biodiversity and metabarcoding) and Dr Jonas Astrin (Biobank and DNA barcoding), together with an external collaborator, Dr Christopher Quince from Warwick University (food web, meta-analysis), offering the student to gain knowledge and training in Bioinformatics, Ecology, Genomics, Conservation and Biodiversity. The PhD candidate should be highly motivated, with good computer command line skills and with a strong enthusiasm for environmental molecular biodiversity. The candidate will have

to spend some time in the Eifel NP (driving license not necessary, but helpful). Desirable skills are molecular biology (e.g., DNA/RNA extraction, PCR) and bioinformatic environmental meta-analyses experience (HTP). Students are expected to acquire and develop new skills but candidates with prior expertise in HTP meta-analysis will be given preference. The candidate should have a Master's degree, or be close to completing a Master's degree in Biology or related discipline. Fluent spoken and written English is essential. The Center for Molecular Biodiversity Research at the Zoological Research Museum Alexander Koenig offers a pleasant and stimulating research environment with a modern molecular laboratory and a state-of-the-art high-performance computing cluster. Current research projects in the department deal with DNA barcoding and metabarcoding terrestrial biodiversity (German Barcode of Life, GBOL) and Environmental barcoding of aquatic invertebrates (EBAI, Norway University Museum), as well as other exciting research lines such as the phylogeny of insects (e.g., www.1kite.org) and other groups of organisms and the organization and evolution of insect genomes (e.g., i5K).

Applications should include: (1) Letter of motivation (relevant skills, experience and research interests) (2) Curriculum vitae (3) Official BSc and/ or MSc certificates (4) Contact details of two (ideally academic) references Closing date for Applications: 1st April 2016. Applications should be submitted in English and electronically as a single PDF to Dr Vera Fonseca, vfonseca@uni-bonn.de with 'MetaEIFEL application' in the subject line. Any enquiries, please also contact vfonseca@uni-bonn.de. The ZFMK values equality of opportunity, human dignity, and racial/ethnic and cultural diversity. According to German law, applications by women and by persons with a disability will be given priority in case of superior or equal qualifications. Women are especially encouraged to apply. The position is remunerated according to TV-L E13 (55 %).

Vera G. Fonseca (PhD) Head Environmental Genomics Zoological Research Museum Alexander Koenig (ZFMK), Centre for Molecular Biodiversity Research, Adenauerallee 160, 53113 Bonn, Germany Tel.: +49 (0)228 9122 283 Fax: +49 (0)228 9122 295 www.zfmk.de www.bolgermany.de Vera Fonseca <vfonseca@uni-bonn.de>

Jobs

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Chicago TheFieldMuseum MammalCollectionManager

Collection Manager, Mammals

The Field Museum, Chicago, IL

The Field Museum seeks to hire a Collection Manager of Mammals. This position involves all aspects of care, maintenance, and accessibility of The Field Museums mammal collection. This large, actively growing collection is home to many research and education initiatives by both resident and extramural scientists. Duties include overseeing all aspects of specimen preparation, identification, care, and organization of specimens; training, supervision and coordination of staff, students, and volunteers in their collection-related activities; assistance to visitors in their use of collection, processing of recently collected specimens, as well as supervision of outgoing and incoming specimen loans, loan recalls, and loan returns, all conducted in consultation with curator(s) of mammals. Primary responsibilities include

the maintenance of records relevant to the collection (electronic catalog, loan invoices, accession files, permits, field notes), providing the public, professionals, and officials with information they need from the collection (including digitizing specimens), and updating records as the collection grows or identifications change. The Collection Manager of Mammals interacts with the Museum's Science Action, Integrative Research, and Learning centers, as well as with Exhibits programs. The position involves a heavy public engagement component through collections tours, donor engagement, and museum programming, grant writing, liaising with federal and state authorities as needed, and working with other mammal collections and researchers. The Collection Manager will have opportunities to conduct collection-based research, but these will be secondary to collection management responsibilities.

For more information about this position including duties and qualifications, and to apply, please visit the Field Museum employment website: (<https://www.fieldmuseum.org/about/careers?id=3D58135>)

Ben Marks

Head of Zoological Collections

Collection Manager, Birds
 Science and Education
 Field Museum of Natural History
 1400 S. Lake Shore Dr.
 Chicago, IL. 60605
 bmarks@fieldmuseum.org
 Ben Marks <bmarks@fieldmuseum.org>

CornellU UC Irvine ResAssist PlantPollinatorEvol

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

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

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

Qualifications: 1) Education: some undergraduate education in biology, ecology, or related field, or equivalent

experience 2) Experience: experience with and enthusiasm about working outdoors, and/or previous field research experience. Previous experience working with plants, bees, or insects is preferable but not required. 3) Tasks: perform repetitive tasks with attention to detail, daily hiking 4) Personality: interpersonal skills and willingness to live and work in close quarters with other researchers in a house.

Compensation: transportation to and from California, a private room with Internet access in the field house, and pay (\$13-\$15 an hour depending on experience) will be provided. Applicants will be responsible for securing their own housing in Ithaca for July and August.

The deadline for applications is March 20, 2016. Applicants should submit: 1) a short (1 page maximum) cover letter describing their qualifications as well as future academic and professional goals; 2) a resume or CV outlining previous work experience and relevant courses (completed or in progress), extracurricular activities; and 3) contact information for two references.

Cornell University is an affirmative action/equal opportunity employer. Cornell University and we in the Geber lab have a commitment to support equality of education and employment opportunity by affirming the value of diversity. We welcome and encourage scientists of all backgrounds to apply to work with us! <http://blogs.cornell.edu/geberlab/> Email to: Monica Geber, Professor of Ecology and Evolutionary Biology mag9@cornell.edu

Katherine Eisen <kee39@cornell.edu>

DukeU ResAssoc EvolAnthropology

The Nunn Lab at Duke University (<http://people.nunnlab.org>) is looking for a part-time or fulltime Associate in Research. The position will provide unique opportunities to participate in research first-hand, with an emphasis on statistics and phylogenetic comparative methods in R, development of online resources, and construction of original databases on primate behavior, ecology and morphology. Duties will also include general lab management, research at the Duke Lemur Center, and opportunities to participate in additional research projects in the Nunn Lab depending on interests and skills.

The ideal candidate would be an upcoming (or recent) graduate from an undergraduate program in evolution-

ary anthropology, biology, statistics, or computational biology. Applicants should have basic skills in statistics, computer programming, and/or phylogenetics, and an interest in developing those skills for future research endeavors. The initial duration will be one year, with possibilities for a second year of employment based on performance. The position would ideally start on June 1, 2016, although some flexibility in the start date is possible. The position is funded partly through the National Science Foundation for research on 'Using Primate Comparative Biology to Understand Human Uniqueness' (BCS-1355902).

Applications should include a cover letter, CV, and names and contact information for two references. Applications will be evaluated starting on April 4, 2016, and will continue until the position is filled. Please send application materials and questions directly to Prof. Charles Nunn, charles.nunn@duke.edu.

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

Charles Nunn Department of Evolutionary Anthropology & Duke Global Health Institute Director, Triangle Center for Evolutionary Medicine (TriCEM) Biological Sciences 106 Duke University Durham NC 27708

nunn-lab.evolutionaryanthropology.duke.edu tricem.org

Office: (919) 660-7281 Cell: (510) 206-5716

Charles Nunn <charlesnunn@gmail.com>

EvolutionaryGenomicsInc MolBiol

Scientist: Molecular Biology

Evolutionary Genomics, Inc. (<http://www.evolgen.com>), a biotechnology/genomics company based in Longmont, Colorado, is seeking a skilled molecular biologist at the Scientist or Senior Scientist level. Candidate will join a multi-functional team working in both plant and human biology applications.

The position requires a wide variety of molecular and cell biology skills, including vector design and construction, transformation, transgenic analysis, protein expression and protein biochemistry.

Candidates must have strong analytical and communication skills as well as a demonstrated ability to work in a team setting. Candidate should have an MS degree in molecular biology. Experience in industry is absolutely required.

Send CV to:

Dr. Walter Messier at wmessier@evolgen.com

ImperialCollege London PartTime ResAssist

Research Assistant

Imperial College London

Job details: This is a 50% part-time position for 30 months. You must have a BSc (or equivalent) in biological sciences and have experience of working in a laboratory. An MSc or MRes in ecology, evolution, plants or fungi is desirable. Experience in DNA extraction, sequencing and editing, PCR, bioinformatics or phylogenetics would also be desirable. Experience of working in a team, the ability to develop and apply new concepts and have a creative approach to problem-solving are essential. You must have good interpersonal and organisational skills, excellent verbal and written communication skills and the ability to pay close attention to details. You must also be able to organise your work with minimal supervision and prioritise it in response to deadlines. You will

be based at the Royal Botanic Gardens, Kew. For informal queries please contact Dr Martin Bidartondo by email at: m.bidartondo@imperial.ac.uk. Closing date: 3 April 2016. More information at <http://www.jobs.ac.uk/job/ANE943/-research-assistant/> “m.bidartondo@imperial.ac.uk” <m.bidartondo@imperial.ac.uk>

Morton Arboretum Illinois ResAssist

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

Classification: Full-time, Non-exempt

Department: Science and Conservation

General Summary: The Morton Arboretum is seeking a full-time Research Assistant to be supervised by the Forest Ecologist and Tree Conservation Biologist. These research programs combine elements of field ecology, forestry, natural history, genetics, modeling, mathematical biology, and management and study of living collections (e.g. arboreta). Research assistants are closely involved in all aspects of research: s/he will participate in planning and executing laboratory and field work, utilize a variety of scientific instruments, assist with lab management, train and oversee volunteers and work in close collaboration with colleagues, attend and contribute to lab group discussions, organize data and perform analysis, discuss results, and help prepare manuscripts. The Research Assistant will also organize and order lab supplies. There is opportunity to collaborate on papers, present research at national meetings, and work with collaborators on international projects. Eventually, the individual may be responsible for developing and executing new research projects. The ideal candidate is one who seeks professional development as a scientist and is therefore interested in reading current scientific literature and being intellectually engaged on research projects.

Qualifications: Bachelor’s degree required in Ecology, Genetics, Evolutionary Biology, Botany, Mathematical Biology, or similar biological field, and at minimum one year experience in laboratory, field, or relevant mathematical research, especially in a molecular lab and/or in field ecology; Master’s degree preferred. Must possess a valid driver’s license, which is subject to insurability and an annual Motor Vehicle Record (MVR) report. Proficiency with Microsoft Office Suite and Gmail and other Google applications beneficial.

Success Factors: Must be well organized, enthusiastic, able to work (after training) without constant supervision, able to quickly learn new skills, have very strong attention to detail and meticulous lab notebook keeping, show capacity to work both independently and collaboratively, be strongly self-motivated, communicate clearly and cooperate with supervisors and co-workers, and solve problems. The successful applicant will have a strong background including coursework and research in plant sciences, ecology, evolutionary biology, informatics and/or molecular biology with both lab and field experience. The applicant must demonstrate curiosity, enthusiasm for ecology and genetics, and an interest in developing a broad range of skills in forest biodiversity science.

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

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

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

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

Review of applications will begin immediately. The position will start as soon as possible.

To apply, visit <http://mortonarb.org/employment> The Morton Arboretum is an equal opportunity employer committed to achieving a diverse workforce.

Colleen Emrick | Human Resources Specialist The Morton Arboretum | 4100 Illinois Route 53 | Lisle, Illinois 60532 T 630-719-7997 | F 630-725-2040 | cemrick@mortonarb.org | mortonarb.org

Colleen Emrick <cemrick@mortonarb.org>

MuseumNatSci Raleigh InvertCollectionsManager

NC Museum of Natural Sciences, Collections Manager
of Invertebrates

JOB CLASS TITLE: Natural Science Curator I

POSITION NUMBER: 60034981

DEPARTMENT: Dept of Natural and Cultural Resources

DIVISION/SECTION: NC Museum of Natural Sciences,
Research and Collections RECRUITMENT RANGE:
\$35,474- \$50,000

SALARY GRADE / SALARY GRADE EQUIVALENT:
67

APPOINTMENT TYPE: Permanent Full-Time

WORK LOCATION: Raleigh, NC (Wake County)

OPENING DATE: 03/15/16 CLOSING DATE:
04/15/16 5:00 PM Eastern Time

DESCRIPTION OF WORK: Pending Reclassification Approval This position will be primarily responsible for the management and maintenance of the Museum's Non-Molluscan Invertebrate Collection and associated curatorial duties (databasing, specimen inventory and management, managing loan activity, collection expansion, etc.). This position will be responsible for coordinating, training, and supervision of volunteers and others who might work with this Collection. This position will be expected and encouraged to participate in active research projects in invertebrate biology, taxonomy, and/or ecology, leading to publication of results in peer-reviewed scientific journals and popular media outlets. The position will participate in various educational and outreach activities of the Museum, including (but not limited to): annual signature events; regular, short science presentations offered to the public; and 'behind-the-scenes' tours of the Collections facilities. This position might also be called upon by other state agencies or external organizations to provide collections information and other assistance.

KNOWLEDGE, SKILLS AND ABILITIES / COMPETENCIES: Management prefers Master's Degree and experience with management or curation of natural sciences collections, including experience with electronic relational databases.

The ideal applicant will have the following skill and abilities: * A demonstrated knowledge of invertebrate taxonomy and/or biology. * Experience with microscopy, scientific illustration, and/or other methodological skills related to working with invertebrate specimens * Strong communication skills, including professional interpersonal communications and public speaking abilities * Strong organizational skills and ability to accomplish assigned tasks in a timely manner

MINIMUM EDUCATION AND EXPERIENCE REQUIREMENTS: Minimum Education and Experience - Graduation from a four-year college or university with a degree in biology, zoology, or a science curriculum related to the area of expertise and two years of experience in specialty area: a master's degree in natural science area may be substituted for experience; or an equivalent combination of education and experience.

SUPPLEMENTAL AND CONTACT INFORMATION: The Department of Natural and Cultural Resources (DNCR) selects applicants for employment based on required education and experience and job-related knowledge, skills, and abilities without regard to race, religion, color, national origin, sex, age, disability, genetic information, political affiliation or political influence.

Please be sure to complete the application in full. See posting and application link at: http://agency.governmentjobs.com/northcarolina/-job_bulletin.cfm?JobID=3D1380909. Resumes may be uploaded with your application, but will not be accepted in lieu of a fully completed application and will not be considered for qualifying credit. "See Resume" or "See Attachment" will NOT be accepted.

Degrees must be received from appropriately accredited institutions. Transcripts, and degree evaluations may be uploaded with your application.

To obtain veterans preference, you must scan and upload a copy of your DD-214 or discharge orders.

Technical issues submitting your application, please call the NeoGov Help Line at 855-524-5627.

Applicants requesting and receiving an accommodation under the Americans with Disabilities Act (ADA) are eligible to submit paper applications via mail or by fax. Please call the human resources office for assistance.

If multiple applications are submitted to an individual posting, only the most recent application received prior to the closing date will be accepted. Applications must be submitted by 5:00 PM on the closing date.

Due to the volume of applications received, we are unable to provide information regarding the status of your application over the phone. To check the status of your

application, please log in to your account. Upon the closing date, applications are “Under Review” and will be screened by Human Resources for the qualified applicants. The hiring process may take an average of 6 - 8 weeks.

It is the policy of the State of North Carolina and the N.C. Department of Natural and Cultural Resources that all employees provide proof of employment eligibility (immigration and naturalization) on the first

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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>

NordU Norway EvolutionFishDomestication

ERC-LINKED POSITIONS NORD UNIVERSITY NORWAY

A five-year researcher position (ref. 30065360), a three-year postdoctoral position (ref. 30065361) and a three-year PhD fellowship (ref. 30065360) in epigenetics of fish domestication are available at the Faculty of Biosciences and Aquaculture (FBA), Nord University (Bodø, Norway).

FBA invites applications from outstanding candidates for the above positions within the project Innovative Epigenetic Markers for Fish Domestication (EPIFISH), which has been recently funded by the EU H2020 excellence programme ERC consolidator grant. The project leader, Professor Jorge Fernandes is affiliated with the Strategic research group marine genomics.

About EPIFISH Domestication is a fascinating and very complex example of evolution in action, involving a combination of random genetic drift, artificial selection for desirable traits and adaptive selection to new environmental conditions. EPIFISH is a timely project that will address fish domestication at its research frontier using a multidisciplinary approach combining evolutionary biology, functional genomics, epigenetics and aquaculture. The rapid pace of substantial phenotypic changes during adaptation to new environmental conditions in fish undergoing domestication raises the hypothesis that epigenetic mechanisms are involved in this process. Thus, the overarching aim of EPIFISH is to ascertain the role of epigenetics in fish domestication using the Nile tilapia

(*Oreochromis niloticus*) as a commercially important model species.

Additional information about the positions, including qualifications, requirements, salary and how to apply can be found at <http://www.nord.no/en/about/jobs>. Contact persons Information about the project: Prof. Jorge Fernandes (e-mail: jorge.m.fernandes@nord.no; telephone +47 75 51 77 36). Administrative queries: Ms Irene Stork Wisth (e-mail: irene.s.wisth@nord.no; telephone +47 75 51 74 42).

DEADLINE FOR APPLICATIONS: MONDAY, 14 MARCH 2016.

Jorge Manuel De Oliveira Fernandes
<jorge.m.fernandes@nord.no>

NorthCarolinaMuseumNatSci InvertCollections

NC Museum of Natural Sciences, Collections Manager of Invertebrates

JOB CLASS TITLE: Natural Science Curator I

POSITION NUMBER: 60034981

DEPARTMENT: Dept of Natural and Cultural Resources

DIVISION/SECTION: NC Museum of Natural Sciences, Research and Collections

RECRUITMENT RANGE: \$35,474- \$50,000

SALARY GRADE / SALARY GRADE EQUIVALENT: 67

APPOINTMENT TYPE: Permanent Full-Time

WORK LOCATION: Raleigh, NC (Wake County)

OPENING DATE: 03/15/16 CLOSING DATE: 04/15/16 5:00 PM Eastern Time

DESCRIPTION OF WORK:

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to participate in active research projects in invertebrate biology, taxonomy, and/or ecology, leading to publication of results in peer-reviewed scientific journals and popular media outlets. The position will participate in various educational and outreach activities of the Museum, including (but not limited to): annual signature events; regular, short science presentations offered to the public; and 'behind-the-scenes' tours of the Collections facilities. This position might also be called upon by other state agencies or external organizations to provide collections information and other assistance.

KNOWLEDGE, SKILLS AND ABILITIES / COMPETENCIES:

Management prefers Master's Degree and experience with management or curation of natural sciences collections, including experience with electronic relational databases.

The ideal applicant will have the following skill and abilities:

* A demonstrated knowledge of invertebrate taxonomy and/or biology. * Experience with microscopy, scientific illustration, and/or other methodological skills related to working with invertebrate specimens * Strong communication skills, including professional interpersonal communications and public speaking abilities * Strong organizational skills and ability to accomplish assigned tasks in a timely manner

MINIMUM EDUCATION AND EXPERIENCE REQUIREMENTS:

Minimum Education and Experience - Graduation from a four-year college or university with a degree in biology, zoology, or a science curriculum related to the area of expertise and two years of experience in specialty area: a master's degree in natural science area may be substituted for experience; or an equivalent combination of education and experience.

SUPPLEMENTAL AND CONTACT INFORMATION:

The Department of Natural and Cultural Resources (DNCR) selects applicants for employment based on required education and experience and job-related knowledge, skills, and abilities without regard to race, religion, color, national origin, sex, age, disability, genetic information, political affiliation or political influence.

Please be sure to complete the application in full. See posting and application link at: http://agency.governmentjobs.com/northcarolina/-job_bulletin.cfm?JobID=3D1380909 .Resumes may be uploaded with your application, but will not be accepted in lieu of a fully completed application and will not be considered for qualifying credit. "See

Resume" or "See Attachment" will NOT be accepted.

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Applicants requesting and receiving an accommodation under the Americans with Disabilities Act (ADA) are eligible to submit paper applications via mail or by fax. Please call the human resources office for assistance.

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SpelmanCollege Atlanta ResTech MicrobeEvolution

Applications are invited for a full-time research technician in the Tekle lab in the Biology Department at Spelman College Atlanta, GA. General research areas in the laboratory include eukaryotic microbial evolution and behavior with emphasis in amoeboid microorganisms. The technician is expected to carry out isolation, culturing and maintaining of microorganisms, molecular and behavior studies. Duties will include: DNA/RNA extraction and purification, PCR and RT-PCR, NGS as

well as light and fluorescence microscopy; supervising undergraduate researchers; general lab maintenance.

The candidate should have a Bachelor's degree in biology, molecular biology, biochemistry, bioinformatics or a related discipline and 1-3 years of relevant research experience or equivalent combination of experience, training and/or education is required. The ideal candidate will have experience with basic molecular techniques (DNA extraction, PCR), limited field experience, good organizational skills and attention to detail, and an ability to work well with and supervise undergraduate students. Previous experience working with microorganisms and basic programming (bioinformatics) skills are desirable.

This is a full-time, one-year position with the possibility of two additional years subject to performance review. Salary is commensurate with experience and includes benefits.

Please email a letter of interest, CV, and names of and contact information for 2 references to ytekle@spelman.edu. For more information on the lab: <http://faculty.spelman.edu/yonastekle/>. Please feel free to email me with questions at the above email address.

Yonas Tekle Assistant Professor Department of Biology Spelman College 350 Spelman Lane SW Atlanta, GA 30314-4399 Office: 404-270-5779

Yonas Isaak Tekle <yonastekle@gmail.com>

StateUNY Oswego 1yr TeachingEvolGenetics

The Department of Biological Sciences at the State University of New York at Oswego invites applications for a one year Visiting Assistant Professor position.

Description of Responsibilities: Will teach a 160+ seat genetics lecture course and genetics laboratory sections in the fall semester. Additional courses could include general education offerings or courses within the applicant's own expertise during the spring semester. This position is a one year sabbatical replacement.

In addition, this position will be expected to display a demonstrated potential for excellence in teaching and scholarship, commitment to undergraduate and/or graduate education, and possess communication and interpersonal skills sufficient to work effectively with an increasingly diverse array of students and colleagues.

Requirements: Required Qualifications: Ph.D. is re-

quired Preferred Qualifications: Prior teaching experience.

Application Instructions: Submit a letter of application addressing qualifications, a copy of unofficial transcripts, curriculum vitae, and contact information for three professional references electronically at: <https://oswego.interviewexchange.com/jobofferdetails.jsp?JOBID=3D69746> Review Date: Review of applications will begin April 15 and will continue until the position is filled.

If you have any questions about the position, please call or e-mail:

Sofia T. Windstam, Search Committee Chair

315 312 3043

sofia.windstam@oswego.edu

Please indicate "VAP Genetics search" in subject line if e-mailing

Founded in 1861, SUNY Oswego is a public comprehensive college located in Central New York on the beautiful shores of Lake Ontario, 45 minutes from Syracuse. Named one of "Top Up-and-Coming Schools" in U.S. News "America's Best Colleges" in 2010, a Kiplinger's "Best College Value" for 2015, and a "Best Northeastern College" by Princeton Review every year since the first edition in 2003, Oswego offers its 8000 undergraduate and graduate students preminent academic programs in the arts and sciences, business, communications, and teacher education. The College's success is built on providing students outstanding educational experiences with attention to a liberal arts and sciences foundation, practical applications, interdisciplinary approaches, independent scholarly and creative work, and skills for living in multicultural and global communities. The emphasis on faculty-mentored student research and creative projects is evidenced by Quest, a daylong symposium spotlighting original student research; a stipend program for students engaged in research and creative work; and the Global Laboratory, a STEM-based research abroad program at top-ranked universities around the world. SUNY Oswego is an unusually collegial and vibrant community and is in a time of wonderful opportunities with extensive facilities construction and renovation, a forward-looking strategic plan, and expanded outreach to regional, national, and international communities.

SUNY Oswego is committed to enhancing its diversity. SUNY Oswego is an Affirmative Action/Equal Opportunity Employer and is actively engaged in recruiting, supporting, and fostering a diverse community of outstanding faculty, staff and students. We encourage applications from qualified applicants regardless

of age, race, color, gender, creed, nationality, marital status, sexual orientation, gender identity or disability or protected veteran status. Click here for our full non-discrimination policy. In accordance with USCIS regulations, successful applicants must be legally able to work in the United States per the Immigration Reform and Control Act of 1986.

Requests for reasonable accommodations of a disability during the application and/or interview process should be made to the Human Resources Office by calling 315-312-2230 or emailing hr@oswego.edu.

Christopher Chandler <christopher.chandler@oswego.edu>

SUNY Oswego LabTech Evolutionary Genomics

Applications are invited for a full time lab technician in the Chandler lab in the Department of Biological Sciences at the State University of New York at Oswego. The technician will join an NSF-funded project looking at the evolution of sex chromosomes and sex chromosome dosage compensation in terrestrial isopod crustaceans. Duties will include maintenance of a laboratory population of terrestrial isopods, molecular genetic analyses (e.g., DNA/RNA isolation, PCR, gel electrophoresis), occasional field work with local isopod populations, data entry and analysis, ordering supplies, and attending group lab meetings. The technician will also be expected to help train and work with undergraduate students involved in this project.

Required qualifications: - Bachelor's degree in biology, zoology, bioinformatics, or a related field - Excellent communication and organizational skills

Preferred qualifications: - Experience with basic molecular techniques (e.g., DNA/RNA isolation, PCR), and/or bioinformatics tools (e.g., Unix command line, genome/transcriptome assembly, variant calling) is desirable

This is a one-year position with renewal possibility for two additional years contingent on satisfactory progress.

To apply: Please submit a letter of application addressing qualifications, CV/résumé, and names and contact information for two references electronically at:

<https://oswego.interviewexchange.com/-jobofferdetails.jsp?JOBID=3D69601> Review of applications will begin April 15, 2016.

Please direct additional questions to Christopher Chandler at christopher.chandler@oswego.edu.

SUNY Oswego/The Research Foundation is committed to enhancing its diversity and is an Affirmative Action/Equal Opportunity Employer actively engaged in recruiting, supporting, and fostering a diverse community of outstanding faculty, staff, and students. We encourage applications from qualified applicants regardless of age, race, color, gender, creed, nationality, marital status, sexual orientation, gender identity or disability or protected veteran status. Requests for reasonable accommodations of a disability during the application and/or interview process should be made to Christopher Chandler, 315-312-2774 or christopher.chandler@oswego.edu.

"christopher.chandler@oswego.edu"
<christopher.chandler@oswego.edu>

UBern Switzerland LabTech Speciation

The Division of Evolutionary Ecology in the Institute of Ecology and Evolution at the University of Bern is focused on identifying the genetic and molecular mechanisms that underlie evolutionary processes. We use the threespine stickleback (*Gasterosteus aculeatus*) fish as a model system to identify genetic and genomic mechanisms that underlie phenotypes that contribute to adaptation and speciation. Our studies utilize a combination of high throughput molecular and cytogenetic techniques, animal work in the laboratory, and field-work.

We offer the position of a Technician, 100 %

Responsibilities In addition to overseeing our stickleback fish facility, the technician will assume responsibility for independent work on research projects, assist in the design of experiments, and in troubleshooting methodological problems. This position will be for 1 year, with the possibility of extension for 1 year given satisfactory performance.

Requirements The ideal candidate will possess the following minimal qualifications: - Bachelor's degree in Biology or equivalent qualifications - Several years of stickleback husbandry experience - Ability to perform standard molecular procedures (DNA preparation, PCR, genotyping and sequencing) in a high throughput manner - Experience in molecular cytogenetic methods - Experience with library preparation for next-generation

sequencing - Computing skills (Microsoft office, R) - Fluency in English (written and spoken) - Ability to work independently

The applicant should be extremely organized, work well with others, have a willingness to learn, and be able to participate at many levels in the laboratory.

The position will be available from 1 August 2016.

Please apply by email (cpeichel@fhcrc.org) with a cover letter and curriculum vitae by 15 April 2016

cpeichel@fhcrc.org

UCalgary InvertebrateSystematics

The University of Calgary has an opening for a tenure-track Instructor in Invertebrate Zoology, with primary teaching responsibility in a course in invertebrate systematics and diversity.

The ad text is below and will appear in the CAUT Bulletin and University Affairs:

The Department of Biological Sciences, Faculty of Science, at the University of Calgary invites applications for a full-time, tenure-track, Instructor in Invertebrate Biology. The primary activity for faculty members in the Instructor-stream is in teaching and learning, especially in undergraduate programs. Scholarship (pedagogical and discipline-specific) and service are also expected, but form smaller components of the position. We seek a broadly trained individual familiar with systematics who can teach both lab-based and field-based courses to enrich our undergraduate programs and complement existing strengths in animal physiology, development, comparative anatomy and paleobiology. Preference will be given to candidates with strengths in aquatic invertebrate biology.

The successful candidate will teach a range of invertebrate zoology courses, including courses integrating invertebrate systematics, diversity, function, behaviour and ecology. There will also be the possibility of teaching advanced topics in invertebrate zoology at the senior undergraduate level and supervising undergraduate research projects. Responsibilities also include participation in pedagogical, course, and program development.

Applicants must have a Ph.D. in Zoology. Post-doctoral experience will be an asset. The successful candidate will have a strong record of teaching experience and possess a broad knowledge and interest in biological educa-

tion pedagogy. Candidates must demonstrate a strong commitment to teaching and learning as evidenced by established successes and use of contemporary approaches to teaching, and a desire to support student learning inside and outside of the classroom.

Application deadline is April 30, 2016. Short-listed candidates will be contacted for an interview.

The University of Calgary believes that a respectful workplace, equal opportunity and building a diverse workforce contribute to the richness of the environment for teaching, learning and research, and provide faculty, staff, students and the public with a university that reflects the society it serves. All qualified candidates are encouraged to apply; however Canadians and permanent residents will be given priority. In this connection, at the time of your application, please answer the following questions: Are you a Canadian citizen or a permanent resident of Canada? (Yes/No)

How to apply: Applicants should submit a curriculum vitae, statement of teaching interests, evidence of teaching effectiveness, and the names and contact information of three references to:

Dr. Robert Barclay, Head, Department of Biological Sciences University of Calgary, 2500 University Drive Calgary, AB T2N 1N4 Fax: (403) 289-9311 Email: head-bio@ucalgary.ca

The Department of Biology at the University is committed to student engagement and creating an innovative, student-centered learning environment. Information about the Department and its programs can be found at <http://bio.ucalgary.ca>. The University of Calgary is home to the recently announced Taylor Institute of Teaching and Learning. The Taylor Institute is designed to transform teaching at the University of Calgary and place us at the forefront of pedagogical advance and the integration of teaching and research across North America. More information about the Taylor Institute and its programs can be found at <http://www.ucalgary.ca/-taylorinstitute/>. About the University of Calgary The University of Calgary is a leading Canadian university located in the nation's most enterprising city. The university has a clear strategic direction to become one of Canada's top five research universities by 2016, where innovative teaching and ground-breaking research go hand in hand, and where we fully engage the communities we both serve and lead. The strategy is called Eyes High, inspired by our Gaelic motto, which translates to 'I will lift up my eyes'.

To succeed as one of Canada's top universities, where new ideas are created, tested and applied through first-class teaching and research, the University of Calgary

needs more of the best minds in our classrooms and labs. We're increasing our scholarly capacity by investing in people who want to change the world, bringing the best and brightest to Calgary to form a global intellectual hub and achieve advances that matter to everyone.

To view a listing of all available academic opportunities and to find out more about what the University of Calgary has to offer, please visit our Academic Careers website.

About Calgary, Alberta Calgary, Canada's fastest growing major city, offers a vibrant,

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

UCalifornia ConservationGenomics ProgramManager

Under the University of California, Presidents Office Catalyst program, a three-year award has been made to establish a conservation genomics network among 6 UC campuses. The goal of the program is to support research, develop new analytical tools, educate graduate and post-graduate students via workshops, and interface with conservation managers and planners as well as the general public. We will translate our results into management recommendations for California species of conservation concern, ranging from mountain lions to abalone, sea otters to ochre seastars, and side-blotched lizards to valley oaks.

We are seeking a Program Manager who will work with the PIs and project participants to initiate and manage proposal goals (see <https://uconservergenomics.eeb.ucla.edu/>) and who will direct their own research program. The position will be based at University of California, Los Angeles, and is available immediately (applications due by April 8th). A PhD with experience in empirical, analytical or bioinformatic research as well as some management experience is preferred. Please submit your application, including a CV and a 1-2 page cover letter discussing qualifications for the position, on the project website (<https://uconservergenomics.eeb.ucla.edu/positions/hiring-executive-director/>)

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, age, disability, protected veteran status, or any other characteristic protected by law.

annabel.beichman@gmail.com

UCalifornia ConservationGenomics ProjectManager

UC Conservation Genomics Program Manager. The UC Conservation Genomics Consortium is seeking a program manager for a proposal funded by the UC Catalyst grant program who will work with the PIs and project participants to initiate and manage proposal goals (see <https://uconservergenomics.eeb.ucla.edu/>). The position will be based at University of California, Los Angeles, receive a starting salary of 3,300 per year and will have a separate travel and research budget. The position is available immediately and we aim to hire by the end of April. A PhD with empirical, analytical or bioinformatic training in molecular genetics is preferred with management experience required. Under the supervision from the Project Director, the Program Manager will oversee the President's Office Catalyst program. The Program Manager will assess progress, identify problems, provide standardize protocols, and critically, oversee the graduate, post-graduate and public outreach components of the project. The incumbent will oversee the production of 3-4 workshops per year, arrange speakers and graduate and post-graduate staffed labs associated with the workshops. The Program Manager will organize and assist in the development of environmental DNA sampling kits and their distribution to 500-1000 field researchers, students and public and direct efforts to assure the kits timely return. The Program Manager will organize presentations to the public on the use of kits and presentation of results based on them. The Program Manager will organize meetings with stakeholders, NGOs, and managers in State and Federal organizations involved in conservation. The Program Manager will be in charge of developing, enhancing and curating a multi-level website which will have public blogs and private sections for researchers and sections for uploading of data and protocols. Lastly, the incumbent will be require extensive travel among 5 collaborating campuses and oversee the successful completion of project goals.

Please submit your application, including a CV and a 1-2 page cover letter discussing qualifications for the position, on the project website < <https://uconservationgenomics.eeb.ucla.edu/positions/hiring-executive-director/> >.

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, age, disability, protected veteran status, or any other characteristic protected by law.

annabel.beichman@gmail.com

UCalifornia ConservationGenomics ProjectManager Correction

Apologies the text formatting of evoldir deleted some important information from within the below posting. Particularly, the starting salary is \$ 53,300 (fifty-three thousand, three hundred dollars) per year. Reposted below:

UC Conservation Genomics Program Manager. The UC Conservation Genomics Consortium is seeking a program manager for a proposal funded by the UC Catalyst grant program who will work with the PIs and project participants to initiate and manage proposal goals (see <https://uconservationgenomics.eeb.ucla.edu/>). The position will be based at University of California, Los Angeles, receive a starting salary of \$ 53,300 per year and will have a separate travel and research budget. The position is available immediately and we aim to hire by the end of April. A PhD with empirical, analytical or bioinformatic training in molecular genetics is preferred with management experience required. Under the supervision from the Project Director, the Program Manager will oversee the President's Office Catalyst program. The Program Manager will assess progress, identify problems, provide standardize protocols, and critically, oversee the graduate, post-graduate and public outreach components of the project. The incumbent will oversee the production of 3-4 workshops per year, arrange speakers and graduate and post-graduate staffed labs associated with the workshops. The Program Manager will organize and assist in the development of environmental DNA sampling kits and their distribution to 500-1000 field researchers, students and public and direct efforts to assure the kits timely return. The Program Manager

will organize presentations to the public on the use of kits and presentation of results based on them. The Program Manager will organize meetings with stakeholders, NGOs, and managers in State and Federal organizations involved in conservation. The Program Manager will be in charge of developing, enhancing and curating a multi-level website which will have public blogs and private sections for researchers and sections for uploading of data and protocols. Lastly, the incumbent will be require extensive travel among 5 collaborating campuses and oversee the successful completion of project goals.

Please submit your application, including a CV and a 1-2 page cover letter discussing qualifications for the position, on the project website.

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, age, disability, protected veteran status, or any other characteristic protected by law.

annabel.beichman@gmail.com

UCalifornia LosAngeles LabTech ConservationGenomics

Title: UCLA Shaffer Lab Technician/Manager

Body:

The Shaffer Lab at UCLA seeks a full-time Lab Assistant to join our research group. We are a group working with the evolutionary and conservation genomics of reptiles and amphibians, with a strong emphasis on California problems and their solutions. We seek an individual with some molecular genomics experience, a passion for conservation and evolutionary genetics, and the ability to learn new skills, contribute to group projects, and organize and manage the daily flow of work in the lab. The position is open immediately.

The primary duties of the position include producing next-generation and more traditional genetic data for research projects, general maintenance of lab space, organization of tissue samples and their associated database, and helping with the paperwork and permits necessary for herpetological conservation research. The individual should be excited about, and able to learn new techniques quickly. The individual will work closely with lab members to organize and manage research projects.

Some familiarity with bioinformatics, or an interest in learning these skills, is also desirable.

Applications must be submitted through <https://hr.mycareer.ucla.edu>. Job Requisition number is #23440, or simply go to hr.mycareer.ucla.edu/applicants/Central?quickFindg528.

Review of applications will begin immediately. If you have any questions, feel free to contact Brad Shaffer (brad.shaffer@ucla.edu) or Sarah Wenner (sarahwenner2@gmail.com). Los Angeles is a vibrant, diverse, and stimulating city, and the lab works closely with the Department of Ecology and Evolutionary Biology (<https://www.eeb.ucla.edu>) and the UCLA La Kretz Center for California Conservation Science (<http://www.environment.ucla.edu/lakretz/>).

Mario Colon I Administrative Assistant I UCLA La Kretz Center for California Conservation Science 818-519-7740 I mario.colon@ucla.edu I <http://www.environment.ucla.edu/lakretz/> Mario Colon <mario.colon@ucla.edu>

UCalifornia SantaBarbara KenyaProjectManager

The Young lab at the University of California, Santa Barbara, is seeking applicants for a project manager position to be based in Kenya from Sep/Oct 2016 - Sep/Oct 2017 (exact dates are flexible). The position will involve various administrative and field work-oriented tasks related to our projects studying the role of wildlife decline on disease in the East African tropical savannah system (<https://labs.eemb.ucsb.edu/young/hillary/>). Our current project investigates the role of watering holes in concentrating parasites and increasing disease risk through animal aggregations at water.

Our research sites are based at Mpala Research Centre, located in Laikipia County (www.mpala.org), where a variety of institutions from around the world conduct research and other educational activities. A lively community of scientists and students is present year-round. The project manager would have a private bedroom, access to a shared bathroom, and three meals per day provided. Internet access and laundry are also included, in addition to a \$250 per month stipend for additional expenses. Mpala is located relatively close to the town of Nanyuki (about a 50 minute drive), where additional supplies are available.

The project manager is expected to assist in data collection in the field, data entry, and various administrative and logistical tasks (such as managing additional field assistants, facilitating permit application completion, and completing necessary paperwork in country). The field schedule will be fairly demanding for approximately four one-month periods during the year. During these sampling periods, the project manager will be expected to be spending the majority of the working day in the field for 5-6 days per week (1/2 Saturdays, off on Sundays). Depending on the season, the weather can be quite hot and dry (90+ degrees F), and a typical sampling day will require 5+ miles of walking. Additionally, project managers must be sensible and vigilant, being comfortable working in locations where dangerous animals may be present (snakes, elephants, Cape buffalo). Project managers acknowledge that they are required to be accompanied by a Kenyan field assistant at all times when working in the field. Major holidays and additional time off for personal travel will also be granted exact time periods are negotiable based on field schedules and personal requirements.

Qualifications:

1. Education: Undergraduate degree in Biology, Environmental Science, or similar, or related experience.
2. Experience: Previous field research experience, previous international travel, some previous parasitological experience is preferable but not required.
3. Other: Able to comfortably walk 5+ miles per day in hot conditions, perform repetitive tasks with attention to detail, ability to take detailed notes and record ecological information.
4. Personal: Good interpersonal skills, ability to live in close quarters with other researchers, critical thinking and problem solving skills, data entry skills, and ability to provide good written and verbal communication.

Compensation:

Travel to and from Mpala Research Centre (flights, taxis), a private room at Mpala with shared bathroom, 3 meals per day, internet access, laundry, plus a \$250 monthly stipend.

Interested applicants should submit the following:

1. Resume or CV that includes previous work experiences and related coursework.
2. A cover letter describing in detail previous research experience, previous international travel, personal research interests, future academic/professional goals, and any other information relevant to the job description.
3. Contact information for two academic or professional

references.

Please send all application materials to Georgia Titcomb and Hillary Young (georgiatitcomb@gmail.com & hillary.young@lifesci.ucsb.edu) by April 9th, 2016. We encourage scientists of all backgrounds and diversities to apply!

georgiatitcomb@googlemail.com

UCalifornia SantaBarbara TeachingEvolution

Lecturer with Potential Security of Employment - Biological Sciences

The Department of Ecology, Evolution, and Marine Biology and the Department of Molecular, Cellular, and Developmental Biology at the University of California Santa Barbara jointly invite applications for a position of Lecturer with Potential Security of Employment (PSOE). The successful candidate will assume responsibility for courses in Introductory Biology for majors and non-majors, and a course in the candidate's area of expertise. Courses will cover topics in biochemistry, cell biology, development, genetics, animal and plant physiology, ecology and evolution. Applicants should have a record of teaching excellence with experience and expertise in the appropriate disciplines. The appointment is for the academic year with the option of additional summer quarter teaching. Salary will be commensurate with qualifications. This position requires a PhD in biology or a closely related field at the time of appointment.

Applicants should submit a cover letter, a curriculum vitae, a statement of their teaching experience and interests, a statement of teaching philosophy, teaching evaluations (if available), and three to four letters of recommendation from persons with the ability to evaluate the candidate.

Submit applications electronically at: <https://recruit.ap.ucsb.edu/apply/JPF00687>. Information about the Departments can be obtained from the website: <https://www.lifesci.ucsb.edu>. The review of applications will begin March 31, 2016 and will continue until the position is filled.

The University of California is an affirmative Action / Equal Opportunity / Americans with Disabilities Act 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.

Thomas Even <tom.even@lifesci.ucsb.edu>

UEastAnglia EvolutionaryBiolEcolConservation

4 Lecturer Positions Including one specifically in the Evolutionary Biology remit, plus three others where candidates could have an Evolutionary background/focus

ATR1304 - Lecturer in Evolutionary Biology/Ecology/Conservation

Research areas include biodiversity, host-pathogen interactions, population genetics/genomics, sexual selection and conflict, social evolution and applied ecology and conservation.

ATR1302 - Lecturer in Bioinformatics

Research areas include regulatory small RNAs, developmental biology and evolution. We particularly welcome applications from investigators with experience in analysing next-generation sequencing data (transcriptome, genome or epigenome sequencing).

ATR1303 - Lecturer in Biomedicine

Research areas include cancer and cancer immunology, stem cells, developmental biology and live imaging, health and disease of the musculoskeletal and cardiovascular systems, ageing, and food and health research (including gut biology).

ATR1305 - Lecturer in Microbiology

Research areas include molecular microbiology (e.g. host-microbe interactions, environmental microbiology and bio-geochemical cycling), medical microbiology, bacterial physiology and microbial biochemistry.

More information about our Research Themes can be found at: <https://www.uea.ac.uk/biological-sciences-research/research-themes> Research Themes - UEA www.uea.ac.uk In BIO our research area is divided into four main themes: Organisms and the Environment Cells and Tissues Molecular Microbiology Plant Sciences

Applications from candidates whose research is interdisciplinary across these themes are very welcome.

All 4 positions are available from 1 August 2016 on a

full-time indefinite basis.

Closing date for all applications: 12 noon on 27 April 2016.

Further particulars and an application form are available on our website: www.uea.ac.uk/hr/vacancies/ or Tel. +44 1603 593493

Lecturer in Evolutionary Biology/Ecology/Conservation
\$B!(B Ref: ATR1304

The specific research areas for this particular post include biodiversity, host-pathogen interactions, population genetics/genomics, sexual selection and conflict, social evolution and applied ecology and conservation.

More information about our Research Themes can be found at: <https://www.uea.ac.uk/biological-sciences/research/research-themes> Applications from candidates whose research is interdisciplinary across these themes are very welcome.

This post is available from 1 August 2016 on a full-time indefinite basis.

Closing date: 12 noon on 27 April 2016.

Further particulars and an application form are available on our website: www.uea.ac.uk/hr/vacancies/ or Tel. +44 1603 593493.

The University is a Bronze Athena Swan Award holder, currently working towards Silver

David S Richardson Professor in Evolutionary Ecology and Conservation Centre for Evolution, Ecology and Conservation School of Biological Sciences, UEA, Norwich NR4 7TJ, England e-mail: david.richardson@uea.ac.uk http://biobis.bio.uea.ac.uk/biosql/fac_show.aspx?ID=3D325cid:image001.jpg@01CF9090.081618F0

UK Top 15 (14th in the Guardian University Guide 2015; 15th in the Complete University Guide 2015) UK Top 3 for Student Experience (Times Higher Education Student Experience Survey 2014) World top 1% (Times Higher Education World Rankings 2013-14) World Top 100 (Leiden Ranking 2014)

“David Richardson (BIO)”
<David.Richardson@uea.ac.uk>

UGeorgia ResTech EvolSexChromosomes

The laboratory of Michael White in the Department of Genetics at the University of Georgia is seeking applicants for a research technician to help explore the mechanisms driving the evolution of sex chromosomes in the threespine stickleback fish. The successful candidate will have the opportunity to work on a number of exciting evolutionary genomics projects using a combination of molecular and bioinformatic techniques. This position is ideal for recent biology graduates who are seeking additional research experience.

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

Qualifications: - Bachelor's degree in biology or a related field. - Experience with general molecular biology techniques (ex. PCR, DNA extraction, and running gels). - Proficiency with computers and Microsoft Excel. - Highly organized and detail-oriented. - Experience with bioinformatics.

Interested candidates should apply at https://www.uga.jobsearch.com/applicants/jsp/shared/-Welcome_css.jsp using the job posting number: 20160460.

Please include a cover letter explaining qualifications and interest in the position, a CV, and contact information for three references.

Any questions can be sent to: whitem@uga.edu.

Michael White Assistant Professor Department of Genetics University of Georgia 706-542-2464 whitem@uga.edu

UHawaii Hilo Evolution

POSITION POSTING Assistant Professor of Biology, pos. #83380

Assistant Professor (Biology), position number 83380, University of Hawai'i at Hilo, College of Arts & Sciences,

tenure-track, full-time, general funds, nine-month appointment to begin approximately August 2016, pending position clearance and availability of funding.

Duties: Teach undergraduate courses in Ecology, Evolution, and Biostatistics. Develop an independent research program in area of expertise that is supported by extramural funding; advise students; participate in departmental governance and related University and community service; participate in the Tropical Conservation Biology and Environmental Science graduate program.

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

Desirable Qualifications: Demonstrated teaching experience in undergraduate and graduate courses in areas related to Ecology, Evolution, Biostatistics, and Molecular Biology. Demonstrated record of student advising and training; a successfully funded research program in one or more areas of Ecology and Evolution, and the ability to develop an active, externally funded research program in Hawai'i or the Pacific region that supports graduate students and provides mentorship and training for undergraduates.

Salary Information: Commensurate with qualifications and experience.

To Apply: Submit a cover letter indicating the position title and position number and how you satisfy the minimum and desirable qualifications, a curriculum vitae, academic transcripts, and statements of research and teaching interests. Please note that copies of transcripts are acceptable for application; however, original documents issued by a university registrar are required upon hire. Provide contact information for three (3) references. Electronic submissions are preferred. Mail Application To: Dr. Rebecca Ostertag, Biology Department, University of Hawai'i at Hilo, 200 W. K  wili St., Hilo, Hawai'i, 96720, or electronically to ostertag@hawaii.edu. Please refer to position number 83380.

Inquiries: Dr. Patrick Hart, Chair, Department of Biology, University of Hawai'i at Hilo, 200 W. K  wili St., Hilo, Hawai'i 96720; pjhart@hawaii.edu

Closing Date: March 24, 2016

UH Hilo is an EEO/AA Employer D/M/V/W.

– Elizabeth Stacy Professor of Biology and TCBES University of Hawaii Hilo 200 West Kawili Street Hilo,

HI 96720 Phone: 808-932-7715 Fax: 808-932-7295
<http://www2.hawaii.edu/~estacy/> Elizabeth Stacy
 <estacy@hawaii.edu>

UKonstanz 3 EvolutionaryBiology

At the University of Konstanz we currently seek to fill three Full Professorships in (broadly) organismal biology with an emphasis on ecology and evolution.

We are aiming, together with the nearby Max-Planck-Institute for Ornithology in Radolfzell (currently both Martin Wikelski and Iain Couzin are directors there and also Professors in the Department of Biology at the University of Konstanz), to build on the exiting strengths in Konstanz in limnology, ecology, evolution and adjacent fields.

Please click on the links for more detailed descriptions on the three professorships.

Full Professor of Organismal Interactions <http://www.uni-konstanz.de/stellenangebote/?cont=-3Dstellausw&seite=3D2016/054&id=3> *Full Professor of Aquatic Ecology* <http://www.uni-konstanz.de/stellenangebote/?cont=3Dstellausw&seite=3D2016/055&id=3> *Full Professor of Genetic Adaptation in Aquatic Systems* <http://www.uni-konstanz.de/stellenangebote/?cont=3Dstellausw&seite=3D2016/056&id=3> Please pass this information around also to your senior postdocs and in particular to female researchers as we are hoping to increase the number of female faculty in Konstanz.

Deadline for applications is the 15th of April 2016.

If you have questions, please feel free to contact any of the researchers in Konstanz who work predominantly on organismal questions.

Prof. Axel Meyer, Ph.D. Chair in Zoologie and Evolutionary Biology Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon + 49 (0)7531 88 4163 fax + 49 (0)7531 88 3018

secretary: Christiane.Weber@uni-konstanz.de tel. + 49 (0)7531 88 3069

www.evolutionsbiologie.uni-konstanz.de Axel Meyer
 <axel.meyer@uni-konstanz.de>

UMaryland EvolutionaryEcol

We will consider applications from all areas of ecology, including evolution (most suitable candidates would probably have expertise in ecological genomics, landscape genomics, etc).

Kind regards,

Matt

Terrestrial Ecologist Faculty Position

The Appalachian Laboratory (AL) of the University of Maryland Center for Environmental Science (UMCES) seeks applicants to fill an open-rank tenure-track/tenured faculty position in Terrestrial Ecology. We invite applications from individuals with research interests in areas of ecology and closely aligned disciplines that complement AL's existing research strengths in landscape ecology (including landscape genomics and ecological genomics), ecohydrology, biogeochemistry, and other spatial analysis of ecosystem processes. Preference will be given to candidates who demonstrate breadth of experience and vision for interdisciplinary, collaborative research that integrates across spatio-temporal scales and that improves understanding of how ecosystems are affected by current and emerging global change processes. If a successful applicant has also demonstrated outstanding experience in the theory and practice of restoration of ecosystem services in human-impacted watersheds at local and regional scales, this position may be considered for a new UMCES endowed chair in Sustainable Ecosystem Restoration.

The UMCES mission includes advancing basic and applied research, promoting graduate-level education, conducting science outreach and application, and providing scientific expertise for regional environmental policies on topics such as air, land, water, and wildlife management/conservation. UMCES' research domains encompass "genes-to-ecosystems" and "mountains-to-the-sea" in the Chesapeake Bay watershed and beyond. The successful candidate will be expected to mentor graduate students and carry a modest graduate-level teaching load. The AL is located in Frostburg, MD, a small college town (home to Frostburg State University) in the heart of the central Appalachian Mountains, with excellent recreational and cultural activities. The AL offers strong administrative support and excellent research, computing, and teaching facilities, including isotopic,

molecular, plant, soil, and water analysis laboratories, growth chambers, and a greenhouse.

Applicants should send the following electronically: (1) a curriculum vitae; (2) statement of research interests and a brief discussion of how their research aligns with the job description and would complement ongoing research at AL; (3) statement on experience with and approach to graduate-level teaching and mentorship; (4) up to five selected reprints and preprints; and (5) names of four references (including title, mailing address, telephone, and e-mail address) to PIsearch@al.umces.edu. Review of applications will begin on April 25, and will continue until the position is filled. Inquiries may be addressed to the AL Director, Dr. Eric A. Davidson: edavidson@al.umces.edu or Search Committee Chair, Dr. Matt Fitzpatrick: mfitzpatrick@al.umces.edu. UMCES is an equal opportunity employer. Women, minorities, individuals with disabilities and veterans are encouraged to apply.

Matt Fitzpatrick Appalachian Lab University of Maryland Center for Environmental Science website scholar profile

Matt Fitzpatrick <mfitzpatrick@al.umces.edu>

UMinnesota Director MuseumNatHist

The University of Minnesota has an exciting opportunity for an Executive Director who will oversee the Bell Museum of Natural History and Planetarium's (BMNHP) mission through its personnel, research/programs and facilities. The BMNHP mission is to ignite curiosity and wonder, explore our connections to nature and the universe, and create a better future for our evolving world. Specifically, the Executive Director will:

Be a visible leader at the University, local, regional, and national level who will represent the BMNHP and build support for the institution;

Advance innovative educational programs and visitor experiences that deepen science literacy and serve the educational needs of a diverse, urban community;

Engage in fundraising efforts and events to develop major donor support;

Ensure strong, evidence-based operations that are efficient and fiscally responsible;

Create a dynamic social gathering space for life-long

learning and informed discussion of scientific and environmental issues;

Oversee and facilitate the museum's curatorial mission.

A new, state-of-the-art museum facility with improved exhibits space, a versatile 120-seat planetarium/digital theater and expanded educational areas is scheduled to open in St. Paul on the University of Minnesota campus in 2018. This new, \$64M facility will showcase University of Minnesota research, scholarship and education in natural science. The Museum's exhibits and public programming will foster scientific literacy for all ages and will serve as a vital interface between the University and the larger community.

For more information about this position and to apply go to the University of Minnesota employment website (<http://www1.umn.edu/ohr/-employment/index.html>) and search for requisition #307546.

Sharon Jansa Associate Professor, Ecology, Evolution, and Behavior Curator of Mammals, Bell Museum of Natural History University of Minnesota 140 Gortner Laboratory 1479 Gortner Avenue St. Paul MN 55108 jansa003@umn.edu 612-624-6293

"jansa003@umn.edu" <jansa003@umn.edu>

UNewBrunswick Plant EvolutionaryEcol

Plant Evolutionary Ecology

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

agement, the Canadian Rivers Institute, the Canadian Forest Service's Atlantic Forestry Centre, and Agriculture and Agri- Foods Canada's Fredericton Research and Development Centre.

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

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

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

Applications should be sent to the search committee:

c/o Melanie Lawson

Department of Biology, UNBâPO Box 4400âFredericton, NB

E3B 5A3 Canada

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. Applicants should indicate current citizenship status.

This position is subject to budgetary approval.

The University of New Brunswick is committed to the principle of employment equity. All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority.

Jason Addison <ja.addison@gmail.com>

UOregon ResAsst MicrobialEcol

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

The Institute of Ecology and Evolution at the Univer-

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

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

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

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

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

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

– INSTITUTE OF ECOLOGY AND EVOLUTION 5289 University of Oregon, Eugene OR 97403-5289 F (541) 346-2364 <http://IE2.uoregon.edu> EO/AA/ADA institution committed to cultural diversity. The University

encourages all qualified individuals to apply, and does not discriminate on the basis of any protected status, including veteran and disability status.

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

UOslo 3yr EvolutionDefenceSystems

Researcher in aquatic evolutionary ecology

A researcher position is available at the Centre for Ecological and Evolutionary Synthesis, (CEES), Department of Biosciences.

The position is for 38 months, and with start date as soon as possible after June 1st 2016. The successful candidate will work on the project "The evolution of defence systems: theory and experiment" (EVODEF) funded by the Research Council of Norway.

Project description

The EVODEF project focuses on the evolutionary ecology of organismal defence traits. Organisms may use an impressive diversity of defences against their natural enemies. Evidence from a range of animal and plant systems suggests that the different defence traits expressed by an organism cannot be understood in isolation from each other, but must be studied as parts of complex suites of traits. The project combines theoretical models (mainly developed by the PI) with empirical experiments (conducted by the candidate) to understand the properties of such defensive systems and how they evolve under different selective conditions. Topics of interest include how defence lines are phenotypically co-expressed and coevolve, how defences against different enemies (e.g. predators or parasites) affect each other, and the role of non-genetic inheritance (e.g. maternal and epigenetic effects) in defence expression. In the theoretical part of the project we will develop mathematical models of organismal defence relevant to several empirical systems. In the experimental part of the project, we will use the inducible defences of *Daphnia* to test novel predictions from theory; the results will in turn stimulate further theory development.

The successful candidate will join our team and study the defence traits of *Daphnia* in the lab. The project provides a unique opportunity to design and run experiments that test novel theoretical ideas and inform ongoing theoretical work. The ideal candidate will make a major contribution to the planned research, but will also develop his/her own complementary lines of re-

search that reflect the candidate's own expertise and interests and that broadly fit within the project's main goals. There is growing interest in developing a research environment for *Daphnia* at the department and it is highly desirable that the candidate will take an active part in this, as well as contribute to developing future collaborative projects that build upon achieved results.

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 PhD-degree or other corresponding education equivalent to a Norwegian doctoral degree in biology or a related field. The successful candidate will be responsible for the establishment and maintenance of *Daphnia* cultures, the daily running of experiments, imaging, morphometrics, and data analysis. A proven, solid record of running lab experiments with small aquatic organisms (preferably *Daphnia*) and maintaining them in culture is required.

The ideal candidate has extensive lab experience with *Daphnia*, strong statistical and writing skills, pays careful attention to detail and theoretical context when designing experiments, and has some experience with field sampling. A background from evolutionary ecology or evolutionary biology is considered an advantage. Field sampling is planned for the summer 2016, and it is desirable that applicants are available to start by this time. A research stay abroad is planned during one section of the project.

The successful candidate will work in close collaboration with the project PI and other members of the team. We seek a highly motivated, enthusiastic person with the ability to think creatively and critically, and with the ambition to gain new insights and publish papers in leading, international journals. Applicants must show good interpersonal skills and be willing to work in close collaboration with others, as well as have the ability to work independently. Applicants should have a good publication record for the career stage.

A good command of English is required.

Salary

Position code 1109, Pay Grade: 57-63 (NOK 483 700 - 540 200 per year, depending on qualifications).

The application must include: Application letter including a statement of interest, briefly summarizing your scientific work and interests and describing how you fit the description of the person we seek CV (summarizing

education, research positions, and other qualifying activity) Copies of educational certificates and transcript of records A complete list of publications, and up to 5 peer-reviewed publications that the applicant wishes to be considered by the evaluation committee Names and contact details of 2-3 references (name, relation to candidate, e-mail

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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>

UPuertoRico EvolutionaryBiol

The Department of Biology, University of Puerto Rico, Mayagüez (UPRM, <http://biology.uprm.edu>) invites applications for a Tenure-track Position as Assistant Professor to begin July 2016. A Ph.D. degree in Biology, Evolutionary Biology, Zoology or related field is required, post-doctoral experience is preferred. Candidates with good communication skills in both English and Spanish will be preferred.

Candidates should have good teaching skills and the ability to develop undergraduate and graduate courses including, but not limited to, General Biology, Zoology, Evolution and other departmental needs, including the ability to design and develop courses in their area of expertise. Demonstrated experience with biodiversity of tropical fauna, either marine or terrestrial, is preferred. Successful candidates will be expected to teach at undergraduate and graduate level. The appointment will consist of a full-time teaching load (12 credits/semester). Benefits include health insurance, retirement plan and tuition waivers in the UPR system for immediate family members.

UPRM is a Land-Grant, Sea-Grant, and Space-Grant institution; interaction with faculty and researchers in these fields is encouraged.

The University of Puerto Rico stimulates collaboration with active faculty and students in a wide range of the Biological Sciences and Biotechnology.

HOW TO APPLY Please send Curriculum Vitae, statement of teaching interests, and three (3) letters of reference (at least one letter must attest to the candidate's teaching abilities) by April 7, 2016 via e-mail to brendam.soto@upr.edu.

For further information please contact:

Prof. Ana V. Vélez Department of Biology School of Arts and Sciences Call Box 9000, Mayagüez, PR 00681-9000 Phone (787) 832-4040 ext. 2335 Fax: (787) 834-3673 Email: ana.velez@upr.edu Authorized by the State Election Commission of Puerto Rico, Certification CEE-C-16-089 <http://home.uprm.edu/hrjobs/showjob.php?id=3D632> Dimaris Acosta Mercado <dimaris.acosta@upr.edu>

UQuebec Rimouski EvolutionaryTheory

Integrative Biology-Tier II Canada Research Chair

The Université du Québec Ã Rimouski invites applications from scholars with a strong research profile for a Tier II Research Chair (CRC) in one of the following areas : integrative biology/theoretical ecology/system biology. Possible disciplinary focus area could include global climate change, biogeography, macroecology, macrophysiology, evolutionary theory, and ecosystem functions. Preferences will be given to candidates who transcend different scales of biological organization and who have a multidisciplinary focus. The candidate will integrate a departmental team working in evolutionary physiology, animal and plant ecology, forestry, limnology, paleoecology, macroevolution, and molecular ecology. One of the three main research axis developed by the Université du Québec Ã Rimouski is northern studies. Candidates must have the potential to contribute to our understanding of northern ecosystem functions through their own research discipline.

The basic qualifications for the outline position are

- Ph.D. in Biological Sciences or equivalent
- Postdoctorate experience
- Excellent skills in bioinformatics or ecological modelling or theoretical ecology
- Outstanding publication record

The Université du Québec Ã Rimouski is a small dynamic institution (it has repeatedly been among the three best small research universities in Canada these past years) that hosts 200 B.Sc. students in biology , 100 graduate students, and 21 faculty. The working language is french.

The chosen candidate will apply for a Tier 2 Canada

Research Chair (CRC). Tier 2 Chairs are intended for exceptional emerging scholars (i.e., candidates must have been an active researcher in their field for fewer than 10 years at the time of nomination). (www.chairs-chaires.gc.ca). He or she will be appointed to a tenure-track position at the assistant or associate professor level, commensurate with qualifications provided CRC nomination. Successful candidates are expected to mount an independent, externally funded research program and to participate in teaching at the undergraduate and/or graduate level (one course per year).

All qualified candidates are encouraged to apply however Canadians and Permanent Residents will be given priority. The universit  du Qu bec Ã Rimouski is committed to diversity and equity in employment. It welcomes applications from women, native people, ethnic minorities, and visible minorities.

For additional information, please see <http://www.uqar.ca/rh/emplois/rh/professeure-regulier-en-biologie-titulaire-dune-chaire-de-recherche-du-cana/>

Starting date : June 1st 2017 (conditional to success at the CRC)

Applications should consist of a letter stating why they think they would be a good fit for the Research Chair position, a current CV, a three page research program description considering potential involvement with the Northern Studies focus of the Universit  du Qu bec Ã Rimouski.

Electronic applications should be sent to Dominique Arseneault, Departement chair of Biology, 300 all e des ursulines, Rimouski, Qc, Canada, G5L3A1, dominique_arseneault@uqar.ca no later May 20, 2016, however, applications will be reviewed as they are received.

“France_Dufresne@uqar.ca”
<France_Dufresne@uqar.ca>

UTromso AncientDNA

Researcher in ancient DNA at Troms  University Museum, UiT - The Arctic University of Norway

Application deadline: April 15th 2016

Ref.2016/2307

Troms  University Museum, UiT - The Arctic University of Norway, has a five year fixed term contract vacant as researcher. The position is on the project ECOGEN -

Ecosystem change and species persistence overtime: a genome-based approach. The project is a collaboration among Tromsø University Museum, Department of Marine and Arctic Biology, Department of Geology, and Department of Archaeology and Social Anthropology at UiT - The Arctic University of Norway, as well as University of Oslo, University of Southampton, University of York, University Joseph Fourier, Århus University, ETH Zürich, Swiss Federal Research Institute WSL, AMU - Adam Mickiewicz University, University of Bern, and University of Lausanne. In addition to the researcher, the project plan to employ 2 PhD students, 2 post docs (3 years each) and a technician for one year (to be employed later).

Application documents must be submitted electronically via the application form available on this page.

Further information about the position is available by contacting Professor Inger Greve Alsos, e-mail inger.g.alsos@uit.no, phone +47 77 6207 96.

Position project

The main goal of the project is to develop high taxonomic resolution ancient environmental DNA methods in order to evaluate how drivers of change (human, climate, biota) affect species persistence and ecosystem tipping points in arctic-alpine biomes. The subgoals are to: 1) Improve methods for full genome analyses of environmental DNA, 2) Compile palaeodata to plan a balanced design of climatic and human impacts, 3) Do full genome analyses of lake cores to obtain information on past presence and abundance of vascular plant species and key herbivores, 4) Identify biotic drivers and disentangle their effects from human land use and climate change on ecosystem resilience and ecosystem services, 5) Estimate species persistence across periods of changes and identify factors causing extinction, and 6) Provide methods and knowledge to inform species conservation and ecosystem management.

Position responsibilities

The researcher will be responsible for the daily management of the project including co-supervising the PhD students. He/she will lead the fieldwork required to core about 20 lakes in northern Fennoscandia and 20 lakes in the Alps. He/she will also take active part in the processing of the sediment cores, the molecular work and data analyses, as well as the publication and outreach of the project. One purpose of this project is to strengthen the research group, and the successful candidates should contribute to this through active collaboration with the involved researchers. The successful applicant must also be willing to engage himself/herself in the ongoing development of his/her discipline and the university as

a whole.

Position affiliation

This position is attached to the Department of Natural Sciences, which is responsible for developing and maintaining scientific collections of objects (animals, plants, fossils and minerals) as well as public outreach including Tromsø Arctic Alpine Botanical Garden. The department has a permanent staff of 16, of which 9 are in academic positions. At the moment, 3 PhD students and one post doc are connected to the department. The position is within the research group in taxonomy and biodiversity, which focuses on diversity, phylogeography and taxonomy of northern organism using molecular as well as traditional methods. The department has laboratories for modern and ancient DNA analyses, and is currently involved in two large projects: Ancient DNA of Northwest Europe and Norwegian Barcode of Life. The latter includes full genome sequencing of the entire Norwegian flora. For more information about the Department of Natural Sciences, visit this site. The successful applicant is expected to spend most of the time in Tromsø but there will also be extensive fieldwork in northern Fennoscandia and in the Alps. The candidate is also expected to have research stay abroad at one or several of the project collaborators for up to 6 months.

Qualification requirements

A Norwegian doctoral degree in the subject area concerned or a corresponding foreign doctoral degree recognised as equivalent to a Norwegian doctoral degree is required. Post doctoral research experience or research experience at this level are considered an advantage. Experience in palaeoecology is most relevant, and additional experience in vascular plant ecology, arctic-alpine biodiversity, molecular biology, and bioinformatics/biostatistics is advantageous. Experience in management, administration and supervision is advantageous. The personal suitability and teamwork skills will be emphasised.

Applicants must have a good command of English and preferably also a Scandinavian language.

The remuneration for a Researcher is in accordance with the State

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UZurich Paelogenetics

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

We are looking for a young and dynamic personality at an early stage in his/her career, flexible and willing to contribute significantly to this dynamic research area. Successful candidates will have demonstrated ability to independently conceive novel research projects and bring them to successful completion. We seek individuals with the following qualifications:

- Training in the field of biomedicine (MD and/or PhD)
 - Expertise in molecular biology and DNA sequencing; experience with analysis of ancient remains - Internationally recognized scientific track record - Interdisciplinary networking with translational research prospects - Excellent social skills; open and integrative personality - Interest for modern teaching methods
- Knowledge of the German Language is not mandatory, however to acquire some proficiency in German over time is expected. The University of Zurich is an equal opportunity employer. The Faculty of Medicine implements specific measures in the selection process to increase the proportion of women with a faculty position.

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

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

Dr. phil. Caroline Krüger Leiterin Stab Berufungen

Universität Zürich Medizinische Fakultät, Dekanat Pestalozzistrasse 3/5 CH-8091 Zürich +41 44 634 10 67 Telefon www.med.uzh.ch caroline.krueger@dekmed.uzh.ch Anwesend: Di, Do, Fr

“caroline.krueger@dekmed.uzh.ch”
<caroline.krueger@dekmed.uzh.ch>

WheatonCollege 3yr Teaching

VISITING ASSISTANT PROFESSOR - The Biology Department at Wheaton College is seeking applicants for a temporary full time Visiting Assistant Professor with the ability to teach genetics with lab, introductory biology, and additional courses as needed by the Department. Applicants with the ability to teach physiology as well as genetics will be highly competitive. This is a three year non-tenure track position with annual renewal based on performance starting 01 July 2016. We are very interested in candidates that can commit to the entire three years. Though primarily a 3/3 teaching position, modest financial support is available for engaging Wheaton undergraduates in an active research program.

The successful candidate must have a Ph.D. at the time of appointment. Applicants should submit a cover letter, CV, statement of teaching philosophy, and 3 letters of recommendation. To apply, please go to <https://jobs.wheatoncollege.edu>. The deadline for application is 08 April or until position is filled.

Wheaton is a private coeducational liberal arts college within easy commuting distance of Boston and Providence. We have 1,600 undergraduates from 39 US States and 72 countries. More than 20% of our undergraduates are U.S. students of color and 11% are international students. The Department of Biology includes 7 tenure-track professors plus 2 instructors and serves majors in Biology, Biochemistry, Bioinformatics, Environmental Science, and Neuroscience. Resources include a state-of-the-art LEED-certified science center, a new zebrafish and animal care facility, and well equipped molecular labs for teaching and research. Information about the Biology Department may be found at <http://wheatoncollege.edu/biology/>. Wheaton College is an equal opportunity/affirmative action employer and does not discriminate against any individual or group on the basis of gender, sexual orientation, gender identity or expression, age, race, color, religion, national origin, veteran status, genetic information, or disability. In a continuing effort to maintain and enrich an intellectually diverse learning environment, the Department and the College actively encourages applications from women and members of underrepresented groups.

Individuals must possess these knowledges, skills and abilities or be able to explain and demonstrate that the

individual can perform the essential functions of the job, with or without reasonable accommodation, using some other combination of skills and abilities.

S. Shawn McCafferty Associate Professor, Chair Biology
Department Wheaton College Norton, MA 02766

Ph: 508-286-5642 email: mccafferty_shawn@wheatoncollege.edu

“mccafferty_shawn@wheatoncollege.edu”

WillametteU 1yr Visiting EvolBiology

Dear Colleagues,

The Department of Biology at Willamette University welcomes applications for a non-tenure-track, visiting assistant professor position to begin August 2016. The appointment will be for one year, with potential for renewal up to three years depending on the department's teaching needs and satisfactory progress towards mutually agreed upon teaching outcomes.

We are seeking a broadly trained biologist who could teach courses in one or more of the following areas: Physiology, Evolution and Ecology, and/or Molecular Cellular Biology. Teaching ability and adaptability are more important than expertise in a particular discipline. The successful applicant will be strongly committed to excellence in both teaching and research at the undergraduate level, and will be expected to teach 6 course units a year (1.0 unit/lecture, 0.5 unit/lab). The teaching assignments will include an introductory non-majors biology course (BIOL 110 Principles of Biology), a course in the Biology Major's Core Curriculum (either Biology 244, Biology 125, or Biology 130), and upper-division courses in the candidate's area of expertise. Course sizes range from 12 to 48 students.

Applicants must have a Ph.D. in Biology or a related field; prior teaching and/or postdoctoral experience is preferred but not required. A.B.D candidates will be considered, but the Ph.D. must be completed before beginning the appointment. This position is eligible for medical and dental benefits. This position is not eligible for any Visa or employment sponsorship.

About Biology at Willamette: Our faculty view themselves as teacher-scholars; teaching in our department is inspired by Vision and Change (NSF, AAC&U, 2011) and research training is deeply imbedded in the curriculum at all levels. 60% of our graduates enter careers

in science and technology. The Department is committed to mentoring and career development for visiting faculty, and we have a strong track record of placing visiting faculty in tenure-track positions at both research-intensive and teaching-focused institutions. Shared research space is available for use by visiting faculty, and significant department funding is available to support teaching and scholarship. Visiting faculty are strongly encouraged to apply for these department funds and to seek extramural funding for research and pedagogical projects. Willamette's Office for Faculty Research and Resources has an outstanding record of helping faculty to find and win grant funding. For more information about the Department of Biology, please visit <http://www.willamette.edu/cla/biology>. Willamette University, founded in 1842, is the oldest institution of higher education in the Far West. Willamette University is a selective residential liberal arts college in the heart of the Willamette Valley. Situated in Oregon's capital city, Willamette includes the College of Liberal Arts (approximately 2000 students), and graduate programs in Law and Management. The academic year is divided into two semesters, beginning in late August and ending in May. The academic undergraduate profile is competitive. Recent students have received prestigious NSF, Watson, Truman, Fulbright, and Goldwater fellowships.

Salem is located in the center of the Willamette Valley, approximately an hour's drive from the Pacific Coast, the Cascade Mountains, and the cities of Portland and Eugene. To learn more about Willamette University, please visit <http://www.willamette.edu>. Believing that diversity contributes to academic excellence and to rich and rewarding communities, Willamette University is committed to recruiting and retaining a diverse faculty, staff and student body. We seek candidates, particularly those from historically under-represented groups, whose work furthers diversity and who bring to campus varied experiences, perspectives and backgrounds.

All applicants for this position are asked to provide a statement describing their experience working with students from diverse backgrounds. The successful applicant must have demonstrated experience working in diverse, multicultural environments.

Apply at: <https://jobs.willamette.edu/postings/1906>
The following materials will need to be uploaded as part of your online application:

1. A cover letter describing your interest in the position.
2. A copy of your CV
3. A statement of teaching philosophy
4. A research statement
5. A diversity statement describing your experience working with students from diverse backgrounds.
6. Copies of your graduate transcripts.
7. Three reference letters*

*As part of the online application, please include three references and notify them that they will be contacted electronically. The email from Human Resources will include a link where they will be able to submit a

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African Arabidopsis samples

Other: Arabidopsis thaliana collection from African sky islands

We are seeking collaborators to help collecting Arabidopsis thaliana seeds from east Africa. Preliminary studies

(part of the Arabidopsis thaliana 1001 Genomes project) have shown that lines from east-African “mountain islands” are very distinct from all others worldwide, presenting interesting opportunities for population genetics and biogeography studies. The lines were collected near “Ketumbeine Forest Reserve” (2.8738 S, 36.2 E), elevation at around 2700 m. We are seeking collaborators who are familiar with these habitats to help collecting more seeds from east Africa.

Please contact for more details: Cheng-Ruei Lee cheng-ruei@uwaterloo.ca

ruei.lee@gmi.oeaw.ac.at

Magnus Nordborg magnus.nordborg@gmi.oeaw.ac.at

“cheng-ruei.lee@gmi.oeaw.ac.at” <cheng-ruei.lee@gmi.oeaw.ac.at>

AGA2016 Awards

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

Several awards are available to cover registration for graduate students who present posters. Six abstracts will be selected for oral presentations, and these students will receive \$500 awards. Details and registration are available at the AGA website: <http://www.theaga.org>
APPLY BY Monday, APRIL 4TH

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

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

Sally Aitken University of British Columbia Jill Anderson University of Georgia Zach Cheviron University of Montana Emily Dittmar Michigan State University Suzanne Edmands University of Southern California David Field Inst. Science and Tech, Austria Lila Fishman University of Montana Jannice Friedman Syracuse University Steve Keller University of Vermont John Kelly University of Kansas Brian Langerhans North Carolina State University Curtis Lively Indiana University Robert Reed Cornell University Douglas Schemske Michigan State University Rena Schweizer UCLA Kerry Shaw Cornell University Peter Tiffin University of Minnesota

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

AGAJOH@oregonstate.edu

ASN awards regional meetings

ASN Awards for Support of Regional Meetings in Ecology, Evolution and Behavior

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

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

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

Renee Duckworth <rad3@email.arizona.edu>

ASN RegionalMeetings Awards

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

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

Renee Duckworth <rad3@email.arizona.edu>

Bangor FishEvolution Jul

Dear all, This is a reminder that the FSBI 2016 international symposium on "Fish, Genes and Genomes", to be held at Pontio Arts and Innovation Centre, Bangor, UK is now welcoming registrations (<http://www.fsbi.org.uk/conference-2016/registration-2/>) and, very importantly, EARLY-BIRD registration (Å£190 GBP vs. full rate of Å£220) and student registration (Å£110 GBP) will remain open until 29th of April, 17:00 UK time.

We therefore suggest that you visit the link and register as soon as possible.

We very much look forward to welcoming you to Bangor, in July, for what promises to be an exceptional symposium (see the programme to wet your appetite!)

You can also follow us on twitter: @FSBI2016

Kindest regards, Stefano Mariani & Gary Carvalho, on behalf of the FSBI 2016 Scientific and Organising Committees.

"S.Mariani@salford.ac.uk" <S.Mariani@salford.ac.uk>

Budget Cryobox Organization

Hi all!

I'm hoping some of you may be able to suggest a route to take with the organization of ~800 cryoboxes. Currently, these boxes are being stored across the lab that I am a part of: in cold rooms, in fridges, and in freezers. They are stacked without much order, so that when a box is removed it is put back without thought to location. This has caused issues with accounting for samples in a database. Boxes get misplaced... and end up being "lost" for several weeks before they "show up" again.

Ideally, we would like to purchase metal freezer racks to better influence how/where boxes are stacked and stored. However, this can be costly for the quantity we require. Does anyone know of a vendor that sells metal freezer racks at a reduced cost? Does any lab have unneeded racks that we could acquire? OR, can anyone think of a cheaper alternative to the metal racks? We've tried plastic bins, but have been unable to find anything with dimensions that maximize cryobox storage.

Any insight will be greatly appreciated!

Thank you, Mary Burak mary.burak@yale.edu

"mary.burak@yale.edu" <mary.burak@yale.edu>

DigitizingHerbarium Specimens Feedback

Dear colleagues,

We are planning an application to NSF's 'Advancing Digitization of Biodiversity Collections' (ADBC) program this coming October to fund the digitization of fossil and herbarium pteridophyte specimens from U.S. institutions (pteridophytes defined broadly to include ferns, lycophytes, and their extinct relatives).

In preparation for this application, we are soliciting

feedback from the community (anyone who might use pteridophyte collection data) and from potential collaborators/data providers (curators, collection managers, etc). If you fall into either category and can spare the time to answer the following questions, those responses would be very much appreciated. Please forward this email to crothfels@berkeley.edu with your responses embedded in the email, following the questions in the text, or log your responses directly using this google form: <http://goo.gl/forms/yI03afFCZW> .

Respondent information: 1. Contact name: 2. Contact email: 3. Contact institution: 4. Institution address:

From the broad community: 1) In what ways could digitization of fossil and herbarium pteridophyte specimens be of use to you?

- 2) What scope (geographic, taxonomic) would be most useful?
- 3) Would a Symbiota portal or related infrastructure be valuable?
- 4) Other suggestions or requests?

From potential data providers (curators/collection managers of U.S. institutions with paleo and neo plant collections):

Herbarium specimens 1) How many specimens in your institution are potentially available for digitization (databasing and digital imaging)?

- 2) Does your collection have particular geographic strengths? (While the project will be able to digitize only those specimens housed at U.S. institutions, the specimens themselves can potentially be from anywhere).
- 3) Who are the major collectors associated with your pteridophyte collection?
- 4) How many of your pteridophyte herbarium specimens are already databased?
- 5) How many of those databased records are skeletal (i.e., lacking most data), and how many are georeferenced?
- 6) How many are already imaged?
- 7) What digitization equipment could potentially be available for this project?
- 8) Does your institution have a webpage with this information summarized? If so please provide us with the url.

Fossil specimens 9) How many pteridophyte specimens in your institution are potentially available for digitization?

- 10) What is the preservation type, e.g., coal balls, mi-

croscopic slides/peels etc.?

- 11) Does your collection have particular geographic strengths? (While the project will be able to digitize only those specimens housed at U.S. institutions, the specimens themselves can potentially be from anywhere).
- 12) How many of your pteridophyte fossil specimens are already databased?
- 13) How many of those databased records are skeletal (i.e., lacking most data), and how many are georeferenced?
- 14) How many are already imaged?
- 15) What digitization equipment could potentially be available for this project?
- 16) Does your institution have a webpage with this information summarized? If so please provide us with the url.

Sincerely,

The Fern TCN Initiation Draft Committee: Barbara Thiers (NYBG) Brent Mishler (UC Berkeley) Carl Rothfels (UC Berkeley) Cindy Looy (UC Berkeley) Diane Erwin (UC Berkeley) Emily Sessa (U. of Florida) Ian Glasspool (Field Museum) Matt Von Konrat (Field Museum) Michael Sundue (U. of Vermont) Richard Rabeler (U. Mich)

crothfels@yahoo.ca

DiversifyEEB

Dear evoldir members,

Meg Duffy and I have created the DiversifyEEB list to aid those who wish to develop a diverse and exceptional conference or seminar series. This list contains the names, contact information and other relevant and useful information for >650 women and/or underrepresented minorities who are either post-doctoral researchers, pre- or post-tenure faculty, or research scientists.

All potential speakers have added themselves to this list and support you in your effort to create and maintain diversity in ecology and evolution. More context behind the list's creation can be found here: <https://dynamicecology.wordpress.com/2016/03/01/-diversifyeeb-introducing-a-new-resource-for-ecology-and-evolutionary-biology/> Best

Gina Baucom

TO ACCESS THE LIST The DiversifyEEB list can be downloaded from this page: <https://diversifyeeb.wordpress.com/list-2/> TO ADD YOURSELF TO LIST (Self-nominations only) Self-nominations are still being accepted via a google form (<https://diversifyeeb.wordpress.com/>). Please note that the DiversifyEEB list is for those who already have a PhD.

GRADUATE STUDENTS (Self-nominations only) A sister list has been created for graduate students (<https://diversifyeebgrads.wordpress.com/>) to help diversify young investigator seminar series.

– Regina S Baucom Assistant Professor 2059 Kraus Natural Science Building 830 North University Dept of EEB University of Michigan Ann Arbor, MI 48109 (734) 647-8490 <http://sites.lsa.umich.edu/baucom-lab>

Dominican Republic VolField Assist Woodpeckers

TWO field assistants needed for a study of ecology of colonial, cooperative breeding and foraging behavior in the Hispaniolan Woodpecker in the Dominican Republic. Field research assistants will participate in data collection during an intensive ~3.5-month field season. Assistant duties will include (but are not limited to) nest monitoring, focal behavioral observations (including nest watches and foraging records), assisting with tree-climbing, color-band reading, nest-searching, assisting with bird capture and processing, and data entry. I am currently looking for:

TWO (2nd term) half-term assistants are needed to arrive between 15 and 30 April (flexible) and remain until 30 July. Applications will be accepted until positions are filled, but preference will be given to those submitted by 26 March.

Location: Piedra Blanca (near Jarabacoa and close to Salto Jimenoa I), La Vega province, Dominican Republic

Job description: The Hispaniolan Woodpecker (*Melanerpes striatus*) nests colonially, ranging from 2 to as many as 20+ simultaneously active nests in the same tree, making it very unique among woodpeckers (only one other picid species of the more than 200 is known to nest in colonies). Additionally, the Hispaniolan Woodpecker is the most sexually size dimorphic of *Melanerpes*

woodpeckers. Since 2012, I have been color-banding and observing these woodpeckers to better understand the social organization of colonies. Fieldwork in the 2016 field season will focus on further studying social organization of colonies, attempting to answer such questions as:

1) How do nesting substrate (live vs. dead trees) and its availability influence colony size and structure?

2) What information do prospecting birds utilize to “decide” where to nest, and how does this information use influence variation in colony size?

More generally, we will collect data to help test hypotheses regarding the costs, benefits, and consequences of group living, the operation of sexual selection in cooperative societies, and the evolutionary factors driving the woodpecker’s exceptional size dimorphism. An important secondary objective of our work will be studying how parasitic fly larvae in the genus *Philornis* impact nesting success.

Field research assistants will participate in data collection during an intensive 3.5-month field season. Assistant duties will include (but are not limited to) nest monitoring, focal behavioral observations (including nest watches, dominance watches, and foraging records), assisting with tree-climbing, color-band reading, nest-searching, assisting with bird capture and processing (including metal- and color-banding), and data management and entry. All volunteers will have the opportunity to learn various tree-climbing techniques. Assistants will be trained to set up, operate, and take down a unique elevated mist-net system developed specifically for this project but with applications to other ornithological studies.

Days will be long and the work will be physically and mentally demanding, but for those seeking to gain experience in field research, you won’t be disappointed. The workweek will typically be 6 days long in humid, mosquito-filled fields and forests, involving hiking sometimes muddy, steep hills, climbing barbed-wire fences, and avoiding bulls; this work will leave you exhausted at the end of the day! Assistants will be involved in all aspects of the project, including discussions of the conceptual framework of the project.

Neotropical bird species are generally poorly known with many aspects of their natural history incomplete or wholly unknown. Hispaniola is an island with many poorly known native or endemic species that will reveal their intriguing secrets to those motivated and patient enough to look. While our work will focus primarily on Hispaniolan Woodpecker, opportunities to collect data on the islands other avian denizens may arise, and

we will exploit these opportunities when possible. Any such observations of other bird species made by field assistants may result in publications (so an added bonus of this fieldwork is the possibility of not only adding a publication to your CV but making a real contribution to our knowledge of Hispaniolan birds and Neotropical ornithology). That having been said, the woodpecker research takes priority.

Dates:

Spring/summer assistants- Start: ~15 April, End: ~30 July 2016. (~3 months)

College graduates and undergraduates are encouraged to apply. Current college students are encouraged to apply for academic credit for their work at their home institution.

Salary: Housing, drinking water, and research-related travel within the Dominican Republic will be covered.

Additionally, some funding is available to partly or fully cover airfare to/from the Dominican Republic. Assistants will have to cover their food expenses (~\$30 USD per week).

Deadline: Until positions are filled. Preference will be given to those

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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>

Draba verna samples

We are starting a research project on the ploidy and ecological characteristics of this small spring (or winter) annual, known as 'whitlow grass', *Draba verna*, or *Erophila verna* and hoping to get seed from as many sites globally as possible. If you are able to find plants and can send samples, here are some guidelines as to what we are looking for, below. PLEASE FORWARD this request to botanists and naturalists in other places, including outside of the U.S. (so instructions are included for collections made outside of the U.S.).

Please wait until the plant is finished flowering and seeds are ripe (but before dispersal, of course). Please note the exact latitude, longitude and if possible elevation of the site, with photos of the plants and location if possible.

Please include your own name, email or other contact information, and institution or address. FROM THE U.S.: If you can send whole, pressed, air dried plants, please send 12-15 whole pressed plants with seeds, or, save seeds only from the plants and send dried seeds packaged separately from each plant. FROM OUTSIDE OF THE U.S.: The USDA does not allow whole plants, so please send seeds only. Their requirements are at the bottom of this note.

If you have seeds from fewer plants, that is also useful, please send what you can collect. If you have seeds from other species of *Draba* or *Erophila*, please identify the species and send those, they may also be useful for our research project. Our contact information is: Jessica Gurevitch jessica.gurevitch@stonybrook.edu AND Jesse Hollister jesse.hollister@stonybrook.edu

Mailing address: Jessica Gurevitch, Department of Ecology and Evolution, Stony Brook University, Stony Brook NY 11794-5245 USA

Thanks very much in advance! Here is the USDA requirements for seeds sent to us from outside the U.S. (i) A typed or legibly printed seed list/invoice accompanies each shipment with the name of the collector/shipper, the botanical names (at least to genus, preferably to species level) listed alphabetically, as well as the country of origin, and country shipped from, for each taxon. Each seed packet is clearly labeled with the name of the collector/shipper, the country of origin, and the scientific name at least to the genus, and preferably to the species, level. The invoice/seed list may provide a code for each lot, which may be used on the seed packets in lieu of the full list of required information. In this case, each packet must at least include the appropriate code, which is referenced to the entry for that packet on the seed list/invoice. (ii) There are a maximum of 50 seeds of 1 taxon (taxonomic category such as genus, species, cultivar, etc.) per packet; or a maximum weight not to exceed 10 grams of seed of 1 taxon per packet; (iii) There are a maximum of 50 seed packets per shipment; (iv) The seeds are free from pesticides; (v) The seeds are securely packaged in packets or envelopes and sealed to prevent spillage [Note: we recommend that seeds are packed in resealable, clear plastic envelopes to facilitate inspection]

Jessica Gurevitch Professor Department of Ecology and Evolution Stony Brook University Stony Brook, NY 11794-5245 USA +1-631-632-8567

Jessica Gurevitch <jessica.gurevitch@stonybrook.edu>

HorizontalGeneTransfer Rate

Hello All,

I am interested in knowing the typical value of rate/probability of horizontal gene transfer in case of present day bacteria. I will be grateful if any reference is also given.

Thanks and regards,

Ashutosh

ashutosh vishwa bandhu <ashutoshvb@gmail.com>

Inquiry Book UnknownSpecies

German press inquiry - book "50 unknown species"

Dear Sir or Madam,

I am a freelancing German science writer and biologist by profession.

At present I am working on a book that is intended to tell 50 portraits of hardly known species (animals).

The intention is to tell the reader there is much more in the world than main predators, elephants, rhinos and dolphins. More than killing, mating and foraging.

Moreover I intend to tell the reader there is a fascinating world outside that is worth being protected.

My question is if there is anyone out there who knows species that are unique, pretty unknown and somehow fascinating to the general audience.

Besides I would like tell some anecdotes from the fieldwork that are linked to a certain species - being lost in the desert while doing a survey or being stuck in the mood while chasing an insect or whatsoever. A fascinating blend of fieldwork and diversity.

My first ideas are the stinking ant (*Paltothyreus tarsatus*) and the *Demodex* family that is closely linked to man and still hardly known.

I would be happy if you could send me one or two ideas.

Looking forward to hearing from you, best Tim

Tim Schroeder Science Writer Hackenweg 79a

D - 26127 Oldenburg www.schroeder-tim.de Tel. 0049/441/9833238 Fax. 0049/441/9833239

Schröder <kontakt@schroeder-tim.de>

Island Conservation

Dear friends,

Already is available another outreach video from our Lab, focused in explain the environmental danger of pets and feral cats on islands: < <https://vimeo.com/140250256> >

In this case we focused on the problem of the introduction of pets in island ecosystems (we have worked this issue in the National Park of the Atlantic Islands of Galicia in Spain). Aware of the problems that we the ecologist have, to make the population aware about this problem, we believe this video could be used to raise public awareness about this complex environmental problem. You are free to share it in your social networks, if you want. PD: By clicking on the button CC (choose captions) it is possible to choose subtitles in several languages

Sincerely yours,

Luis Navarro

Luis Navarro phone 1: (+34) 986 812619 Depto. Biología Vegetal phone 2: (+34) 647 343097 Facultad de Ciencias fax: (+34) 986 812556 As Lagoas-Marcosende email: lnavarro@uvigo.es Universidad de Vigo <http://webs.uvigo.es/lnavarro> 36200-Vigo <http://webs.uvigo.es/plantecology> Spain <http://www.divulgare.net> Luis Navarro <lnavarro@uvigo.es> Luis Navarro <lnavarro@uvigo.es>

Joshua Tree Genome Project

Dear Evoldir members,

I am writing to share the exciting news about an initiative to sequence the genome of the Joshua Tree (*Yucca brevifolia sensu lato*). Todd Esque (USGS), Leslie DeFalco (USGS), Jim Leebens-Mack (University of Georgia), Mike McKain (Danforth Plant Sciences Center), Jeremy Yoder (University of British Columbia) and I

are collaborating on a project that we hope will allow us to identify genes involved in climate adaptation and coevolution with yucca moths.

As part of the project we're starting a social media campaign to generate public engagement, and promote public understanding of conservation genomics. You can check out our project page here: <http://joshuatreegenome.org/>, follow us on twitter: @JTGenome, and join our Facebook group here: <https://www.facebook.com/jtgenome/>.

We've also launched a crowd-funding project raise money to pay for pilot sequencing. You can donate to our crowdfunding campaign here: <https://experiment.com/joshuatree> This project is part of Experiment.com's liberal arts college competition; the project with the most donors on March 16th will get an additional \$2000 from Experiment. Please help us to spread the word!

Why Sequence The Joshua Tree Genome?

A Joshua tree reference genome would open the doors to answering many questions, of both scientific and conservation importance.

Understanding the genetics of coevolution. Like all yuccas, Joshua trees rely on a specialized group of moths to move their pollen from plant to plant. Amazingly, female moths actively collect and distribute yucca pollen after laying their eggs in the flowers they pollinate. Yucca moths effectively farm yucca seeds as nutrition for their offspring. In exchange for reliable pollination, yuccas sacrifice some of their seeds to the moths larvae. Joshua tree flowers exhibit a suite of adaptations that promote active moth pollination while deterring larval consumption of all their developing seeds. The genetic bases of these adaptations, however, are currently unknown. Sequencing of a reference Joshua tree genome would pave the way for association mapping to identify genes contributing to co-evolved adaptations to yucca moth pollination and larval seed predation.

Discovering genes that allow adaptation to desert environments. The Mojave Desert contains some of the hottest and most arid regions of North America. To survive in these inhospitable environments, Joshua trees have developed an array of physiological and morphological adaptations, from thickening of the waxy cuticle on the outside the leaves, to reduced stomatal pore size, and the presence of water storage cells. Sequencing the Joshua tree genome will help to identify the genetic basis of these adaptations, and will identify existing genetic variation in Joshua trees that may allow some individuals to survive and adapt to warmer temperatures. We will combine genome-wide-association studies with gene expression assays in common gardens to deter-

mine which genes have enabled Joshua trees to survive in the Mojave.

A genomic approach to conservation. Ensuring that Joshua trees will persist into the future means preserving not only the plants themselves, but also the genetic variation that will allow them to adapt to changing climates and environments. We will use a landscape genomics approach to measure the total amount of genetic variation in different populations, and estimate genetic differentiation between populations. This information will allow us to identify which populations of Joshua tree have the greatest potential to adapt to future environmental changes, and give these areas the highest priority for conservation.

Genome archeology. Like the vast majority of species within the Agavoideae, Joshua trees have five large chromosomes and twenty-five small chromosomes. The bimodal karyotype is hypothesized to have originated with an ancient allopolyploidy event. Sequencing the Joshua tree genome will allow us to test this hypothesis by comparing gene content and organization between the large and small chromosome sets. Further, comparisons with related genomes just outside of the Agavoideae will reveal how the putative subgenomes have changes since polyploidization.

Christopher Irwin Smith Associate Professor and Chair
Department of Biology Willamette University Salem,
OR 97301 ph: 503-370-6181 fax: 503-375-5425

Google Calendar <<https://www.google.com/calendar/selfsched?sstoken=3DUUxEQ1FKYkxPdTF1fGRlZmF1bHR8OGIwZjRlNjE1OTFjNjkyOWY2NjcxNTIyZDVhNjk0NTE>>

Lab Website: <http://www.willamette.edu/~csmith/ChrisSmith.htm> Biology at Willamette:

Our students: Through a research-rich curriculum that affords high-impact

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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>

Laboratory Fees

Apologies for any cross-postings of this message.

Please send all replies to brent.p.thoma@jsums.edu

I am sure most of you can commiserate with university systems continually facing budget cuts in recent years. At our university, this has resulted in little to no money available to purchase basic supplies and equipment for undergraduate teaching labs. There are a number of funding opportunities to update or advance undergrad laboratory equipment and activities but few, if any, provide funds for long-term support and maintenance.

I am aware that many departments with lab courses have created 'lab fees' to help ameliorate the funding of innovative and informative lab activities; however, I have found little written text containing such information. Thus, I am writing in hopes that you would provide me with any information on the implementation of 'lab fees' at your respective institutions.

This information will be compiled and presented to our university in hopes to implement our own lab fees to supply our students with a more robust curriculum including both field and laboratory exercises.

I appreciate your consideration and time in this endeavor. I will post the results of this inquiry for those of you who are interested.

Cheers, Brent

Brent P. Thoma PhD Assistant Professor of Biology
Jackson State University

Tel. Ph.: 601-979-3461 *Cell Ph.:* 337-371-8700
E-mail: brent.p.thoma@jsums.edu *Website:*
www.brentthoma.info "brent.p.thoma@jsums.edu"
<brent.p.thoma@jsums.edu>

Liverpool Proteomics BSPRLecture

'What has proteomics ever done for us?' Professor Rob Beynon (<http://www.liverpool.ac.uk/cpr>), a biochemist who works in close collaboration with the Mammalian Behaviour and Evolution Group (<http://www.liverpool.ac.uk/mbe>) in Liverpool UK, is the BSPR Lecturer this year (<http://www.bspr.org/news/bspr-lecturer>). He has been asked to deliver two types of talk, one of which promotes the application of proteomics to new areas of science. To this end, and with a little trepidation, he is offering to deliver one of his lectures to Departments with a strong interest in Evolutionary Biology and Animal Behaviour. He promises to keep the nerdy jargon down to a minimum! This is

the abstract for this talk:

The proteomics of sex

Robert J Beynon, Centre for Proteome Research, Institute of Integrative Biology, University of Liverpool

Most of evolutionary biology and animal behaviour is about sex! Sex is, in part, mediated through proteins and their interactions with other proteins. Thus, the study of proteins involved in topics such as sexual reproduction, sperm competition, mate selection and inbreeding avoidance could provide valuable new insights into the drivers of speciation and evolution. In my talk I will explore how successful collaborations between protein chemists and evolutionary biologists can yield new insights in this area. The biologists bring the big ideas, while the protein chemists find sneaky and novel ways to test their hypotheses, developing a truly interdisciplinary team approach - a model of modern biological research. I will target my talk towards the biologist, make few assumptions about the technical level of understanding of protein chemistry or mass spectrometry, and illustrate throughout with some fascinating studies we have conducted with the Mammalian Behaviour and Evolution Group here in Liverpool. If there is time I'll discuss the recipe for a productive collaboration across these two disciplines.

If you would like Rob to deliver a talk, please make direct contact with him (r.beynon@liv.ac.uk) or BSPR (see link)

Prof Paula Stockley Mammalian Behaviour & Evolution Group Institute of Integrative Biology University of Liverpool Leahurst Campus Chester High Road Neston CH64 7TE UK

www.liverpool.ac.uk/mbe "P.Stockley@liverpool.ac.uk"
<P.Stockley@liverpool.ac.uk>

MaxPlanckInst Seewiesen Volunteer SexualSelectionParrots

MaxPlanckInst_Seewiesen.SexualSelectionParrotsVolunteers

Where: Loro Parque Fundacion, Tenerife, Spain When: Immediately until 31 August What: Volunteers Research Assistants

The Department of Behavioural Ecology and Evolutionary Genetics at the Max Planck Institute for Ornithology in Seewiesen, Bayern, Germany (see <http://www.orn.mpg.de/2622/Department.Kempenaers>), is

seeking two volunteers to start working immediately and until 31 August 2016 (the position requires a minimum of 2 months).

The volunteers will assist in the collection of courtship displays and egg laying data. This work would be part of a project that aims to understand the evolution of sexual selection in parrots of the world. The work will be done at the facilities of the Loro Parque Fundacion, located in Tenerife, Spain.

Work will include:

§recording courtship displays §following up reproduction (egg laying, hatching, and fledging) §maintenance of electronic equipment §setting up experimental equipment §data collection, entry, and management

Successful candidates should have experience with video-recording equipment. Experience with monitoring animals is desirable. Applicants should also be highly motivated and well organised, with capabilities of working both in a group and independently. Work will be 5-6 days per week starting early in the morning and potentially continuing into the evening. The working language at the Institute is English, so good knowledge of the language is required. A basic working knowledge of the Spanish language would be advantageous. Eligibility is sadly restricted to UK and EU students. The Max Planck Institute for Ornithology employs a dynamic, dedicated, and international group of researchers who are focused on exploring the fields of evolution, ecology, genetics, and neurobiology.

Benefits will include accommodation and travel-related expenses in Tenerife.

If you are interested in applying for one of the volunteer positions as described above, please apply (including your CV and cover letter) via email to lcarballo@orn.mpg.de.

Deadline 20 April 2016 or until the positions are filled.

Luisana Carballo Department of Behavioural Ecology and Evolutionary Genetics Max-Planck-Institute for Ornithology Eberhard-Gwinner-Straße, House 8 82319 Seewiesen Germany

“Carballo, Luisana” <lcarballo@orn.mpg.de>

microMORPH Funding

Reminder, Applications due March 15!

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 per 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, Pamela” <pamela.diggle@uconn.edu>

MissouriBotanicalGarden REU ConservationBiol

Summer 2016 REU in Botany, Conservation Biology and Ethnobotany

The Missouri Botanical Garden in St. Louis, MO will be offering an NSF-funded Research Experiences for Undergraduates summer program in 2016. Ten students will be chosen to participate in a ten-week program involving full-time work on an independent research project, with the guidance of a staff mentor, in addition to educational seminars, discussion sessions and field trips. Available research projects deal with subjects including taxonomy, speciation, population genetics, conservation biology, restoration ecology, biodiversity modeling, crop development, ethnobotany, and climate change. Students will receive a weekly stipend as well as housing, food, transportation, and funding for research supplies. Eligible students are U.S. citizens or permanent residents who will be returning to school in the fall semester after the REU program. Students from schools with limited research infrastructure and from underrepresented groups are particularly encouraged to apply. Applications must be received by April 15. Further information on the program, available mentors and projects, and how to apply can be obtained from the website: www.mobot.org/reu. If the website does not answer your questions, please email reu@mobot.org.

Wendy Applequist <wendy.applequist@mobot.org>

MolecularClock question

Dear Evoldir members,

I need to understand how to calibrate a molecular clock in beast using Minimum and maximum constraints. If you know about manuals, tutorials, papers or any other readings about it, please help me telling me where to find them

I'll appreciate your collaboration --

Cordialmente,

MANUEL HOYOS

Biólogo

Manuel Antonio Hoyos Rodriguez
<mahoyosr@unal.edu.co>

MolecularEcol Prize Nominations

I am soliciting nominations for the annual Molecular Ecology Prize.

The field of molecular ecology is a young and inherently interdisciplinary research area. As a consequence, research in molecular ecology is not currently represented by a single scientific society. Likewise, there is no body that actively promotes the discipline or recognizes its pioneers. To help fill this void, the editorial board of the journal *Molecular Ecology* created the Molecular Ecology Prize to recognize significant contributions to this area of research.

The prize will go to an outstanding scientist who has made significant contributions to Molecular Ecology. Presumably these contributions would mostly be scientific, but the door is open for other kinds of contributions that were crucial to the development of the field. Previous winners are: Godfrey Hewitt, John Avise, Pierre Taberlet, Harry Smith, Terry Burke, Josephine Pemberton, Deborah Charlesworth, Craig Moritz, Laurent Excoffier, Johanna Schmitt, and Fred Allendorf.

Please send your nominations with a short supporting statement (no more than 150 words) by 15 May 2016 directly to me (fred.allendorf@gmail.com).

Thanks on behalf of the Molecular Ecology Prize Selection Committee. We look forward to hearing from you.

Fred Allendorf

fred.allendorf@gmail.com

OmmenPrize EvolutionAndMedicine NominateYourArticle

The firm deadline for nominations is March 31.

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

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 in Durham, North Carolina of the International Society for Evolution and Medicine. <http://evolutionarymedicine.org> rmnesse@gmail.com

Phyloseminar ClausWilke April20

Claus Wilke University of Texas at Austin Wednesday, April 20, 2016, 10:00 AM PDT

Structural and functional constraints on protein evolution

Proteins are under selective constraints to fold stably into their native conformation and to carry out their biological function. These selective constraints shape how proteins evolve, and they cause variation in substitution rates among the sites within a given protein. In particular, sites in the core of a protein, with many residue-residue contacts, tend to be more conserved than sites on the protein surface. Further, catalytic residues in enzymes are highly conserved, and they impart a measurable increase in conservation to much of the enzyme structure, in a distance-dependent manner. (The further a site is from a catalytic residue, the less extra conservation it experiences.) Finally, protein-protein interfaces show a surprising ability for evolutionary divergence, even if they are strongly selected for function.

– Frederick “Erick” Matsen, Associate Member Fred Hutchinson Cancer Research Center <http://matsen.fredhutch.org/> Erick Matsen

<matsen@fredhutch.org>

Phyloseminar JesseBloom March15

Jesse Bloom (Fred Hutchinson Cancer Research Center) Using experiments to inform phylogenetic models of substitution Tuesday, March 15, 2016, 10:00 AM PDT

Computational algorithms to infer phylogenetic relationships or detect sites of positive selection are widely used in diverse branches of biology. However, anyone with a passing knowledge of modern biochemistry can recognize that the quantitative models of the evolutionary process used by these algorithms are woefully oversimplified. I will discuss prospects for making these models more realistic while keeping them computationally tractable. In particular, I will discuss how new sources of high-throughput experimental data can be leveraged to improve algorithms for the analysis of gene sequences.

– Frederick “Erick” Matsen, Associate Member Fred Hutchinson Cancer Research Center <http://matsen.fredhutch.org/> matsen@fredhutch.org

Pyrenees VolFieldTech PlantSpeciation DeadlineExt

Nick Barton’s group at the Institute of Science and Technology (IST) Austria requires volunteers to assist with field work on plant speciation in the Pyrenees (Spain) this coming summer (late May - early August).

The project: We are studying the evolutionary dynamics underlying species diversification in the genus *Antirrhinum* (snapdragons). A major focus of this research involves field work on natural hybrid zones between two subspecies with different flower colours. Most of the field work is contributing to a long-term pedigree project aimed at establishing a direct link from genotype to phenotype to fitness. With 20,000 samples collected over six generations (so far), this provides an exciting and powerful system to examine many outstanding questions in speciation and quantitative genetics in wild populations. We are seeking volunteers to assist with the field work, which involves working in teams mapping the location of

individual plants (GPS), tagging and sampling them for leaves and flowers, measuring quantitative traits, phenotyping them for flower pigmentation and processing material for later DNA extraction. There may also be opportunities to be involved in other projects we are doing on plant-pollinator interactions, pollen fertility and community ecology surveys. Most of the work is outdoors, however we do spend some time indoors processing samples. The work is highly team orientated, typically in groups of 2-3 in the field and larger groups processing samples back at the research station. This is a great opportunity for anybody looking to obtain experience in field work relating to evolutionary biology, plant ecology and plant-animal interactions. You will also be part of a large multidisciplinary team including researchers from IST Austria (Vienna), John Innes Centre (Norwich, UK) and the University of Toulouse.

The field site is located near Ripoll in a beautiful part of the Pyrenees of North Eastern Spain (Catalonia). We stay in comfortable apartments overlooking a picturesque valley, with close access to hiking trails and small villages. All food, accommodation and travel (within Europe) are covered. However, we cannot offer any further stipend.

For these positions we are looking for hard working and enthusiastic biology students with a strong interest in working outdoors with plants. You must be meticulous with recording data and also be comfortable working as part of a team. Experience with field-based projects and plants is preferred but not essential.

We require assistance between late May and late July. Depending on the year and the plants, we may extend our time into August. Length of stay is flexible but a minimum stay of 3 weeks is required.

Please send any questions to the email address below. How to apply? By the closing date of April 7th, please send a statement of your background, CV, why you are interested and the length of time you would be available via email to maria.clara.melo@ist.ac.at

Maria Clara MELO HURTADO
<maria.clara.melo@ist.ac.at>

SouthAfrica VolResAssist SocialMoleRats

SouthAfrica.VolResearchAssistant.SocialMoleRats

Cooperative breeding in Damaraland mole-rats (*Fukomys damarensis*).

Voluntary research assistant: Starting in May 2016 for 6 months

We are looking for one voluntary research assistant to help with our research on the completely subterranean, highly social Damaraland mole-rat (*Fukomys damarensis*).

This position entails assisting in several studies on hormonal effects on social behaviour of mole-rats. We are interested in the effects of prolactin and testosterone on allo-parental care in non-reproducing mole-rats. The research assistant will be involved in all steps of the experiments and will mainly work in the laboratory with our captive mole-rats which are housed in large semi-natural tunnel systems. The responsibilities include behavioural observations, hormonal measures (blood sampling, urine sampling) and hormonal manipulations. The laboratory is situated in the Kuruman River Reserve in the southern Kalahari, Northern Cape province of South Africa.

Additionally, we are conducting a capture-mark and recapture study in which the voluntary research assistant can get involved in. 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 field work is physically demanding (long hours, heavy digging to capture mole-rats) and weather conditions are very challenging (heat during the day, very cold during the night). Field work will make trapping during the night necessary. The assistant will mostly be working along one more experienced scientist but will need to work independently at times.

The successful applicant will work in a team of 5-10 persons. The research station is also the home of several other projects studying meerkats (www.kalahari-meerkats.com), pied babblers, forktailed drongos, bat-eared foxes and hornbills resulting in a stimulating scientific environment. Around 20-30 research assistants are based at the station year round. Research assistants will learn a range of skills such as remote sensing

of behaviour, endocrine sampling techniques, capture-mark-recapture techniques, behavioural observations, data handling and management.

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 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. A zoology related degree and/or previous field experience will be considered an asset. The successful applicant needs to be a team player and generally a person that enjoys collaboration and team work.

Accommodation is provided, and research assistants are paid a monthly allowance to cover their personal costs and food. The bus fare from Johannesburg to the field site can be covered but we do not provide an international airfare, travel insurance, or visa fees for applicants from overseas.

Applications received until the 25th of March 2016 are ensured full consideration. Later applications can be considered if the position has not been filled.

For further information or informal enquiries feel free to get in touch by email.

Please apply by sending a CV & cover letter in a single pdf file to:

Mz338@cam.ac.uk

Dr Markus Zöttl

Research associate

Larg - Department of Zoology

University of Cambridge

Downing Street

CB23EJ - UK

<http://www.zoo.cam.ac.uk/directory/dr-markus-zottl>

Office: +441223336673

Markus Zoettl <mz338@cam.ac.uk>

SouthAfrica Volunteers StripedMouse

Volunteers needed for April, July and end of 2016

Evolution and Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

Opportunity: This is a great opportunity for anybody who wants to get more experience in field work related to animal behavior, evolution, eco-physiology, and ecology before starting an MSc or PhD project.

Project: We study the evolutionary and ecological reasons as well as physiological mechanisms of group living, paternal care, communal nesting and social flexibility in the striped mouse. One focus is on the adaptation to droughts, combining physiological, behavioral, ecological and evolutionary research. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students are preferred as candidates. Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o' clock), and stops its activity with dusk (19 o' clock). Work during nights might also be necessary. Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40°C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small social group.

Work of volunteer field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field. Volunteers will also see how blood samples are collected for physiological measurements. Volunteers are expected to help with maintenance of the research station (water pump, solar power, etc.).

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1450 (around 175 US\$, 100 Euro) must be paid for ac-

commodation at the research station. Students must buy their own food etc in Springbok (costs of about R 3000, approx. 350 US\$ or 250 Euro/month). Including extras (going out for dinner; shopping), you should expect costs of about 600 US\$ / 450 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country.

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: At the moment we are looking for two volunteers starting in April 2016 and two volunteers to start in June / July 2016. Volunteers are expected to stay for 2-3 months. We are also looking for volunteers for later in 2016.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to succulent.karoo.research.station@kabelbw.de.

More information under

http://stripedmouse.com/site1_3_5.htm

Dr. Carsten Schradin

Director of the Succulent Karoo Research Station (South African non-profit organization), Goegap Nature Reserve, PO Box 541, 8240 Springbok, South Africa

<http://www.stripedmouse.com>

Logo..June 2014

Director Succulent Karoo Research station
<succulent.karoo.research.station@kabelbw.de>

SSB Ernst Mayr Award

The Ernst Mayr Award is given to the presenter of the outstanding student talk in the field of systematics at the annual meetings of the Society of Systematic Biologists (SSB). This is SSB's premier award, and is judged by the quality and creativity of the research completed over the course of the student's Ph.D. program. The award consists of \$1000, a certificate of distinction, and a two-year subscription to the journal Systematic Biology.

Members of the Society who are students or have completed their Ph.D. within the last 15 months are eligible.

Applicants may be from any country, but MUST be members of SSB, and are advised to join the Society as soon as possible to be considered. Previous Mayr Award winners are not eligible.

***IMPORTANT:** Submit your abstract early to be sure you will be considered for the award*

How to become eligible for the Ernst Mayr Award

+ To be considered for this award, you MUST submit an abstract of your talk to the Evolution meeting website (<http://evolutionmeetings.org/>) at the time of registration. Instructions for registering as a potential Mayr award contender will be given on the meeting website. + Abstracts should clearly indicate methods used, conclusions, and the relevance to systematics. Presentations focusing on other areas of biology (ecology, behavior, genetics, populations or molecular biology, etc.) that lack a strong systematics emphasis are not eligible. + Applications for this award will be accepted only until the end of early registration (April 30, 2016) or EARLIER if all of the meeting talk slots fill. So APPLY EARLY to ensure that you are considered for the award and are able to present at the meeting. + At the closing of early registration, a subset of applicants will be selected by the SSB Awards Committee to present their talks in the Mayr symposium during the meeting. All applicants will be notified about selection decisions approximately May 15. Applicants not selected for an award will be given a regular concurrent talk in another session at the meeting.

Judging: Based on the submitted abstracts, the Mayr Awards Committee (appointed by the Awards Chair) will select a maximum of 16 applicants for inclusion in the Mayr Award symposium. The Mayr symposium will be held at a single venue as a continuous session. Talks will be judged on creativity, depth and excellence of research, and on quality of presentation. Competitive students are expected to be in the final stages of their doctoral program, presenting results of a major body of work.

Co-Authors: The talk may be co-authored. It is understood that the ideas, data and conclusions presented are primarily and substantially the work of the student presenter, and the intention is that the student presenter will be senior author on the published version of the paper. If a submission includes multiple authors, include a brief section below the abstract that outlines the contribution of each author to the research.

Notification of Winner: The winner of the award will be announced at the SSB business meeting and again during the Super-Social at the conclusion of the Evolution Meetings, whereupon the winner will be given

an award certificate (the check will be mailed). An announcement of the winner will also be published in *Systematic Biology* and placed on the SSB website.

For information about joining SSB, please see: <http://www.systbio.org/membership.html>. Contact: Please email the SSB Awards Director, Tracy Heath at ssb.awards.director@gmail.com if you have any questions.

ssb.awards.director@gmail.com

SSB Grad Student Research Grant

The Society of Systematic Biologists (SSB) announces the 2016 annual Graduate Student Research Award competition (<http://www.systbio.org/graduate-student-research-awards.html>). The application deadline this year is April 24, 2016. The purpose of these awards is to assist students in the initiation (first two years) of their systematics projects and in the collection of preliminary data to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications. Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply. Awards will range between \$1200 - \$2000 and approximately 15 awards will be made.

Some examples of successful proposals are available at: <http://www.systbio.org/graduate-student-research-awards.html>. ++ How to apply ++

Applicants must submit:

- + a curriculum vitae (one page maximum)
- + brief research proposal including objectives, methods, significance, and schedule (maximum of three single-spaced pages including literature cited and any figures and tables)
- + budget (\$2,000 limit) and budget justification (1 page maximum)
- + arrange for two reference letters; one letter must be from the student's current graduate advisor.

The research proposal must clearly state the current stage of the proposed research and the current year and status of the student. PLEASE INCLUDE AP-

PLICANT'S CONTACT E-MAIL ADDRESS AT THE TOP OF THE APPLICATION ITSELF. Both Masters and Ph.D. students in their FIRST TWO YEARS ONLY are eligible. (Ph.D. students with masters degrees are still eligible if they are within the first 2 years of their Ph.D. training.)

Systematics is interpreted broadly to include questions below and above the species level, molecular and morphological approaches, and issues of pattern and process. Funding is not limited to any particular aspect of research, but rather is available for field, museum/herbarium, and/or laboratory work.

All application materials must be in electronic format. Applicants and those writing reference letters are required to use pdf format to minimize difficulties in file transfer. Applicants should send all materials (except reference letters) in a SINGLE pdf file.

Letters of reference should be sent via email (ssb.awards.director@gmail.com) separately by the referees in PDF format; please include the FULL NAME OF APPLICANT in reference letters. In the subject line of the email, indicate "LOR: Student Research" followed by the student's first initial and last name.

Please email all application materials and queries to the Chair of the SSB Awards Committee (Dr. Tracy Heath: ssb.awards.director@gmail.com). IN THE SUBJECT LINE OF THE E-MAIL, PLEASE INDICATE "Student Research" FOLLOWED BY FIRST INITIAL AND LAST NAME.

To be considered for this year's award, application materials, including reference letters, must be received electronically no later than April 24, 2016. Applicants will be notified of their proposal status by the end of June.

For information about joining SSB, please see: <http://www.systbio.org/membership.html>. Please contact the SSB Awards Director (ssb.awards.director@gmail.com) with any questions.

ssb.awards.director@gmail.com

SSB Mini-ARTS Grant

The Society of Systematic Biologists is pleased to offer Mini-ARTS awards to enhance taxonomic knowledge (<http://www.systbio.org/mini-arts-awards.html>). These awards are for revisionary taxonomy and systematics, modeled after the NSF Dear Colleague Letter: Advancing Revisionary Taxonomy and Systematics (ARTS) recently developed within the Systematics and Biodiversity Science Cluster (<http://www.nsf.gov/pubs/2011/nsf11037/nsf11037.jsp>). We are calling these 'Mini-ARTS' grants. These awards are designed to allow SSB members (students, post-docs, and faculty) to spend a summer or semester apprenticed to an expert in a particular taxonomic group or to enhance revisionary taxonomic and systematics research in novel ways. Goals of this award program are to address constraints on our knowledge of undescribed biodiversity, assist in passing on taxonomic expertise before it is lost, increase the number of students with broad training in organismal biology and systematics, and support projects in biodiversity and taxonomy informatics as well as monographic and revisionary taxonomy. Activities can include a trip to the taxonomist's laboratory, pay for the taxonomist to visit the applicant's laboratory for a period of time, or pay for costs of computer time or development of interactive keys for electronic dissemination of systematics results. Requests for support may be in any amount up to \$3,000. We expect to fund between 1-3 of these awards this year.

=How to apply=Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications. A complete application includes:

+ a brief description of the project, including a separate section justifying the importance of the taxon and the revisionary work + an itemized budget (narrative plus budget should not exceed 2 pages) + the applicant's CV + a letter of support from the taxonomic expert or collaborator + If the applicant is a student or post-doc, please also include a reference letter from the advisor

Grant applications should be sent to the chair of the SSB Awards Committee (Dr. Tracy Heath: ssb.awards.director@gmail.com). E-mail submissions are required, and applicants should use pdf format for all documents. In the subject line of the email, please indicate the SSB award category as 'Mini-ARTS'.

The next application deadline for all materials, including letters of support and letters of reference, is March 31, 2016.

For information about joining SSB, please see: <http://www.systbio.org/membership.html> . Please contact Tracy Heath (ssb.awards.director@gmail.com) with any questions.

ssb.awards.director@gmail.com

SSE THHuxleyAward Deadline Apr4

The *Society for the Study of Evolution* Education Committee is pleased to announce the T. H. Huxley award, named in honor of Darwin's very public supporter, which recognizes and promotes the development of high quality evolution education resources. If you have an interesting project or educational activity to share, consider applying for this award. Graduate students and postdoctoral fellows are encouraged to apply. This award provides funding for an SSE member to present evolution education resources at the National Association of Biology Teachers (<http://www.nabt.org/>) annual conference. This years NABT conference will be held Nov. 3-6, 2016 in Denver, CO. *The deadline for applying for the Huxley award is April 4. *

Apply here: <http://goo.gl/forms/8JBIh9oj3w> Questions? Contact Louise Mead (lsmead@msu.edu) or Kristin Jenkins (kristin.jenkins@bioquest.org)

perezke@gmail.com

THHuxley Award SSE

The *Society for the Study of Evolution* Education Committee is pleased to announce the T. H. Huxley award, named in honor of Darwin's very public supporter, which recognizes and promotes the development of high quality evolution education resources. If you have an interesting project or educational activity to share, consider applying for this award. Graduate students and postdoctoral fellows are encouraged to apply. This award provides funding for an SSE member to

present evolution education resources at the National Association of Biology Teachers (<http://www.nabt.org/>) annual conference. This year's NABT conference will be held Nov. 3-6, 2016 in Denver, CO. The deadline for applying for the Huxley award is April 4.

Apply here: <http://goo.gl/forms/8JB1h9oj3w> Questions? Contact Louise Mead (lsmead@msu.edu) or Kristin Jenkins (kristin.jenkins@bioquest.org)

Kathryn E. Perez, Ph.D. Department of Biology The University of Texas Rio Grande Valley perezke@gmail.com; kathryn.perez@utrgv.edu <http://northamericanlandsnails.org> Office: SCNE 3.142, (956) 665-7145 Lab: SCNE 2.240, (956) 665-2849

perezke@gmail.com

UColoradoBoulder REU Phylogenetics

This is a reminder that the deadline for the following REU is this Friday!

We are recruiting two undergraduate students to conduct independent research over 10 weeks this summer (23 May - 29 July) at the University of Colorado Boulder as part of an NSF-funded REU. The project will involve investigating the ecological and evolutionary processes influencing the phylogenetic structure of plant communities across the United States. Students will work in the Smith lab (www.colorado.edu/smithlab) under the guidance of Dr. Julianne Ng and Dr. Robert Laport, primarily generating DNA sequence data, conducting phylogenetic analyses, and accessing and managing large amounts of plant trait data from public databases. More information about the project can be found at the following website: <http://julienneng.weebly.com/reu-summer-2016.html> Students will be provided a stipend of \$500/week, dormitory housing and return flight (up to \$500).

Participants must be U.S. citizens or permanent residents, and an undergraduate during the entire period. We especially encourage students from groups traditionally underrepresented in science to apply.

To apply, please send a personal statement that describes your research interests and how this REU will support your professional goals (no more than half a page), a resume or CV, unofficial transcripts, and the contact details of two professional references (including title, how you know them, phone number and email

address) to Dr. Julianne Ng (julienne.ng@colorado.edu). Applications close 4th March, 2016.

Please direct any questions to Dr. Julianne Ng (julienne.ng@colorado.edu).

julienne.ng@gmail.com

UGeorgia REU EvolutionAndClimateChange

subject: NSF REU position with Anderson lab (UGA) in the ecological and evolutionary consequences of climate change on natural plant populations

body: Jill Anderson and Susana Wadgymar at the University of Georgia are searching for an enthusiastic undergraduate with a strong interest in evolutionary ecology for field research in an NSF REU position (National Science Foundation, Research Experience for Undergraduates) from June-August 2016.

We study the ecological and evolutionary consequences of climate change for natural plant populations. We focus on research on Drummond's rockcress (*Boechera stricta* in the plant family Brassicaceae), a mustard plant native to the Rocky Mountains. Our studies take place around the Rocky Mountain Biological Lab (<http://www.rmbl.org/>), which is located in Gothic, Colorado near the wildflower capital of Colorado (Crested Butte). We quantify plant fitness and traits to ask whether climate change could disrupt long-standing patterns of local adaptation, and to test whether phenotypic plasticity will enable populations to persist in the short-term. We perform large-scale reciprocal transplant experiments to examine patterns of adaptive evolution and natural selection in contemporary landscapes. Since fall 2013, we have planted ~60,000 seeds and seedlings into five experimental gardens ranging in elevation from 2500 m to 3340 m (8202 feet to 11000 feet). Our summer research involves intensive monitoring of these experimental plants to record data on germination success, survival, growth, reproductive success, as well as life history and morphological traits. We conduct most of our work in the field, with a small proportion of indoor lab work.

The successful candidate will assist with ongoing fieldwork. In addition, there are many opportunities for students to develop independent projects associated with our overall objectives, including studies on: 1) population divergence in ecologically-relevant traits, es-

pecially drought, UV tolerance, and herbivore resistance; 2) phenotypic plasticity at multiple spatial scales; 3) population density and species composition of the herbivore community that attacks Drummond's rockcress; 4) flower color polymorphism; and 5) the importance of maternal effects in biological responses to climate change.

We are offering a stipend of \$500/week for a full time REU student (40 hours/week) for 10 weeks. The exact start and end dates are flexible.

We will cover room and board at the Rocky Mountain Biological Laboratory and reimburse travel expenses up to \$500. Fieldwork will involve hiking to experimental gardens through rough terrain (1-3 miles one-way daily).

The University of Georgia is committed to maintaining a fair and respectful environment for living, work, and study. To that end, all qualified applicants from individuals with a strong interest in evolutionary biology will receive consideration for employment without regard to race, color, religion, sex, national origin, sexual orientation, gender identity, disability status, or age. The application consists of a cover letter your qualifications, a CV/ résumé and contact information for two references, all of which can be emailed to Dr. Jill Anderson at: jta24@uga.edu Applications are due by April 1st, 2016.

Feel free to contact Jill or Susana (susanaw@uga.edu) if you have any questions about the position. Additional information about the our work can be found at: <http://andersonlab.genetics.uga.edu/Home.html> Susana Wadgymar <swadgymar@gmail.com>

UGreifswald ExchangeGrants

Reminder: RESPONSE Exchange Grants

To establish new collaborations, the DFG-funded Research Training Group RESPONSE (GRK 2010 - Bio-

logical Responses to Novel and Changing Environments; www.uni-greifswald.de/RESPONSE/) offers Exchange Grants to a limited number of scientists for a stay of 2-12 weeks in Greifswald, Germany. Researchers should collaborate with one of the RESPONSE research projects, i.e. on issues related to environmental change. We are particularly interested in combining various research approaches, like ecology, evolution, genetics, physiology, behaviour, theory or modelling.

Deadline for grant applications is April 15th, 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 grantee's 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 RESPONSE.

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.

Michael Schöner <schoenerm@uni-greifswald.de>

PostDocs

Adelaide Australia AncientHumanGenomics 87	OldDominionU EvolutionCooperativeBehavior . . . 105
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Adelaide Australia AncientHumanGenomics

ARCResearch Associate AustralianCentre for Ancient DNA, The University of Adelaide Salary:Level A \$62,112 - \$84,291 per annum (PhD starting \$78,525), plus up to 9.5% Superannuation applies.

Keywords: Bioinformatics, Human Evolutionary Genetics, Biomedical Population Genetics, Ancient DNA Database.

A2 year post-doctoral position (extendable) is available

studying human genetic selection using ancient genomes - with a focus on GWAS, disease, molecular evolution and the impacts of environmental change. The position will be responsible for managing and extending the Online Ancient Genome Repository (OAGR - <https://www.oagr.org.au>) - the worlds only publicly available complete collection of ancient genomic data and meta-data. The project is co-supervised by quantitative geneticist Prof. Peter Visscher (Queensland Brain Institute - <http://researchers.uq.edu.au/researcher/1487>) and the successful applicant will use OAGR to develop and apply field leading population genetics approaches including imputation and GWAS. The aim of the project is to trace the evolution and spread of important genetic markers through ancient populations and genomes, us-

ing existing and newly generated data, and is part of an internationally competitive research team working closely with genetic analysts, population genetics specialists, archaeologists, and ancient DNA researchers at Harvard University, Max Planck Institutes, and UCSD.

The project is housed within the Australian Centre for Ancient DNA (ACAD) and will combine state-of-the-art genetics, bioinformatics, and genomics tools, and is funded by the Australian Research Council (ARC) for a period of 2 years with immediate start. It forms part of ARC Laureate Project FL140100260 Using ancient genomes and microbiomes to reconstruct human history award to Prof. Alan Cooper.

The position focuses on bioinformatics and population genetics analyses, and there is also scope for the generation of new ancient human data using the large collections of material available at ACAD and through collaborators. The successful applicant will lead a program to develop and integrate analytical methods and pipelines for the analysis of large ancient genomic datasets, and co-supervise a group of postgraduate students in collaboration with QBI, overseas colleagues and the University School of Mathematical Sciences. The position would also be open to an MSc level candidate, who would be expected to provide analytical capacity, but without supervisory responsibilities.

The University of Adelaide is one of Australia's leading Group of Eight, research-intensive universities and is consistently ranked among the top 1% of universities in the world. Established in 1874, it is Australia's third oldest university with a particularly strong reputation for scientific research. The Faculty of Sciences is one of five faculties at the University of Adelaide. As the first university in Australia to grant degrees in science (1882), science has long been at the cornerstone of the institution and this continues today. As a research and education leader in fields such as biomedical sciences, agricultural, environmental and earth sciences, the faculty offers an exciting and innovative work environment. ACAD sits within the Flagship Environment Institute, and is an international-level ancient DNA research centre, regularly publishing in high-impact journals such as Nature and Science. The applicant would be expected to operate at this level.

Position requirements

To be successful you should have:

A PhD or MSc involving bioinformatics, biostatistics, quantitative genetics, population genetics, biomedical or ancient DNA research, or other relevant disciplines.

Expertise in UNIX based systems, including scripting in bash and at least one pre-compiled language (prefer-

entially Python), as well as proficiency in working on Linux clusters and databases.

Demonstrated knowledge and experience with Next Generation Sequencing and genomics datasets, including filtering/processing large datasets, multivariate statistical analysis, developing analytical methods and pipelines, and performing population genetics analyses.

Proficiency in coding and developing bioinformatics pipelines to address unique genetic questions.

Demonstrated ability to publish in scientific journals, and present research at international conferences.

Excellent written and oral communication skills with the ability to liaise, collaborate and interact with a wide range of national and international scientific researchers.

Salary: Level A 2,112- 4,291 per annum plus up to 9.5% Superannuation applies. Salary is commensurate with qualifications and experience - PhD Starting salary level 8,525

Please address and upload your responses addressing the selection criteria section of the position description and include the contract details of

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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>

Barcelona Bioinformatics

Bioinformatics postdoctoral position at the Evolutionary and Functional Genomics Lab. Institute of Evolutionary Biology (CSIC-UPF). Parc de Recerca Biomèdica de Barcelona.

http://www.biologiaevolutiva.org/gonzalez_lab/ The Evolutionary and Functional Genomics Lab led by Josefa González is seeking a highly motivated postdoctoral researcher to join our research team at the Institute of Evolutionary Biology (CSIC-UPF). The postdoctoral researcher will work on a project funded by a European Research Council Consolidator Grant that aims at identifying the genetic basis, the molecular mechanisms, and the functional traits relevant for environmental adaptation.

The postdoctoral researcher will be responsible for the identification and the in silico analyses of the candi-

date adaptive mutations. The tasks involved in the postdoctoral research project are: de novo assembly of *Drosophila melanogaster* genomes (short and long NGS reads), implementation of pipelines to detect de novo transposable element insertions in genomes, searching for evidence of selection at the DNA level (e.g. Fst, iHS, environmental association methods, detection of polygenic adaptation) and ChIP-Seq analyses, among others. A PhD in Populations Genetics or a related field, good programming skills, and good writing skills are required. Previous postdoctoral experience will be considered.

We offer a full-time position for 2 years with the possibility of extension. Salary will depend on the experience of the candidate. Starting date September 2016 but alternative dates can be discussed. Application: Please send your CV and a brief letter of motivation before the 15th April 2016 to: josefa.gonzalez@ibe.upf-csic.es

Josefa González, PhD Ramón y Cajal Researcher Institut de Biologia Evolutiva (CSIC-UPF) Passeig Marítim de la Barceloneta 37-49 08003 Barcelona. Spain. +34 932309637 New lab publication in bioRxiv Our most recent collaboration with the Petrov Lab in Molecular Ecology Lab website: www.biologiaevolutiva.org/-gonzalez_lab Science Outreach: La Ciència Al Teu Món “GONZALEZ PEREZ, JOSEFA” <josefa.gonzalez@ibe.upf-csic.es>

BrownU Phylogenetics

The Edwards Lab at Brown University is currently looking for a post-doctoral research associate in the area of phylogenetics/phylogenomics. We are open to anyone with a strong interest and background in evolutionary biology, and hopefully plants, but the successful candidate will also have considerable bioinformatics expertise. There is guaranteed funding for one year, with negotiable extension. We would like to fill the position as soon as possible, but can be very flexible for the right person.

Brown University is located in the heart of Providence, RI. Also home to the Rhode Island School of Design and the Johnson and Wales Culinary Institute, Providence has an active and creative arts, music, and food scene. All in all, Providence is a wonderful place to live.

Please send a CV and names/contact info for three references to erika_edwards@brown.edu. Brown is an equal

opportunity employer.

- Erika Edwards Associate Professor of Ecology and Evolutionary Biology Brown University

Box G-W 80 Waterman St Providence RI 02912

phone: 401.863.2081 fax: 401.863.2166

lab website: http://www.brown.edu/Research/-Edwards_Lab/index.php “erika_edwards@brown.edu” <erika_edwards@brown.edu>

CIRAD France VirusPopGenetics

We are seeking a post-doc fellow to investigate potential adaptive mechanisms behind the ability of viruses transmitted by arthropod vectors to infect cyclically both mammals and arthropods. To that end, you will analyse how the genetics of Bluetongue virus populations changes while they switch between mammals and insects hosts. This funded project will use bioinformatic analysis of NGS data generated from infections of mammals and insect vectors as well as experimental evolution of viral populations in cell culture. We will consider candidates able to conduct both bioinformatic and experimental approaches, as well as those autonomous in one and willing to develop its skills in the other. The candidate will work in our fully equipped labs in Montpellier - South of France, home of a vibrant scientific community - in a new and dynamic structure within the CMAEE research unit (<http://www.cirad.fr/en/research-operations/research-units/control-of-emerging-and-exotic-animal-diseases>).

Funding is dependent on a grant from a funding scheme (www.agreenskills.eu) the candidate must apply for (basic salary is already available but the candidate must obtain the funding from the Agreenskills call to be selected). This grant provides a highly competitive salary (over 3 000 EUR per month) for French living standards. If interested, please check on the Agreenskills web site whether you are eligible before contacting us. The deadline for application is 29th April 2016 but an eligibility check is required before application submission.

Informal enquiries may be made to Serafin Gutierrez or Etienne Loire (serafin.gutierrez@cirad.fr, etienne.loire@cirad.fr).

– Serafin Gutiérrez, PhD

Scientist

Virology team CMAEE Unit - Control of Exotic and

Emerging Animal Diseases

CIRAD TA-A15/G, Campus International de Bail-larguet (bureau G 204) 34398 Montpellier Cedex 5 France

tél:+33 4 67 59 39 11

fax:+33 4 67 59 37 98

<http://umr-cmaee.cirad.fr/l-unite/les-equipes-disciplinaires/virologie/contexte-objectifs>

Serafin Gutierrez <serafin.gutierrez@cirad.fr>

ClemsonU StreptococcusGenomics

Vince Richards lab in the Department of Biological Sciences at Clemson University is accepting applications for a post-doctoral position. The position is broad in scope covering various aspects of Streptococcus genomics. Approaches such as comparative genomics, population genomics, transcriptomics, and metagenomics will be used to address various questions pertaining to this important group of pathogens. The candidate should have a strong publication record, a background in population and evolutionary genetics, experience analyzing next-generation sequence data, and be well versed in Linux/bash. Strong communication and writing skills are essential.

The position will begin July 1st, 2016 and is available for two years with the possibility of extension. Applicants should contact Vince Richards directly at vrpricha@clemson.edu. Please provide a cover letter describing research interests, experience, and career goals, CV, PDFs of representative publications, and contact information for three references. Salary is commensurate with experience and the position is benefits eligible. Review of applications will begin immediately and continue until the position is filled.

Clemson University is ranked 21st among national public universities by U.S. News & World Report and is located on Lake Hartwell near the Blue Ridge mountains in beautiful Upstate South Carolina.

Vincent P Richards, Ph.D. Assistant Professor Department of Biological Sciences Clemson University Clemson, SC 29634 email: vrpricha@clemson.edu Lab website: <http://www.vrprichards-lab.com> Vincent Paul Richards <vrpricha@clemson.edu>

CNRS MuseumMankind Paris AdmixturePopulationGenetics

POSTDOCTORAL POSITION in Paris, France: Population Genetics - Admixture (Human and Plant)

**

Project METHIS:

METHIS: Influence of admixture histories on the genetic evolution of hybrid populations.

The METHIS project aims to develop a novel comprehensive population-genetic framework for studying, reconstructing, and predicting how complex historical admixture processes influence genetic diversity and evolution of hybrid populations.

The post-doctorate candidate will be mainly in charge of developing (and ultimately releasing to the community) a flexible forward-in-time simulator of genome-wide genetic data, based on the mechanistic admixture models developed in Verdu and Rosenberg /Genetics/ 2011. This simulator shall be used to investigate, a priori, the evolution of genetic diversity in hybrid populations experiencing complex histories of admixture. Furthermore, *the simulator will be integrated into an Approximate Bayesian Computation framework that will be specifically adapted to infer the parameters of the historical admixture processes* that gave rise to hybrid populations, using genetic data.

*The candidate will be able to apply this new methodology to two "real life" case-studies.*First, using available genetic data, the post-doctorate candidate will be able to apply the new methodology to *reconstruct and predict the influence of admixture processes on the survival and adaptation of /Arenaria grandiflora/.* This plant species is targeted by a hybrid re-introduction program conducted since 1999 in the Fontainebleau forest to restore its nearly extinct population, and more than 600 samples gathered in 2007, 2011, 2014 and 2015 have already been genotyped to monitor the genetic diversity of the re-introduced populations.

Second, we will investigate recent histories of admixture in human populations. In particular, the post doctorate candidate will be able to apply the new simulator and ABC tools to *reconstruct, from genome-wide data,* *how variable admixture histories influenced the genomic diversity of admixed populations that arose, on different

sides of the Atlantic, during the history of European colonization and the Atlantic Slave Trade.* This case study will focus on *publically available genome-wide data *from African, European, Caribbean and American populations (including admixed Barbadian, Puerto Rican and Columbian populations), *as well as novel genome-wide data* for 400 individuals (75 are already available in the lab) *from Cape Verde* generated during the project METHIS.

**

Required abilities:

Candidates are expected to have a strong background in population genetics/genomics principles and statistical tools, as well as extensive programming skills. Ideally, candidates should have prior experience with ABC and genetic data analysis at the genome-wide scale.

Lab:

UMR7206 Eco-Anthropology and Ethno-Biology

Evolutionary Anthropology team (Dir. Evelyne Heyer and Frédéric Austerlitz)

Location: Museum of Mankind, 17 place du Trocadéro 75016 Paris (yes, offices and labs are located in the newly renovated Musée de l'Homme, and viewing the Eiffel Tower)

**

Post Doctorate Supervisor: Paul Verdu (CNRS tenured researcher)

Funding: ANR (French National Research Agency) project METHIS (PI- Paul Verdu)

Duration Post Doctorate: 2 years

Start date: 2016, to be determined with the candidate

Salary: Based on prior experience of the candidate, between 2,000 and 2,400 euros per month after taxes (net salary) and including French Social Security and Benefits.

To apply, please send your CV, the contact details of two references, and a letter describing your research interests and skills to Paul Verdu (verdu@mnhn.fr).

Paul Verdu, PhD. Chargé de Recherche CNRS / CNRS researcher CNRS/MNHN/Univ. Paris Diderot/Sorbonne Paris Cité UMR 7206 Ecoanthropology and Ethnobiology Musée de l'Homme 17, place du Trocadéro 75016 Paris France verdu@mnhn.fr <http://www.ecoanthropologie.cnrs.fr/spip.php?article203> tel: +33 1 44 05 73 17 fax: +33 1 40 79 32 31

Paul Verdu <verdu@mnhn.fr>

ColdSpringHarborLab ComputationalGenomics

Postdoctoral Positions in Computational Genomics.

Position Description: Postdoctoral positions are available in Dr. Adam Siepel's research group in its new location at the Simons Center for Quantitative Biology at Cold Spring Harbor Laboratory.

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- and NSF-supported projects in 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.

Relevant recent papers include the following:

Kuhlwilm M, Gronau I, Hubisz MJ, et al. Ancient gene flow from early modern humans into Eastern Neanderthals. *Nature*, 530(7591): 429-433, 2016.

Gulko B, Hubisz MJ, Gronau I, Siepel A. A method for calculating probabilities of fitness consequences for point mutations across the human genome. *Nat. Genet.* 47(3): 276-283, 2015.

Rasmussen MD, Hubisz MJ, Gronau I, Siepel A. Genome-wide inference of ancestral recombination graphs. *PLOS Genet.* 2014. 10(5): e1004342.

Arbiza L, Gronau I, Aksoy BA, et al. Genome-wide inference of natural selection on human transcription factor binding sites. *Nat. Genet.* 2013. 45(7):723-729.

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 phylogenetics, a serious interest in 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, matlab, 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>

CornellU EvolutionaryGenomics

Postdoctoral position in evolutionary genomics and speciation.

P.I.: Dr. Kerry Shaw, Cornell University Research Project: A postdoctoral position is available to join an NSF-funded Dimensions of Biodiversity project in the laboratory of Kerry Shaw at Cornell University to study population genomics, functional genomics of behavior, and speciation in the Hawaiian cricket genus *Laupala*. *Laupala* species are recently diverged and ecologically and morphologically similar, but differ in traits involved in sexual isolation. We seek to understand speciation and species interactions across a temporally well-characterized landscape in conjunction with on-going studies of other native arthropods by our collaborators at UC Berkeley, University of Maryland and University of Hawaii. A draft genome is available, and we seek to exploit this resource in the identification of SNPs for evolutionary inferences in these native Hawaiian insect

species.

Requirements: The desired candidate will possess an interest in / experience with molecular tools, next gen sequencing, population genetics and associated bioinformatics skills (such as basic Linux knowledge, read mapping, SNP calling). Cornell University has many labs and research groups dedicated to the study of evolution, genomics, behavior and ecology of evolutionary ecology and speciation. There is a strong community of scientists interested in the study of non-model genomics. As such, it provides a rich academic environment for those interested in training further in evolutionary genomics and speciation.

To apply, email a statement of research interests, a curriculum vitae, and the email addresses of three references to Kerry Shaw (KLS4@cornell.edu). At least two years of funding are available.

“Kerry L. Shaw” <kls4@cornell.edu>

CzechRepublic PDF PhD ClimateAdaptation

We are offering 1 postdoc and 1 PhD position to model the consequences of climate change for freshwater fish populations and fisheries at the Institute of Hydrobiology of the Biology Centre of the Czech Republic.

For details see http://www.hbu.cas.cz/en/Cds/-Download/?filename=3556-Announcement_Fellow
The deadline for applications has been extended to 16 March 2016.

Informal enquiries are welcome - please contact Prof. Jan Kubecka (kubecka@hbu.cas.cz).

David Boukal <boukal@entu.cas.cz>

Duke-NUS Singapore EvolutionDiseases

We are currently recruiting a post-doc to work with Professor Mariano Garcia-Blanco and Assistant Professor Julien Pompon in the Programme in Emerging Infectious Diseases (<https://www.duke-nus.edu.sg/content/garcia-blanco-mariano>). The group studies host factors of fla-

vivirus infection in human tissue culture and mosquitoes. The group is located in a dynamic, well-funded and well-equipped environment (<https://www.duke-nus.edu.sg/>), with access to cutting-edge genomic, transcriptomic, proteomic and insectary facilities.

We were recently awarded a Tier3 grant from the MOE of Singapore to study the saliva-assisted transmission of pathogenic viruses by blood-feeding arthropods for 4 years. The project includes experts in entomology, protein structure, immunology and mouse model from Duke-NUS, NUS, SMART, UTMB, A-Star, NIH, University of Oxford and Baylor College of Medicine. The project aims at identifying and functionally characterizing mosquito saliva at the proteomic and transcriptomic levels. In this stimulating environment, the post-doc will tackle the characterization of saliva composition and the influence of dengue and chikungunya infection on saliva-assisted transmission. The work will include entomological study, generation of transcriptomic and proteomic datasets and functional characterization of saliva proteins using functional genetics in mosquitoes as well as molecular and cell biology. The project should provide a basic understanding of how viruses hijack mosquito physiology to enhance their transmission, thereby identifying targets that could be used to develop transmission blocking strategies.

The ideal candidate will have experience in molecular entomology, functional studies and arthropod-borne diseases. The candidate should have a track record of publications, a high level of intellectual engagement and excellent problem-solving skills. The ability to work independently and generate hypotheses is essential.

Singapore is a safe, lively and stimulating country with a profound commitment to supporting cutting-edge scientific research. Salary is attractive and will depend upon experience. The position is a one-year contract renewable for up to 4 years. Only selected candidates will be invited for interview.

Please send a CV and cover letter to:

Julien.pompon@duke-nus.edu.sg

– Julien Pompon, PhD | Assistant Professor Emerging Infectious Diseases | Duke-NUS Medical School 8 College Road, Singapore 169857 | www.duke-nus.edu.sg
Julien Pompon <julien.pompon@duke-nus.edu.sg>

DukeU Epigenetics

Postdoctoral Position in Ecological Epigenetics at Duke University

A Postdoctoral Researcher is wanted to participate in an NSF funded project on the ecological epigenetics of trans-generational environmental effects in *Arabidopsis thaliana*. The project aims to examine variation in the stability of epigenetic inheritance and the conditions under which the stability of epigenetic modifications is adaptive. Methods include genome-wide methylation profiling, QTL analysis of epigenetic stability, and whole-organism phenotyping. Candidates must have demonstrated expertise in genomic data analysis and motivating interests in the genetic basis of adaptation. Experience working with plants is strongly preferred.

Available as early as 1 April 2016. Competitive salary and full Duke benefits. Duke University is an Equal Opportunity/Affirmative Action employer.

Please send CV and names and contact information for three references to Kathleen Donohue: k.donohue@duke.edu

DEADLINE FOR PRIORITY CONSIDERATION: 15 MARCH, 2016

Kathleen Donohue <k.donohue@duke.edu>

GeorgeWashingtonU Microbial-SaprobeCommunityStructure

Postdoctoral position in saprotrophic microbial community structure/function A postdoctoral position is available in the Zanne lab at George Washington University with a flexible start date. The postdoctoral scientist will work on collaborative projects related to the microbial colonization of wood. These projects include: 1. Analyzing multi-year microbial community data from an NSF-funded project in St. Louis, MO, USA, and 2. Measuring plant anatomical, morphological and chemical wood traits and characterizing fungal community composition using DNA-based and functional approaches for an Australian Research Council-funded

experiment in Sydney, Australia, in collaboration with Will Cornwell (University of New South Wales) and Jeff Powell (Western Sydney University). Possibilities also exist to work on projects examining the relative roles of microbes and termites in breaking down wood in tropical Australia. The position is one year but has the potential to be extended. The postdoc would be based at GWU located in the heart of Washington, DC, USA with easy access to numerous science-, conservation-, and policy-based institutions. However, the postdoc would spend at least 1-2 months based in Sydney and Richmond, NSW, Australia working in the Cornwell and Powell labs. Motivated applicants with skills in microbial community analyses are especially encouraged to apply. Applicants should have a PhD in a relevant field and strong writing and quantitative skills. Applications will be reviewed as received and the position will remain open until filled. Applications should include a research statement, including relevant skills for the project and future goals (max: 1-2 pages), curriculum vitae, and contact information for three references (including emails and phone numbers). Materials should be sent to Amy Zanne: aezanne@gmail.com.

Dr. Amy Zanne *Note: I am on sabbatical through August 2016, based out of: UMR BIOGECO, INRA - University of Bordeaux, Bat B2, Allée Geoffroy St-Hilaire, CS 50023, 33615 Pessac Cedex, France

Home Institution:

Department of Biological Sciences

Science and Engineering Hall

800 22nd Street NW

Suite 6000

Washington, DC 20052 Office: 6690 SEH Office Phone: (202) 994-8751 Lab: 6420 SEH Lab Phone: (202) 994-9613 Fax: (202) 994-6100 Website: <http://www.phylodiversity.net/azanne/> Amy Zanne <aezanne@gmail.com>

GeorgiaTech Evol Biol

The Paaby lab at Georgia Tech is seeking a creative and enthusiastic postdoctoral scholar in evolutionary biology, with an anticipated start date in fall 2016 or spring 2017.

Our lab explores the evolution of complex traits using genetics, molecular biology, cell biology, genomics and

field work. Our strength is using creative engineering approaches to test the functional consequences of natural genetic variation. (For more information, please visit my website: <http://genaamics.org/>.) The successful candidate will be a critical thinker pursuing research in evolutionary genetics, quantitative genetics or evo-devo and have a PhD in one of these, or a related, area.

The research project will include both experimental benchwork and computational research or analysis and will be defined jointly by the postdoc and myself, Annalise Paaby. The project could originate entirely from the candidate, from an existing project in the lab (which currently includes research in *C. elegans* and related *Caenorhabditis* species), or it could be something in between. The postdoc will be free to develop an independent research program with the support and expertise of the lab.

WHY GEORGIA TECH?

The School of Biology at Georgia Tech is a medium-sized department with an outstanding group of evolutionary biologists. We include at least seven highly interactive labs with a primary focus on the genetic basis of evolutionary dynamics, and additional labs using computational approaches in evolutionary genomics or field- and lab-based approaches in ecological genetics. Located within a world-class engineering institute, we have truly unique opportunities for collaboration, especially for experimental model systems.

WHY ATLANTA?

Atlanta is a lush, green city with loads of restaurants and great quality of life. The city offers all the perks of a major metropolis but is affordable. The North Georgia mountains are only an hour's drive and the region includes some of the most beautiful outdoor landscapes on the east coast.

WHY THE PAABY LAB?

My lab is new (established fall 2015) and what I can't yet offer in reputation I aim to make up for as an engaged colleague! I am committed to working productively with all members of my lab and I enjoy opportunities to mentor the development of independent researchers.

HOW DO YOU PRONOUNCE PAABY?

It's "poe-bee".

WANT TO APPLY?

The most important criterion of the successful candidate is demonstrated enthusiasm and aptitude for scholarship in evolutionary biology. If this sounds like you, please send me (annalise.paaby@biology.gatech.edu) a combined PDF of your CV and a short cover letter that

includes the email addresses of three references and very, very brief info on:

- the topic of your dissertation research and current research (if any) - topics you'd like to pursue as a postdoc and why - ideal start date - microscopy experience and skills (if any) - coding experience and skills (if any) - any questions you may have!

Annalise Paaby Assistant Professor School of Biology Georgia Institute of Technology

website: genaamics.org

"annalise.paaby@biology.gatech.edu"

GhentU ComparativeGenomics

Postdoc position in Evolutionary and Comparative Genomics *Job description*

A two year postdoctoral position is available in the Van de Peer lab in the Department of Plant Systems Biology (VIB), Bioinformatics Institute Ghent N2N (BIG N2N), Ghent University, starting August 1st 2016.

Our research group is considered a center of excellence in gene prediction and genome annotation, and comparative and evolutionary genomics. We are currently looking for someone to strengthen our genome annotation and genome analysis team, in particular someone to work on the comparative analysis of mites, of which many are important pests for plants. Amongst other things, we want to unravel the genetic/genomic cause for specific adaptations linked to lifestyle and herbivory. You will also be involved in the study of gene and genome duplications, another major interest of the research group.

Required Qualifications

The ideal candidate holds a PhD degree in a relevant field (or equivalent through experience), is highly interested, ambitious, curiosity-driven and likes interdisciplinary work. He/she will need to interact productively with evolutionary biologists, genome biologists and computer scientists. Further requirements include a strong bioinformatics background and deep interest in evolutionary and comparative biology. Programming/scripting experience (e.g., Perl, Python, R,) and experience working in a Linux environment are essential. The project will make extensive use of RNA-seq and genomic data sets (using data from Illumina and PacBio platforms). Therefore, a background in genomic, tran-

scriptomic and/or epigenetic research and experience in evolutionary and/or comparative genomics would be ideal. Since English is the working language of the laboratory and the institute, excellent English communication skills are imperative.

Working environment

The successful candidate will work in the Department of Plant Systems Biology (VIB) at Ghent University. VIB and BIG N2N (<http://www.bign2n.ugent.be/>) offer a supportive and stimulating environment, with access to excellent computer and academic facilities. The Van de Peer lab is a computational group and consists of a mix of molecular and evolutionary biologists and computer scientists. More information on our research and research topics can be found at <http://-bioinformatics.psb.ugent.be/> . *Contact details*

To apply, please send a single document including a letter of motivation describing your research motivation and experience, a detailed CV with a list of publications, and contact details for at least two referees to yves.vandeppeer@psb.ugent.be.

Yves Van de Peer, PhD.

Professor, Department of Plant Biotechnology and Bioinformatics, Ghent University Group Leader, Department of Plant Systems Biology, VIB Technologiepark 927 B-9052 Ghent Belgium

Phone: +32 (0)9 331 3807 Cell Phone: +32 (0)476 560 091 Fax: +32 (0)9 331 3809 email: yves.vandeppeer@psb.vib-ugent.be

<http://bioinformatics.psb.ugent.be/> <http://-www.nucleotides2networks.be/> <http://-www.plantgenomeevolution.com/> Part-time Professor at the Genomics Research Institute, Department of Genetics, Pretoria, South Africa

Yves Van de Peer <yves.vandeppeer@psb.vib-ugent.be>

HobartWilliamSmithColleges MilkweedPhylogenomics

POSTDOCTORAL POSITION IN MILKWEED PHYLOGENOMICS

An NSF-funded postdoctoral position investigating milkweed (*Asclepias*) phylogenomics is available in the Straub Lab at Hobart and William Smith Colleges in

Geneva, New York. The diversity of *Asclepias* in North America is the product of a recent, rapid evolutionary radiation. Because milkweed species diversified over a short evolutionary time span, reconstructing their evolutionary relationships requires genome-scale data. Targeted sequencing of the nuclear genome of *Asclepias* combined with sampling of many individuals per species will allow us to distinguish common causes of gene tree discordance: incomplete lineage sorting and introgression. The postdoc on this project will be responsible for 1) performing targeted sequencing of the *Asclepias* nuclear genome, 2) phylogenomic analyses, 3) manuscript preparation, and 4) public outreach. This research will be conducted in collaboration with Dr. Mark Fishbein at Oklahoma State University.

Required Qualifications:

- Ph.D. in plant systematics, evolution, genomics, bioinformatics or related discipline
- Background in phylogenetics
- Strong record of publication
- Strong organizational, oral, and written communication skills

Desired Qualifications:

- Strong computational skills, including knowledge of one or more programming languages (Python, Perl, R/BioConductor etc.)
- Laboratory skills for preparation of Illumina libraries
- Experience with analysis of NGS data

The initial appointment will be for one year with the possibility of renewal for a second year contingent on satisfactory performance. The start date for this position is flexible with a latest start date of September 1, 2016. Salary is commensurate with experience and the position is benefits eligible.

Applications should be submitted through Interfolio <https://apply.interfolio.com/30948> and consist of 1) a cover letter describing the candidate's research interests and experience, 2) a CV, and 3) the names and contact information for three references. Questions about the position should be directed to Shannon Straub at straub@hws.edu. Review of applications will begin on April 15, 2016 and continue until the position is filled. EOE?

“STRAUB@hws.edu” <STRAUB@hws.edu>

IndianaU Bloomington 3 EvoDevo

THREE POSTDOC POSITIONS IN EVO DEVO AND ECO DEVO OF HORNED BEETLES

(Moczek-Lab, Indiana University, Bloomington)

Three (3) full-time postdoctoral positions are available in Armin Moczek's lab, Department of Biology, Indiana University, Bloomington. Our lab conducts research in the evolutionary developmental (evo-devo) and ecological developmental (eco-devo) biology of insects. We focus on the genetic, developmental, and ecological mechanisms, and their interactions, that mediate the origins and diversification of novel complex traits (such as beetle horns, firefly lanterns, or treehopper helmets) and functions (such as nutrition-responsive development, sexual dimorphisms, or alternative reproductive tactics).

The first position will focus on identifying the genes and pathways underlying the origin and diversification of horns in the extraordinarily diverse beetle genus *Onthophagus*. Specifically, the work will use genomic and candidate-gene approaches to identify and functionally characterize the developmental-genetic mechanisms that regulate horn morphology (size, shape, position), context-dependent expression of horns (sex- and nutrition-specificity), and how evolutionary changes in these mechanisms have mediated diversification within and among species.

The second position will utilize diverse horned beetle species and populations to explore the role of developmental plasticity in facilitating, biasing, or hindering phenotypic evolution. Focusing on morphological and physiological phenotypes, this work will combine genomic, transcriptomic, and candidate-pathway approaches to contrast ancestral and descendant patterns of gene expression and function in natural as well as mesocosm populations.

The third position will explore the relative significances of - and interactions among - the horned beetle microbiome, niche construction behaviors, and nematode symbionts in the ecological radiation of horned beetles. This work will combine genomic, transcriptomic, and candidate-pathway approaches in both beetles and nematodes to characterize the role of co-development in the ecology and evolution of dung beetles, and the developmental mechanisms and evolutionary consequences of interspecific epistasis.

All postdoctoral candidates would have opportunities to develop additional independent lines of research in these and related areas.

We seek three collegial, self-motivated, independent, and intellectually curious individuals with recent PhDs in Evolutionary Biology, Developmental Biology, or related fields. Applicants for either position must have strong bench skills, and familiarity with techniques such as RNA interference, qPCR, cloning, immunohistochemistry, and the bioinformatic analyses of next-gen sequencing data is strongly desirable (though training in these techniques will also be provided as necessary). In addition, candidates must have demonstrated written and oral communication skills. Experience working with insects is helpful but not required. All three positions are initially available for 24 months, with possible extension for a third year funds permitting. Salary will be commensurate with experience, and full benefits are included.

Indiana University has a large and interactive group at the interface of evolutionary and developmental biology and ecology. Bloomington is situated in scenic, hilly southern Indiana, near several parks and wilderness areas. The cultural environment provided by the University is exceptionally rich in art, music, and theater.

To apply, please submit a letter of application indicating which position is being applied for, a CV, a statement of research interests, and the contact information for three references to <https://indiana.peopleadmin.com/postings/2277> or send to Jeremy Bennett, 1001 E. Third St., Bloomington, IN 47405 (jebennet@indiana.edu). Review of applications will start immediately and will continue until positions are filled. Preferred start date is July '16 (position #1) and September '16 (positions #2,3) though some flexibility exists. Inquiries about each position can be directed to Armin Moczek (armin@indiana.edu). Additional information about research in the Moczek lab can be found at <http://ecoevodevo.com/>. 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.

Armin P. Moczek Professor of Biology, Indiana University Associate Chair for Teaching <http://ecoevodevo.com/> “Moczek, Armin P” <armin@indiana.edu>

IowaStateU EvolutionaryEcol2

A Postdoctoral Research Associate position is available in the laboratory of Fredric Janzen to help lead NSF-funded projects examining the roles of climate, maternal effects, and sex-specific fitness in the evolutionary ecology of environmental sex determination, focusing on the painted turtle. The goal is to explore how these major factors affect population dynamics and sex-ratio evolution in nature. This now 28-year study involves observational and experimental research at (1) a primary field site (Turtle Camp) along the Mississippi River near Clinton, IA, (2) a network of additional sites across North America, and (3) Iowa State University in Ames, IA. The postdoc will be central to most aspects of the projects and thus strong mentoring, communication, writing, and analytical/modeling skills are essential. In addition to facilitating goals of the overarching projects, the successful candidate will be strongly encouraged to develop her/his own independent research. The ideal applicant should have solid experience in field biology, experimental design, climate and demographic databases, and evo-eco modeling, plus a strong background in ecology, evolution, and statistics.

A Ph.D. in ecology or evolutionary biology is necessary. Current funding for the position is available for two years, with annual renewal contingent on performance, emphasizing progress on teamwork, data collation and analysis, modeling, and writing. The successful candidate must be available no later than 1 July 2016. Up to 1 month annually may be spent at Turtle Camp (<http://www.public.iastate.edu/~fjanzen>), but the primary location for the postdoc will be at Iowa State University, where data analysis, modeling, and writing manuscripts will be emphasized.

Examples of recent publications related to these projects include: 1) Refsnider & Janzen (2016) *J Hered* 107:61-70. 2) Schwanz et al. (2016) *Evolution* 70:329-341. 3) Mitchell et al. (2015) *Funct Ecol* 29:268-276. 4) Refsnider et al. (2014) *Evol Ecol* 28:977-989. 5) Spencer & Janzen (2014) *Proc R Soc Lond B* 281:10.1098/rsbl.2014.0831. 6) Mitchell et al. (2013) *Proc R Soc Lond B* 280:10.1098/rspb.2013.2460. 7) Telemeco et al. (2013) *Am Nat* 181:637-648.

To apply, e-mail Fredric Janzen (fjanzen@iastate.edu) with (1) a brief (< 1 page) cover letter explaining your research interests, (2) a CV, and (3) contact informa-

tion for three references. Review of applicants will begin immediately and end on 31 March 2016, shortly after which a suitable candidate will be selected.

“fjanzen@iastate.edu” <fjanzen@iastate.edu>

IowaStateU EvolutionaryEcology

A Postdoctoral Research Associate position is available in the laboratory of Fredric Janzen to help lead NSF-funded projects examining the roles of climate, maternal effects, and sex-specific fitness in the evolutionary ecology of environmental sex determination, focusing on the painted turtle. The goal is to explore how these major factors affect population dynamics and sex-ratio evolution in nature. This now 28-year study involves observational and experimental research at (1) a primary field site (Turtle Camp) along the Mississippi River near Clinton, IA, (2) a network of additional sites across North America, and (3) Iowa State University in Ames, IA. The postdoc will be central to most aspects of the projects and thus strong mentoring, communication, writing, and analytical/modeling skills are essential. In addition to facilitating goals of the overarching projects, the successful candidate will be strongly encouraged to develop her/his own independent research. The ideal applicant should have solid experience in field biology, experimental design, climate and demographic databases, and evo-eco modeling, plus a strong background in ecology, evolution, and statistics.

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Telemeco et al. (2013) *Am Nat* 181:637-648.

To apply, e-mail Fredric Janzen (fjanzen@iastate.edu) with (1) a brief (< 1 page) cover letter explaining your research interests, (2) a CV, and (3) contact information for three references. Review of applicants will begin immediately and end on 31 March 2016, shortly after which a suitable candidate will be selected.

“fjanzen@iastate.edu” <fjanzen@iastate.edu>

Ireland ViralBioinformatics

Hi all, The lab of professor Colin Hill has a two year post-doctoral position available within the APC Microbiome Institute working in the area of bioinformatics of the gut phageome.

Position Summary The APC Microbiome Institute is a trans-disciplinary research centre, with clinicians, clinician-scientists and basic scientists from diverse backgrounds working in teams, sharing ideas and resources. Although focused upon the gastrointestinal bacterial community (the microbiota), the scale and scope of the work has become one of the fastest moving areas of biology. The microbiota is not only a target for treatment and prevention of disease, it is a repository for functional food ingredients and even new drugs and is a source of novel biomarkers of disease risk. The scientific organisation of the APC consists of a matrix of ‘spokes’ or themes of intellectual pursuit which are supported by multiple horizontal or shared technology platforms. This position is within APC’s Gut Phageomics Laboratory, consisting of up to 20 researchers investigating the role of the gut phageome in health and disease. The Post-Doctoral Researcher will have a role in the GUTPHAGE project and will preferably have a PhD in bioinformatics and/or biostatistics, and proven ability to conduct independent research to a very high level.

Salary: €33,975 - 42,394 **Post Duration:** 2 years
Project title: Gut Phageomics (Unique ID SE2)

Key Duties and Responsibilities This title will apply to newly qualified Post-Doctoral Researchers and will be considered as a period of training as the researcher will have dual goals in terms of the research project and their own career development. The researcher will be mentored by a Principal Investigator (PI). It is expected that a researcher would spend not more than 3 years at the Post Doctoral level, subject to the term of the project and would then be eligible to compete for

a Senior Post Doctoral post advertised by the University. The primary focus of the Postdoctoral Researcher will be research however a particular emphasis during this stage should include; - To conduct a specified programme of research under the supervision and direction of a Principal Investigator/Project Leader. - To engage in appropriate training and professional development opportunities as required by the Principal Investigator, School or College in order to develop research skills and competencies. - To gain experience in grant writing. - To engage in the dissemination of the results of the research in which they are engaged, as directed by, with the support of and under the supervision of a Principal Investigator. - To become familiar with the publication process. - To acquire generic and transferable skills (including project management, business skills and post-graduate mentoring/supervision). - To engage in the wider research and scholarly activities of the research group, School or College. - To interact closely with postgraduate research students who are studying for a Masters or a PhD and possibly have an agreed role in supporting these students in their day to day research in conjunction with an academic supervisor. - To carry out administrative work to support the programme of research. - To carry out additional duties as may reasonably be required within the general scope and level of the post. - To contribute to costing research grant proposals and assist in the financial management of a research project.

Criteria

- A PhD qualification in bioinformatics and/or biostatistics. - Appropriate research experience. - Appropriate technical competence and accomplishment. - A capability of working within a project team to achieve results. - Good communication, organisation and interpersonal skills. - A commitment to gaining practical experience working on a research project. - Ability to work well within a team.

For Informal Enquiries on the post candidates should contact: Name: Prof Colin Hill Title Professor of Microbial Food, Principal Investigator APC Microbiome Institute Email Address: Ac.hill@ucc.ie Telephone: +353 21 4901373

To Apply: Please submit a short cover letter quoting the UNIQUE ID SE2, your C.V and the contacts of at least two referees. to Grainne Heelan, APC Microbiome Institute, University College Cork, Cork, Ireland. apc.administrator@ucc.ie, +353 21 4901430, on or before the closing date 6th April 2016. Supplementary Information on the Department/Research Centre and the post is available at the following URL: <http://apc.ucc.ie>
Angela McCann <angie_red2000@yahoo.co.uk>

Kiel Evolutionary Genomics

Postdoc Position on Evolutionary Genomics

Basic Information

Postdoctoral Scientist position for 6 years, starting date 1 July 2016 or soon thereafter, salary at level TV-L E14

Area of Work

Up-to-date research work on genome evolution - with a focus on either antibiotic resistance evolution or the evolution of *C. elegans*-microbe-interactions. Within the 6-years-time frame, an innovative research program in one of these fields shall be developed. In addition, contributions to the teaching activities of the Schulenburg group within the fields of evolutionary ecology, biostatistics, and/or genomics at both Bachelor- and Master-level (four hours per week).

Expectations and Requirements

University degree and PhD in the general area of evolutionary genomics with one of the above listed foci. Experience in the independent performance of research in these areas (e.g., based on a first postdoc project). Excellent knowledge of genome analysis, including population genetics. High competence in English. Ideally, experience in teaching students, supervision of BSc and MSc projects, experience in procurement of third-party funding, and international experience(s) (e.g., postdoc outside of Germany). Kiel University aims at a higher proportion of women in research and education, and, therefore, specifically encourages qualified female scientists to apply. Female scientists will be preferentially considered in case of equivalent qualification, competence and achievements. Kiel University specifically supports employment of severely handicapped people. Therefore, severely handicapped applicants will be preferentially considered in case of suitable qualification. Kiel University specifically welcomes application from people with migration background.

Location

The position will be based in the Schulenburg group at the University of Kiel, Northern Germany. The department provides an international and interactive atmosphere, while Kiel University and connected institutes (e.g., Max Planck Institute in Ploen) offer a stimulating research environment with a particular focus on evolutionary biology and also *C. elegans* genetics. The city

of Kiel is a medium-sized town located at the coast of the Baltic Sea. It is the capital of the most Northern state of Germany, Schleswig-Holstein. It offers many opportunities for leisure activities, including theatres, an opera, the Schleswig-Holstein classical music festival, the heavy metal festival in Wacken, sailing, surfing, cycling, and the famous festivities of the “Kieler Woche” - one of the largest sailing events in Europe.

Applications

Applications should include a motivation letter (max. 2 pages long), CV, publication list, names and contact details of two referees (who are familiar with the applicant’s work), and copies of certificates. Deadline for applications is 08.04.2016. Applications should be sent as a single pdf-document by Email to Hinrich Schulenburg (hschulenburg@zoologie.uni-kiel.de).

Deadline for applications

8 April 2016

Further questions

Send an Email to Hinrich Schulenburg (hschulenburg@zoologie.uni-kiel.de).

Hinrich Schulenburg

Zoological Institute Christian-Albrechts-Universitaet zu Kiel Am Botanischen Garten 1-9 24118 Kiel Germany Tel: +49-431-880-4143/4141 Fax: +49-431-880-2403 Email: hschulenburg@zoologie.uni-kiel.de Web: www.uni-kiel.de/zoologie/evocogen/ Hinrich Schulenburg <hschulenburg@zoologie.uni-kiel.de>

LinkopingUSweden EvolutionOfPersonality

Postdoc required for research on the mechanisms underlying variation in animal personality

Job description:

Dr. Hanne LÅvlie, Linköping University (IFM Biology), is looking to recruit a strong postdoctoral candidate in evolutionary biology. The job description primarily entails analysing and writing up existing data on the underlying mechanisms of variation in personality in the 3-spine stickleback, together with developing further research on the same topic.

Animal personality (i.e. consistent individual behavioural responses), has recently received considerable

research attention. Despite this, fundamental questions remain unanswered, such as why variation in personality arises, and how polymorphism is maintained?

The postdoc will have access to existing data on brain physiology, and gene expression exploring the role of the brain monoaminergic systems (i.e. serotonin and dopamine) underlying variation in personality. The stickleback is a particularly suitable species to investigate personality because of the potential to combine existing understanding of behaviour, physiology and genetics, with the application of a strong experimental design. However, the topic of the project is relatively flexible and can be tailored to fit the skills and interests of the successful candidate. The project is in collaboration with Professor Svante Winberg (Uppsala University).

Requirements:

The successful applicant will be a highly motivated and well-merited candidate with a PhD and potentially also postdoc experience in evolutionary biology, behavioural ecology, neurobiology or similar. Research experience in experimental animal behaviour, good statistical knowledge and analytical ability are merits, as is strong experience in scientific writing. Very good knowledge of written and oral English is required. Both good cooperation skills and the ability to work independently are emphasised. Experience of fish as model is also beneficial.

What we offer:

Linköping University is a modern university with a vibrant and growing biology division. A major research focus at the biology division is animal behaviour, including behavioural genetics and genomics. Linköping is located in central Sweden, only a couple of hours from several other university cities, such as Stockholm, Uppsala and Lund.

Opportunities to gain experience in the supervision of students and other teaching is possible, but not required.

Start date:

Suggested starting date is 1st of June 2016, but this is flexible.

Funding:

According to present rates at the university, postdoc stipends (where no tax will be deducted) are 25 000 SEK per month. The stipend does not give entitlement to sickness benefit, parental allowance, holiday pay or pension. Funding is so far secured for the start up of the project and 50% of the stipend for a period of 2 years. The suitable candidate will apply together with Dr LÅvlie for the remaining funding, with suitable

opportunities available already from 15/4.

Application procedure:

The application should include a 1-2 page cover letter describing your research experience and interests, and your interest in the project, and a full CV (including name and contact details of 2 references who are willing to provide letters of support). The application should be sent as a single PDF to hanne.lovlie@liu.se. The position is open until filled, and applications will be reviewed continuously, but for full consideration please apply before 31st of March 2016.

Contact:

Associate professor Hanne LÅvlie (hanne.lovlie@liu.se), tel +46 (0) 13-286681. <https://www.liu.se/forskning/-foass/hanne-lovlie?l=en&sc=true> Hanne LÅvlie, Associate professor IFM Biology AVIAN Behavioural Genomics and Physiology Group Linköping University 58183 Linköping SWEDEN <http://www.liu.se/forskning/foass/hanne-lovlie?l=en> Hanne Lovlie <hanne.lovlie@liu.se>

Liverpool MosquitoResistanceEvolution

Post-Doctoral Research Associate

We are seeking to appoint an Post-Doctoral Research Associate who will work with Professor Martin Donnelly < <http://lstm-centre.mrmdev.co.uk/about/-people/professor-martin-james-donnelly> > and Dr David Weetman < <http://lstm-centre.mrmdev.co.uk/about/-people/dr-david-weetman> > on the evolutionary genomics of insecticide resistance in the malaria vector *Anopheles gambiae*. It is essential that the successful candidate holds a PhD in Biology or related fields and can demonstrate skills in any or all of the following:

* Molecular biology laboratory skills * Molecular genetics analytical skills * Experience in the design and execution of genomic and transcriptomic studies.

Ref: 088

We are looking for an individual with excellent communication skills (both written and verbal), well developed research and analytical skills, plus the ability to work as an integral and co-operative member of a multi-disciplinary research team. For appointment, you must be prepared to travel to Africa to assist with design and implementation of field collections and to provide

support to post-graduate researchers.

If you are interested in applying, please return your completed Application Form, Personal Details Form and Equal Opportunities Monitoring Form, stating vacancy reference number (088), via email to jobs@lstm.ac.uk, or by post to HR, Liverpool School of Tropical Medicine, Pembroke Place, Liverpool L3 5QA. Please note CVs will not be accepted unless accompanied by a fully completed application form. More details at <http://www.lstm.ac.uk/post-doctoral-research-associate> Please get in touch by email with Martin and David if you would like to discuss the position before applying.

Closing Date for completed applications: 20 April 2016, 12.00pm UK Time

Martin James Donnelly

Professor of Evolutionary Genetics Department of Vector Biology Malaria Programme Liverpool School of Tropical Medicine & Wellcome Trust Sanger Institute Pembroke Place Hinxtton Liverpool Cambridge L3 5QA CB10 1SJ Tel +44(0) 151 705 3296 Fax +44(0) 151 705 3369 Email martin.donnelly@lstm.ac.uk Web <http://donnelly.openwetware.org/Home.html> Skype martin-donnelly; Orcid 0000-0001-5218-1497

Martin Donnelly <Martin.Donnelly@lstm.ac.uk>

Montpellier MosquitoMatingBehaviour

Postdoctoral position for a Bio-engineer on insect acoustic behavior in malaria mosquitoes

A 2 year postdoctoral position in insect acoustic behaviour is available within the Anofeel project funded by the French Agence Nationale de la Recherche (ANR) and hosted by the Research Institute for Development (IRD, Mivegec Lab, Montpellier, France), in collaboration with the IRSS (Bobo-Dioulasso, Burkina Faso) and the NRI (Greenwich University, Kent, UK). The Anofeel project aims at investigating the mating behavior of malaria mosquitoes using state-of-the-art synchronized 3D video and audio recording devices.

Scientific context: Malarial mosquitoes are the most dangerous animal on Earth; they kill more humans than any other animal. Prof. G. Gibson at the NRI and colleagues at the University of Brighton have discovered that mosquitoes use acoustic cues in a unique way to identify and locate mates. The aim of the project is to

discover how this novel behavior might be exploited to control or even eradicate these deadly insects. For example, the development of sterile male release strategies to control mosquito populations highlights the necessity of producing competitive males which will require a detailed analysis of their acoustic capabilities. The findings of the project will also be used to develop new control and monitoring strategies.

Observing mating behavior is technically challenging, as it occurs in mid-flight within a volume $\sim 1 \text{ m}^3$ and in virtual darkness. Prof. Gibson has developed a recording studio designed to mimic the natural lighting and atmospheric conditions mosquitoes encounter during mating flights, and instrumented the space with 3D video recording and high-quality acoustic recording to document every stage of mating behavior. An experienced bio-engineer is required to operate the equipment, to design and construct modifications as required for this project and to write code for capturing and analyzing the video and audio recordings. The Post doc will also be required to set up similar equipment at the IRSS research centre in Burkina Faso, West Africa to build capacity in the field for similar experiments where there is access to wild populations of mosquitoes.

The postdoc fellow will work on acoustic cues emitted by males swarm at the NRI under Prof. Gabriella Gibson's supervision. She/He will conduct the following studies:

- i- Characterise male swarms; record the flight paths of individual mosquitoes in 3D and the simultaneous sounds they emit by their flight-tones.
- ii- Determine the distance of attraction to swarms for males and females.
- iii- Test the effects of pure tones within the range of male and female flight-tones to determine whether pure sounds can trigger similar responses.
- iv- If it can be shown that mosquitoes hear swarms, arrangements will be made with the University of Brighton to conduct key investigations of the sensory physiology underlying this acoustic behavior.
- v- The Postdoc will be expected to contribute to the maintenance of the equipment related to the project and assist with rearing the mosquitoes used in the project.
- vi- The Postdoc will make one - two field trips to Burkina Faso to test for biological activity of recorded sounds in semi-field and field conditions and to assist with setting up a swarming studio equipped with 3D video recording for use by co-PIs on other tasks of the project.

This project is highly challenging, so we are looking for a highly motivated and independent candidate able to think 'out of the box'. A strong background in bio-engineering and programming, preferably in Java, is essential. A background in acoustics and neurophysiology would be desirable, but not essential. The project will require construction of experimental arenas, so ex-

perience and enthusiasm for basic building activities is highly recommended. Gross monthly salary will be between 2150-2500 euro according experience (Net salary of 1700-2000 euro). This salary includes French health insurance, retirement contribution and other social security contributions, but not income tax.

The Natural Resources Institute (NRI) of the University of Greenwich is located on the Medway Campus of the Greenwich University in UK. NRI's mission is to discover, apply and share knowledge in support of global food security, sustainable development and poverty reduction. To apply, please send an email to both Olivier Roux (project PI: olivier.roux@ird.fr) and Gabriella Gibson (Task leader: g.gibson@gre.ac.uk) which includes (all in a single PDF file): - your research interests (including why you are specifically interested in working on this project), - research experience, - CV, - degree certificates - complete contact information for at least two references .

The position will start in April 2016 but is open until filled.

Olivier ROUX Institut de Recherche pour le Développement MIVEGEC (IRD 224-CNRS 5290-NUM)

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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>

MPI Cologne PopulationGenomics

Postdoc position in Population (epi)Genomics

We seek a highly motivated and curiosity-driven individual to join our Evolutionary Genomics research group.

Project Title: Reconstructing the history of epigenetic divergence and transposon activity in Macaronesian Arabidopsis

Location: Max Planck Institute of Plant Breeding Research (MPIPZ), Cologne, Germany

Project Description: Large-scale structural variation mediated by transposons and epigenetic variation may enhance adaptive potential and underlie episodes of rapid adaptation in nature. Arabidopsis thaliana is widespread across Eurasia, but is also found in other

locations worldwide. The population from Cape Verde has been especially intriguing because of the extreme climate, which is defined by a long and severe dry season. Only a single strain has been available from this region, but based on years of study, we know this strain is divergent from other strains for a broad range of organismal phenotypes. It is therefore particularly interesting that this accession is also divergent for methylation and heterochromatin phenotypes and suggests a possible link between phenotypic and epigenetic divergence.

The goal of this project is to retrace the evolutionary history of epigenetic divergence of Cape Verde Arabidopsis and identify associated organismal phenotypes. This project will make use of RNA-seq, bs-seq and genomic data sets (using data from Illumina and PacBio platforms) and phenotypic data generated in our lab.

Research Environment: Research in the Hancock Lab is funded by the European Research Council (ERC) and Max Planck Institute (MPI) and focuses on understanding the molecular basis of evolutionary processes. For more information about work in the lab, see <http://www.mpipz.mpg.de/hancock>. Our research group is housed within the Max Planck Institute of Plant Breeding Research (MPIPZ), a world-class research center, located in the Green Belt' of Cologne, Germany. The Institute houses 25 research groups, its own Genome Center with cutting-edge PacBio and Illumina sequencing capabilities, Mass-Spec facility, Biomolecule Screening Center and Central Microscopy Center.

The MPIPZ is part of a larger network of plant and evolutionary biologists from the University of Cologne and Heinrich Heine University in Düsseldorf, and it is a member of (CEPLAS), a regional cluster of excellence in the area of molecular plant science.

Required Qualifications and Application Instructions:

Preference will be given to candidates with programming/scripting experience (e.g., Python, R) and experience working in a Linux environment with NGS data or other large data sets. Previous background in genomic, transcriptomic and/or epigenetic research would be ideal. English is the working language of the laboratory and the institute, so excellent communication skills in English are imperative.

The position is for two years with the possibility of extension, and salary and benefits are in accordance with the German TVöD scale, based on qualifications and previous experience. 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. The Max-Planck society is committed to increasing the number of individuals with disabilities

in its workforce and therefore encourages applications from such qualified individuals.

To apply, please send a letter of motivation describing your reasons for applying to the position, CV, transcripts and contact details for at least two references. All materials should be sent in English and in a single file to hancock@mpipz.mpg.de

Review of applications will begin April 1 and will continue until a suitable candidate is found.

Angela Hancock <angela.m.hancock@gmail.com>

NewYorkU PlantSystemsBiol

Post-doctoral Position in Plant Systems Biology

Project: NSF - NutriNet: A network inspired approach to improving NUE in crops.

New York University Center for Genomics and Systems Biology

A post-doctoral position at NYU's Center for Genomics and Systems Biology - in the laboratory of Dr. Gloria Coruzzi - is available as part of our NSF Plant Genome Grant entitled: NutriNet: A network inspired approach to improving Nutrient Use Efficiency (NUE) in crop plants.

The successful applicant will have skills and experience in Plant Biology and Genomics. The position will require experimental skills for the generation of -omics datasets such as DNA/RNA isolation, Next-gen sequencing library construction, plant growth (Arabidopsis and Maize) etc. Additionally, working knowledge of R, Python or other programming language is highly desirable. This position also includes Project Management duties, which involve coordinating scientific activities at two participating institutions; organizing group meetings, writing grant reports, paper writing and communicating our work in conferences and meetings.

This project involves the collaboration three institutions. PI: Gloria Coruzzi (PI), NYU, Center for Genomics & Systems Biology (plant genomics); Dennis Shasha (co-PI) NYU, Courant Institute of Mathematical Sciences (bioinformatics); & Stephen Moose (co-PI) U. Illinois, Urbana-Champaign (maize functional genomics).

Overview: Recent advances in genome sequencing, functional genomics, and computational tools enable a systems-level understanding of key physiological and

developmental processes in the model plant *Arabidopsis*, but translating this knowledge to enhancing agriculturally important phenotypes in crop species remains challenging. The goal of our NutriNet project is to develop network-connected modules in crops- exploiting *Arabidopsis* network knowledge - that are predictive of phenotypic variation and enhance the efficiency of genetic gain in crop species, using nutrient use efficiency (NUE) of maize as the target trait. Four aims are proposed to achieve these goals. First, new and existing data for nutrient-responsive gene expression profiles will be integrated with phenotypic variation for NUE to develop a training set that exploits the power of genetic diversity from both *Arabidopsis* (Coruzzi, NYU) and maize (Moose, Illinois). Second, a split-root experimental design combined with RNASeq (Coruzzi) will identify *Arabidopsis* and maize genes that function in root-shoot N-signaling and that control root foraging for nutrients. The third aim is to construct the NutriNet for maize (Coruzzi/Shasha, NYU), which will be combined with *Arabidopsis* network knowledge to define network modules predictive of NUE traits. NutriNet modules will be validated using 'left-out data' and tests of predictive ability in genotypes outside of the initial training set. Finally, information derived from NutriNet modules will be used to select individual genotypes that possess optimal NutriNet configurations from diverse germplasm pools, which will then be evaluated for improved NUE traits in the lab (*Arabidopsis*) and field (maize). A comparative analysis of lab-to-field results will directly assess the translation of knowledge from *Arabidopsis* to cereal crops.

Application: Please send cover letter, resume and 3 letters of reference by email to: coruzzi.lab.nyu@gmail.com.

Please mark the subject line of your e-mail: NutriNet Post-doc

Applications received by April 15, 2016 will receive full consideration for the position.

The Coruzzi lab

Coruzzi lab web page: <http://coruzzilab.bio.nyu.edu/>
 Coruzzi Biology Faculty web page: <http://biology.as.nyu.edu/object/GloriaCoruzzi.html> The Coruzzi lab is located in the historic and vibrant Greenwich Village in downtown Manhattan in New York City. NYU is one of the world's leading research universities and its Center for Genomics and Systems Biology is housed in a new, state-of-the-art facility with 14 faculty members who study Genomics and Systems Biology across all six kingdoms of life. For more information on our Genome Center, please go to: <http://cgsb.as.nyu.edu> Coruzzi Lab

New York University Center for Genomics and Systems Biology

12 Waverly Place, New York, NY 10003

Amanda Heim <amanda.heim@nyu.edu>

NTUSingapore HumanEvolutionaryGenomics

The lab of Irene Gallego Romero (<http://www.ntu.edu.sg/home/igr>) at Nanyang Technological University in Singapore is seeking a self-motivated and enthusiastic postdoctoral scholar to work on any of a number of projects aimed at deciphering the role of gene regulation in human evolution, be that at the inter-species or inter-population level. The lab combines the flexibility of induced pluripotent stem cells (iPSCs) with genomic approaches to address questions about the mechanisms of evolutionary adaptation in humans that are intractable by any other means, and the majority of projects in the lab incorporate aspects of both experimental cell culture and genomics data analysis. As such, applicants will be expected to contribute to both wet and dry laboratory aspects of their project.

The ideal candidate will have an established publication record, as well as previous experience with both cell culture (not necessarily iPSCs) and the analysis of genomic or transcriptomic data. Applicants with limited wet lab or cell culture experience will also be considered if they have a demonstrable expertise in genomics. They will have the opportunity to join a young and active research group and to collaborate with local institutions such as the Lee Kong Chian Natural History Museum or the Singapore Zoo, as well as with local groups based at the Genome Institute of Singapore (A*STAR) and elsewhere.

The position can start at any point between July 1st, 2016 and Jan 1st, 2017, includes attractive compensation and benefits and will be reviewed on an annual basis, with a maximum length of three years. All applicants must hold a PhD degree or have completed all of the requirements necessary for one at the time of appointment.

To apply, please email the following items to Dr Gallego Romero (igr@ntu.edu.sg): 1. a cover letter 2. a CV, including the names, phone numbers and email addresses of three referees 3. up to three of their publications

Any informal enquiries or questions may be sent to the same address.

igr@ntu.edu.sg

Okinawa BeeEvolution

We are looking for a motivated postdoc or technician to join a fully funded multi-disciplinary project investigating quantitative genetics of bee behavior. The overall goal is to understand quantitative trait loci involved in the bee dance language using a backcross design between two different subspecies. Having done dance, we will then wish to tackle other more complex behaviors. This project involves computer vision, bee behavior and genomics. Your principal role will be to wrangle bees, and interface with the computer scientists; so previous experience with bee behavior and beekeeping is required. Other skills, such as knowledge of quantitative genetics or bioinformatics are a plus, but not essential. Successful applicants should be willing to travel to Okinawa for an interview in mid to late April, and can start right away, joining our dynamic multi-disciplinary team. In addition to the main project, you will have opportunities to pursue independent research, if you so desire.

The Okinawa Institute of Science and Technology (OIST) is an interdisciplinary and international university located in the subtropics (long field season!) and chock full of high tech equipment. All aspects of the university's operation are in English. OIST is an excellent environment for an early career scientist, offering a wide range of opportunities for expanding your skill set.

Interested applicants should submit a CV and a brief introductory paragraph to Sasha (alexander.mikheyev@oist.jp).

Alexander (Sasha) Mikheyev Associate Professor Ecology and Evolution Unit < <http://ecoevo.unit.oist.jp/> > Okinawa Institute of Science and Technology 1919-1 Tancha Onna-son, Kunigami-gun 904-0495 Japan

“alexander.mikheyev@oist.jp”
<alexander.mikheyev@oist.jp>

OldDominionU EvolutionCooperativeBehavior

POSTDOCTORAL RESEARCH ASSOCIATE: The Walters Lab invites applications for a postdoctoral research associate position in behavioral ecology and evolution of social behavior beginning in Fall 2016. The successful applicant will work with Principal Investigator Walters and collaborators (Walt Koenig, Joey Haydock), to combine newly-developed tracking technology with long-term demographic data and experimental studies to understand why helper acorn woodpeckers provision young that are not their own and to determine why such striking variability in provisioning behavior exists, thereby providing new insights into the ecological and evolutionary drivers of cooperative behavior in complex societies.

The applicant must have a PhD in behavioral ecology, population ecology, or related field and should have relevant field experience. The applicant will be based at the Hastings Reserve (Carmel Valley, California) but will also spend 2 months per year at the home institution of the PI and / or collaborators.

Job Responsibilities: Oversee the field component of a long-term project examining the behavioral ecology of acorn woodpeckers at Hastings Reserve (Carmel Valley, California);

Work with the PI and collaborators to combine newly-developed tracking technology with long-term demographic data and experimental studies to understand why helpers provision young that are not their own and to determine why such striking variability in provisioning behavior exists, thereby providing new insights into the ecological drivers of cooperative behavior in complex societies;

Coordinate research activities, including (but not limited to): tree climbing; capturing birds to color band, sample blood, and attach nanotags; establishing and maintaining a grid of nanotag base stations; and extensive hiking;

Maintain both long-term field and genetic databases;

Contribute intellectually to the project's further development and success; assist in developing questions, analyzing data, and writing up results to better fulfill the goal of understanding the proximate and ultimate factors affecting helping behavior in acorn woodpeckers;

Oversee hiring, training, and mentoring of field interns integral to the project;

Present results at professional meetings;

Oversee a seminar series incorporating talks by visiting researchers at Hastings Reserve;

Lead a weekly journal club that will incorporate REUs, field assistants, graduate students, the co-PIs, and researchers from other projects when they are on site;

Conduct public outreach that includes managing film crews, providing interpretive programming to visitors of Hastings (including K-12 classes, undergraduate classes, biologists attending training workshops, extension classes, and members of the public)

Applicants should submit a CV, list of publications, statement of research interests, career goals, and contact information for at least three references to ODU Research Foundation <http://www.researchfoundation.odu.edu/> Click on the employment tab and follow the link for position #16010. Applicants must apply through the Research Foundation - DO NOT send application directly to the PI.

Review of applications will begin 31 March 2016 and will continue until the position is filled. The position is for one year and renewable for subsequent years depending upon availability of funding and satisfactory progress.

<http://www.ericwalters.org/-employment.htm#California> Eric Walters

Eric L. Walters, PhD Assistant Professor Dept of Biological Sciences Old Dominion University Norfolk, VA 23529-0266 office ph: (757) 683-5461 lab ph: (757) 683-5620 fax: (757) 683-5283 email: ewalters@odu.edu website: www.ericwalters.org facebook: www.facebook.com/WaltersLab "Walters, Eric L." <ewalters@odu.edu>

PennsylvaniaStateU EvolutionInfectiousDisease

The Boni Lab in the Department of Biology at the Pennsylvania State University is recruiting two highly-motivated postdoctoral scholars to work at the interface of field, theoretical, and computational areas of evolutionary epidemiology. Our lab's research interests can be seen here <http://mol.ax> . Positions will begin in summer/autumn 2016; please inquire if you would like an earlier start date. Our lab is currently based in Ho Chi Minh City, Vietnam, and it will be making a

move to be 50% Penn State Biology Department and 50% Vietnam in August 2016. This means that for the near future, we will have an integrated lab across two sites with computational and theoretical expertise at the Center for Infectious Disease Dynamics (<http://www.cid.dpsu.edu/>) and field and laboratory studies at the Oxford University Clinical Research Unit (<http://www.oucru.org>) in Ho Chi Minh City.

Our current field studies include a large multi-site seroepidemiology study focused on influenza seroprevalence; an mHealth reporting study centered on influenza-like illness patterns in Ho Chi Minh City; and an avian influenza study focused on poultry population dynamics and the effects on H5N1 emergence and persistence. Our computational work focuses on evaluating malaria treatment strategies (<http://mol.ax/pdf/nguyen15.pdf>), exploring seasonality of influenza and ILI in the tropics (<http://mol.ax/pdf/thai15.pdf>), estimating the exposure frequency of avian influenza in the general population (<http://mol.ax/pdf/boni13b.pdf>), and the development of the recombination detection tool 3SEQ (<http://mol.ax/3seq>). The main pathogens of interest in our research group are influenza, malaria, and dengue.

Candidates are encouraged to apply if they are interested in developing new directions for any of the ongoing projects described above, or if they see an opportunity to merge computational and field methods in a novel way. Candidates who would enjoy spending time in the field are encouraged to apply.

The position requires a PhD in one of Ecology, Evolution, Computational Epidemiology, Mathematical Modeling, Population Genetics, Bioinformatics, Statistics, Applied Mathematics, or a related field. The ideal candidate will have experience in one or more programming languages and in a variety of statistical and modeling methods. Complementary expertise in epidemiology, ecology, or immunology may also be helpful. Excellent communication skills, including writing, are required, as is a strong publication record.

Interested applicants should apply at <https://psu.jobs/job/61636> by providing a brief cover letter describing their research interests and career goals, a CV, and names of three professional references. Review of applications will begin immediately and continue until the positions are filled.

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.

Please email Maciej Boni - mfb9@psu.edu - for more information.

Maciej F Boni <mfb9@psu.edu>

QueensU EvolutionaryEndocrinology

We are immediately seeking a talented and highly motivated postdoctoral associate for work on an NSF-funded study on the role of glucocorticoids in mediating responses to environmental challenges and life history tradeoffs in birds. The successful candidate will become a member of the Department of Biological Sciences at Virginia Tech in Blacksburg, Virginia, and will work closely with Ignacio Moore, Fran Bonier (Queen's University), and Mark Haussmann (Bucknell University), with opportunities for visits to each of the PI's labs. The postdoc will be based in the Bonier lab at Queen's University in Kingston, Ontario, Canada.

The project will require that the postdoc spend ~3 months in the field at the Queen's University Biological Station in Ontario, Canada from May until late July, working with a team comprised of undergraduate field assistants and graduate students. The postdoc will coordinate activities at the field sites and supervise the field team. The project will involve large-scale field experiments (manipulations of glucocorticoids, parasites, and/or reproductive effort) and measurement of effects on reproductive investment, parental behavior, immune function, and markers of oxidative stress. The postdoc will have the opportunity to be involved in all aspects of the project, and thus will receive broad training in field and laboratory methods.

***Required Qualifications:** *Must have completed a PhD degree in Biology or related fields prior to the start date. Strong publication record, communication skills, organizational skills, teamwork, and leadership ability required.

***Preferred Qualifications:** *Previous relevant field and lab research experience and some postdoctoral experience preferred.

This is a one-year position with possibility of renewal for an additional year. *Start date May 1, 2016.*

To apply, please send cover letter, CV, and contact information for 2 professional references to Fran Bonier: bonierf@queensu.ca

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Fran Bonier Assistant Professor Queen's University Biology Department Biosciences Complex 3523 Kingston, ON K7L 3N6 Canada

phone: 613-533-6000 x77024 email: bonierf@queensu.ca
<http://post.queensu.ca/~bonierf/index.html>
fbonier@gmail.com

RutgersU PopulationGenomics

Post-Doctoral Position in Population Genomics at Rutgers

The Maslo and Pinsky Labs in the Department of Ecology, Evolution and Natural Resources at Rutgers University are seeking a post-doctoral researcher to participate in a United States Fish and Wildlife Service-funded project examining whether bat populations infected with White-nose Syndrome are experiencing a disease-induced selective sweep. Our approach includes quantification of the standing genetic variation that exists within and among natural bat populations and comparison of genomic signatures of bottlenecks and natural selection.

Candidates should have a Ph.D. in ecology, evolution or related field with strong skills in genomics and bioinformatics. Experience with demographic modeling is preferred. Excellent verbal and written communication skills and proven capacity to publish in peer-reviewed journals are also strongly preferred. The successful candidate will receive training in professional development, research collaboration, presentation and publication of results, and interaction with regulatory agencies.

The preferred start date will be Fall 2016. The position is initially for 1 year, but with the ability to extend, contingent upon a performance review. The position includes a competitive salary and health insurance.

Applicants should submit: 1) cover letter describing research interests/experiences; 2) CV; and 3) names and contact information for 3 references. Send full application packages as a single PDF file to Dr. Brooke Maslo at brooke.maslo@rutgers.edu.

Screening of applications will begin on April 22, 2016.
malin.pinsky@gmail.com

SARS Norway MesodermEvoDevo

Research Fellow (PhD candidate) - 'Evolution of mesoderm development and tissues differentiation'

The Sars International Centre for Marine Molecular Biology (www.sars.no) has available one 4-year research fellow position affiliated with the ERC Consolidator Grant 'EVOMESODERM' recently awarded to Dr. Andreas Hejnol (<http://erc.europa.eu/projects-and-results/erc-funded-projects/evomesoderm>). The Sars Centre belongs to the University of Bergen and is partner with The European Molecular Biology Laboratory (EMBL) www.embl.de/. The position is in collaboration with the Faculty of Mathematics and Natural Sciences at the University of Bergen. The place of work will be at the Sars Centre.

Project/work tasks: The research group 'Comparative Developmental Biology of Animals', headed by Dr. Andreas Hejnol studies a broad range of mainly marine invertebrates using genomic, embryological, and advanced microscopic and molecular methods. The announced PhD positions will focus on a diverse range of invertebrate taxa with the goal to study the evolution of mesoderm specification and its differentiation into cell types and tissues with a focus on haematopoiesis and blood evolution.

Qualifications and personal qualities of the candidate: - the candidate must have completed a master's degree or equivalent in biology, or have submitted a master's thesis for evaluation before expiry of the application deadline. It is a requirement that the master's degree has been completed before the decision to appoint can be made. - Proven experience in molecular biology and microscopy is expected - Strong interest in evolution and developmental biology is desired - Bioinformatic skills are advantageous - It is required that the candidate is able to work independently and in a structured manner and demonstrates good collaborative skills. - proficiency in both written and oral English is expected

About the PhD position The fellowship position is for a fixed term of 4 years, of which 25% will comprise obligatory duties associated with research, teaching and dissemination of results. The employment period may be reduced if you have previously been employed as a

research fellow/research assistant or the like.

The research training programme: As a research fellow you must take part in an approved study programme leading to a PhD degree to be completed within a time period of 3 years. It is therefore a requirement to meet the criteria for admission to the PhD study programme at the University of Bergen. A final plan for completion of the research programme must be approved by the faculty within three months after you have begun working in the position.

We can offer: - a good and professionally challenging working environment - starting salary at grade 50 in the Civil Service pay grade table (code 1017), currently NOK 430.200 gross p.a. Further increases will be made according to length of service in the position. - membership in the Norwegian Public Service Pension Fund - inclusive workplace (IW) - good welfare benefits

Your Application must be in English and include: - a brief statement in English of your research interests and motivation for applying for the position - names and contact details of at least two referees (one of these must be the main supervisor for your master's thesis or equivalent thesis) - CV - transcripts and diplomas showing completion of your Bachelor's and Master's degrees, or official confirmation that your master's thesis has been submitted - relevant certificates/written references - List of publication or any other relevant scientific work

The application and appendices with certified translations into English must be uploaded at Jobbnorge. Please note that applications will be assessed only with the information available in JobbNorge when the deadline expires. It is the applicant's responsibility to ensure that all relevant attachments are submitted by the deadline. Applications submitted by e-mail only will not be considered.

Application deadline: Screening of applications will start 14. March 2016, the announcement will remain open until the position is filled.

General Information: Further information regarding the position and scientific content of the project can be obtained from Group Leader, Dr. Andreas Hejnol, tlf. +47 55 58 43 05/email andreas.hejnol@uib.no. State employment shall reflect the diversity of Norwegian society to the greatest extent possible. Age and gender balance among employees is therefore a goal. It is also a goal to recruit employees of various immigrant backgrounds as well as persons with disabilities. We encourage persons with an immigrant background and

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This message has been arbitrarily truncated at 5000 characters.

To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

TempleU CoralBioinformatics

Post-Doctoral position in Coral Bioinformatics

Project Title: Gene expression analysis of coral stress response

Supervisors: Dr. Erik Cordes and Dr. Rob Kulathinal, Department of Biology, Temple University, Philadelphia PA.

We are looking for a bioinformatics specialist who has experience working with non-model organisms. We have ongoing projects on gene expression and stress responses of deep-water corals. The first is an NSF-funded study of the effects of ocean acidification on the deep-sea coral *Lophelia pertusa*. The second project is an examination of the response of deep-sea octocorals to oil and dispersant exposure that is part of a large, collaborative, research consortium funded by the Gulf of Mexico Research Initiative. The post-doc would be responsible for the analysis of large volumes of RNAseq data from organisms with few existing genomics resources and will have the opportunity to manage and work with doctoral students and a project-dedicated bioinformatician. The post-doc will be expected to disseminate the results of the project at scientific conferences and in peer-reviewed publications that they lead. Ideally, the post-doc would develop additional projects using the existing data sets and also work with the PIs to secure additional funding for further investigations.

Candidates should have a Ph.D. in a related field (either already awarded or awarded by the time of the initial appointment), a good history of publication, and extensive experience with bioinformatics tools. The candidate should have experience with data from multiple sequencing platforms. Excellent writing skills and the ability to work well in a group environment are essential. Experience in a molecular lab, including DNA and RNA extractions and PCR are a plus. The ability and desire to participate in field work, including multiple weeks on offshore research cruises, are also preferred.

The candidate will have access to Temple University's exciting new genomics resources including a large community of computational evolutionary genomicists at the Center for Biodiversity (www.biodiversitycenter.org)

and the Center for Computational Genetics and Genomics (www.cgg.temple.edu).

Temple University is located in the heart of historic Philadelphia, and is the sixth largest provider of graduate school education in the US. Situated between New York City and Washington DC, Philadelphia is home to a large biotech industry and has many outstanding academic, research, and cultural institutions. Temple University is an equal opportunity, equal access, affirmative action employer committed to achieving a diverse community (AA, EOE, m/f/d/v).

The position will begin as soon as possible, but no later than August 15th, 2016. This position will initially be for 12 months, with the possibility of a multi-year extension contingent on additional funding. The initial salary will include full benefits and will be commensurate with experience, according to the schedule published here: <http://www.temple.edu/grad/pfo/index.html> Candidates should send a cover letter, CV, and the names and contact information for three references via email to ecordes@temple.edu. Review of applications will begin immediately and all applications received before April 30th will be given full consideration.

Erik Cordes Associate Professor Department of Biology Temple University BL315, 1900 N 12th St Philadelphia PA 19122 office: 215-204-8876 fax: 215-204-6646 <http://astro.temple.edu/~ecordes/> twitter: @CordesLab

Erik Cordes <ecordes@temple.edu>

UAuckland NZ AdaptivePotential

*Predicting the adaptive potential of the endangered New Zealand hihi (stitchbird; *Notiomystis cincta*)*

We are pleased to offer an 18 month postdoctoral fellowship, funded by a Marsden Fund Grant, with Dr Anna Santure in the School of Biological Sciences, University of Auckland, New Zealand. This project is an exciting opportunity to use statistical genetic approaches to understand and predict the evolutionary potential of the endangered New Zealand hihi (stitchbird; **Notiomystis cincta**), and is a collaboration with Dr Patricia Brekke and Dr John Ewen at the Institute of Zoology, Zoological Society of London, see www.hihiconservation.com. Determining the adaptive potential of wild populations requires that we understand the genetic basis of traits that are important for survival and reproduction in these

populations. We are developing a genomic toolkit to characterise the genetic basis of morphological and life history traits in the reintroduced Tiritiri Matangi Island population of hihi, in order to understand the potential of the species to respond to changing environmental pressures, including anthropogenic climate change. Hihi are an ideal study system because, in addition to being a wonderful example of eccentric New Zealand wildlife, a reintroduced population of birds on Tiritiri Matangi Island has been intensively monitored since introduction and we have a wealth of data on morphological and life history traits, social and genetic relationships, DNA samples and environmental variables. The postdoctoral fellow will be responsible for quantifying selection on morphological and life history traits, and investigating heritabilities and genetic trade-offs between traits that may constrain the adaptive potential of the species. The postdoc will also have the opportunity to contribute to linkage mapping and association analysis, and there is potential to examine signatures of selection in the draft hihi genome and test the impact of drift versus selection on the population.

We are looking for a candidate with a strong background in quantitative and / or theoretical population genetics, as well as a passion for evolution and conservation biology and a track record of publishing in leading journals. Candidates with experience in comparative genomics, statistics, bioinformatics, mathematics, computer programming or similar are also encouraged to apply.

The postdoctoral fellowship is available with a salary range of approximately NZD \$79,159- \$84,931 depending on experience, the start date is negotiable but ideally before September 2016. We welcome informal enquiries, please contact Anna Santure at a.santure@auckland.ac.nz.

Applications should be made through the Auckland University Careers site at: https://www.opportunities.auckland.ac.nz/ps/EMPLOYEE/HRMS/c/HRS_HRAM.HRS_CE.GBL?languageCd=ENG (select Research Fellow - School of Biological Sciences)

The University has an equity policy and welcomes applications from all qualified persons. International applicants are welcome to apply. The University is committed to meeting its obligations under the Treaty of Waitangi and achieving equity outcomes for staff and students.

asanture@gmail.com

UBasel PopulationGenomics

Postdoctoral fellowship in Evolutionary Genomics (100%), University of Basel, Switzerland

The Department of Environmental Sciences is looking for a postdoc to lead the analyses of a unique population genomics data set.

*Topics of research

Research projects could focus on (a) genomic load, (b) distribution of transposable elements, (c) genes of climate adaptation, or other questions of interest to you. Our group has recently re-sequenced populations of *Arabidopsis lyrata* from its entire North American distribution, including two ancestral lineages, core areas, and the southern and northern edges of the distribution. Therefore, population genomic data should reflect a wide range of geographic, climatic and other clines.

*Your profile

The fellowship is for advanced applicants who have done at least one postdoc in Evolutionary Genetics / Genomics already.

*We offer

The initial appointment is for one year; based on performance, the fellowship is renewable for up to three years.

The University of Basel has generous resources for genomic analysis (scientific high- performance computing, data management, training and support). Furthermore, our Department of Environmental Sciences offers a stimulating environment, including a rich spectrum of research activities in life sciences (ecological genomics, population genomics, evolutionary biology, plant ecology, physiology and molecular and cell biology). Finally, Basel is a mid-sized Swiss city, well connected and offering a broad range of cultural and recreational activities.

*Further information and application

For more information, contact Yvonne Willi (yvonne.willi@unibas.ch) or see the following web-pages: www.botanik.unibas.ch/ecol and <http://-evolution.unibas.ch/index.htm>. Application packages should include a letter of motivation, with a one page summary of your ideas for research during the fellowship, a curriculum vitae, and the names and addresses of two referees. Documents should be submitted as a single

PDF file to franziska.grob@unibas.ch. Applications are welcome until the position is filled. We will begin reviewing applications on March 28, 2016.

Yvonne Willi, PhD, Prof.

Department of Environmental Sciences

University of Basel

Hebelstrasse 1

CH - 4056 Basel

Phone: +41 (0)61 267 35 00

Fax: +41 (0)61 267 29 80

Email: yvonne.willi@unibas.ch

Web: botanik.unibas.ch

Yvonne Willi <yvonne.willi@unibas.ch>

UCalifornia Davis HighlandAdaptationPopgenExpression

Postdoctoral Positions on Highland Adaptation in Maize at UC Davis

Two postdoc positions are available in the labs of Jeffrey Ross-Ibarra and Daniel Runcie at UC Davis to study the functional and evolutionary genetics of maize adaptation to highland environments. This is a joint project with labs at Iowa State, USDA-ARS, and Langebio, Mexico. We will draw on population genetics, quantitative genetics, and functional genomics approaches to identify the genetic basis and evolutionary history of highland phenotypes.

The position in Dr. Runcie's lab will be responsible for generating and analyzing RNAseq data on highland and lowland genotypes in the lab and in the field. We are starting two parallel projects. The first will characterize gene expression evolution at a population level, using a diverse sample of landraces from high and low elevation locations. The second will use gene expression to validate and functionally interrogate a strong candidate region for several highland phenotypes. Preference will be given to candidates with experience preparing RNAseq or DNAseq libraries, field tissue collection, and proficiency in unix, R, and other bioinformatics tools. A strong background in evolutionary biology is also desired.

The position in Dr. Ross-Ibarra's lab will be responsible primarily responsible for population genetic analysis

of introgression and adaptation using genotyping and sequence data from replicate populations of wild and domesticated maize in the highlands of Central Mexico. The ideal candidate will have experience in population genetics, proficiency in bioinformatics, and a strong background in evolutionary biology.

Opportunities exist for both positions to additionally collaborate on a number of ongoing projects in both labs, including statistical methods for gene expression analysis, quantitative genetic and functional genomic analysis of adaptive phenotypes, and population genetics of reinforcement or genetic load. Both positions are for one year, with the potential for a second year of support conditional on performance. Start dates are open-ended, with preference for earlier dates.

UC Davis has extremely strong programs in both plant and evolutionary biology. Candidates would have the opportunity to interact with members of the Center for Population Biology and the Genome Center as well as the Dept. of Plant Sciences. Additional information about our labs please visit runcielab.ucdavis.edu or rilab.org.

For more information or to apply, please send a cover letter and a CV with a list of references to deruncie@ucdavis.edu for the first position, or to rossibarra@ucdavis.edu for the second.

UC Davis provides equal opportunity to all qualified individuals and does not discriminate on the basis of race, color, creed, age, marital status, sex, gender, religion, sexual orientation, gender identity or expression, national origin, veteran status or disability. UC Davis provides reasonable accommodations to applicants with disabilities; if you need such accommodation for any part of the application process, please contact the office of Graduate Studies at gradservices@ucdavis.edu.

Jeffrey Ross-Ibarra

Dept. of Plant Sciences 262 Robbins Hall, Mail Stop 4 University of California One Shields Ave Davis, CA 95616

Tel: 530-752-1152 @jrossibarra www.rilab.org "rossibarra@ucdavis.edu" <rossibarra@ucdavis.edu>

UCalifornia Los Angeles OakGenomics

Postdoc:UCLA.OakGenomics

We have a post-doc opening to join an oak genomics project funded by the NSF Plant Genome Research Program to provide a complete, high-quality sequence of the valley oak genome with structural and functional annotations of genic regions and repetitive elements. The project will develop and implement innovative genome assembly tools for the valley oak genome using PacBio sequencing. The postdoc for this position will play a major role in the annotation component of the project and will also conduct gene expression experiments with the goal of improving identification, validation, and annotation of genes underlying phenotypes associated with local adaptation to climate response. The post-doc will design his/her experiments with access to greenhouse, growth chambers, and two common gardens of ca.7000 trees planted at two sites maintained by the US Forest Service. The post-doc should be willing to assist in outreach projects and/or student training.

The post-doc will work in the laboratory of Victoria Sork at UCLA and join a collaborative multi-institutional team that includes Steven Salzberg (Johns Hopkins University Center for Computational Biology), Matteo Pellegrini (UCLA Institute of Quantitative and Computational Biosciences) and Paul Gugger (University of Maryland Center for Environmental Sciences, Appalachian Laboratory), as well as a bioinformatic scientist in the Sork lab, researchers with computational biology expertise in the Pellegrini lab, and computational engineers in the Salzberg lab. For more details of the project see the valley oak genome project website: valleyoak.ucla.edu. Individuals with strong bioinformatic expertise will be eligible to apply for fellowships from the Collaboratory at the Institute of Quantitative and Computational Biosciences (<http://qcb.ucla.edu/collaboratory/lab-projects/>)

Key Requirements: The applicant should possess a PhD or equivalent in the biological sciences, preferably with empirical, analytical or bioinformatics training in molecular or evolutionary genetics. Previous experience in molecular techniques, next-gen sequence analysis, and variant calling are preferable. Candidate should have a research track record with relevant publications in peer-reviewed journals. Interest in plant evolutionary

biology or evolutionary genomics of local adaptation is desirable.

This position will begin September 1, 2016 (flexible), and with possibility of renewal for 1-2 years, based on performance.

Applicants should email their CV, pdf's of 3 publications, statement of research interests, and email information for three referees to sorklab@gmail.com. Cover letter should include a short personal statement describing your research experience and interests that would match this project. Please also include any outreach activities or other broader impacts associated with your previous research or education. Review of applications will begin 15 April 2016 and continue until position is filled. For informal queries, please contact Victoria Sork by email, vsork@ucla.edu

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, age, disability, protected veteran status, or any other characteristic protected by law.

Sork Lab Manager 4140 TLSB *Office:* x41431 *Cell:*(415) 410-3300

"klbeckley@g.ucla.edu" <klbeckley@g.ucla.edu>

UCalifornia Santa Cruz Paleogenomics

PostDoc: UCalifornia_SC Paleogenomics PaleopopulationGenetics

Applications are invited for a Postdoctoral Scholar position in the Human Paleogenomics section of the Paleogenomics Laboratory at the University of California Santa Cruz. The Paleogenomics lab uses genomic data isolated from archaeological human remains to better understand the population history of our species and how genetic diversity is generated and maintained within populations through time. We are especially interested in the role of the interaction of culture and biology in the formation and maintenance of human genetic variability. The Human Paleogenomics section is directed by Professor Lars Fehren-Schmitz (Department of Anthropology). The section was established recently and joined the UCSC Paleogenomics Lab, directed by Professors Beth Shapiro (Department of Ecology and

Evolutionary Biology) and Richard Green (Department of Biomolecular Engineering). Together we combine experimental and computational approaches to address a variety of paleogenomics topics.

We seek a Postdoctoral Scholar to participate in an NSF funded collaboration project with the George Washington University and the Yale University whose general goal is to reveal the impact of the expansion of late pre-Columbian state societies (e.g. Inca) on the genetic structure of Central Andean populations. Beyond this general point we are interested in approaching a number of other factors relevant for the population history of South America using paleogenomic tools, including health/ disease and human adaptation to stress factor acting in high altitude. The Postdoctoral Scholar will be expected to use paleogenomic and population genetic/computational techniques to explore the population history of South America and beyond and preferably be interested in developing/adapting new statistical approaches to allow population differentiation in low diversity environments. Beyond that all members of our lab are encouraged and supported to develop their own project ideas. The successful candidate will attend and participate in lab meetings and journal clubs, and will work cooperatively with a team of scientists, including molecular biologists, archaeologists, biological anthropologists, historical linguists, ethno-historians and biostatisticians.

We have a preference for candidates with experience and expertise in paleogenomics, especially individuals with experience in population genetic approaches to the statistical analysis of genome wide ancient DNA data, and excellent organizational, verbal communication, and collaboration skills and willingness to travel to field sites and museums.

BASIC QUALIFICATIONS: A Ph.D. in biological anthropology, evolutionary biology, genomics, population genetics, bioinformatics, or other relevant fields; laboratory (wet lab or computational) experience; demonstrated record of research and publication; and experience with next-generation sequencing and analysis of paleogenomic NGS data, including phylogenetic and population genetic approaches to the statistical analysis of genomic data (latter is most important).

PREFERRED QUALIFICATIONS: The ideal candidate has experience in the analysis and manipulation of large, population genomic data sets, has programming skills and familiarity working in a UNIX environment. Active wet lab work is not mandatory for this position but experience with ancient DNA extraction, PCR amplification, genomic library preparation, and DNA sequencing protocols would be a plus. Learn More More in-

formation about this recruitment: http://apo.ucsc.edu/academic_employment/jobs/JPF00312-16T.pdf *Open date: *now *Next review date: *April 29th, 2016 Apply by this date to ensure full consideration by the committee. *Final date: *July 31st, 2016

Dr. Lars Fehren-Schmitz Assistant Professor Anthropology Department & UCSC Human Paleogenomics Lab U.C. Santa Cruz 1156 High Street Santa Cruz, CA 95064 Phone: +1 (831)- 459-3851 Email: lfehrens@ucsc.edu HP: <http://ucschpg.wordpress.com/> “lfehrens@ucsc.edu” <lfehrens@ucsc.edu>

UCambridge EvolutionCancer

Position available for a postdoctoral scientist to study the genetics and evolution of transmissible cancers in dogs and Tasmanian devils.

An exciting new opportunity for a Postdoctoral Research Associate has become available within Dr Elizabeth Murchison's laboratory, the Transmissible Cancer Group (TCG), at the University of Cambridge. The TCG is a newly-established small, interactive and international research team based at the Department of Veterinary Medicine, with strong collaborative links with the Wellcome Trust Sanger Institute's Cancer Genome Project. The group's research is focused on the genetics and evolution of clonally transmissible cancers in dogs and Tasmanian devils. The new position is part of a Wellcome Trust-funded project examining genetic diversity in hundreds of dog and Tasmanian devil transmissible cancer samples. The role provides an exciting opportunity to combine cancer genomics with conservation biology and infectious disease genetics to study the emergence, evolution and spread of transmissible cancers. For further information on the position and the Transmissible Cancer Group, please see our website: <http://www.tcg.vet.cam.ac.uk> . Job closes on 28th March 2016.

Twitter: <https://twitter.com/tcgcambridge> Many thanks,

Elizabeth

– Elizabeth Murchison, Ph.D. Reader in Comparative Oncology and Genetics Wellcome Trust Investigator Department of Veterinary Medicine University of Cambridge Madingley Road Cambridge CB3 0ES United Kingdom Phone: +44(0)1223766497 Email: epm27@cam.ac.uk www.tcg.vet.cam.ac.uk Elizabeth

Murchison <epm27@cam.ac.uk>

UCollege London WheatStatisticalGenetics

Research Associate in Statistical Genetics and Bioinformatics, - Ref:1539126

We are recruiting a talented statistical geneticist/bioinformatician to determine the genetic basis of complex phenotypes in populations descended from known founder individuals. The project uses wheat crop improvement as its focus but the methodologies developed apply to many crops and animals. It is also expected to shed light on the population genetics of wheat. The BBSRC-funded post centres on the DIVERSE wheat MAGIC population of recombinant inbred lines. These descend from 16 wheat crop varieties grown commercially in the UK, and have been developed primarily to map genes responsible for important agronomic traits. Many users, both academic and from the plant-breeding community will access the project resources.

The post-holder will join the group of Richard Mott at University College London, a dynamic Institute working on quantitative and population genetics across a range of species. The group is affiliated to the Department of Genetics, Evolution and Environment (GEE) and the UCL Genetics Institute (UGI), which offer one of the most exciting work environments in the UK. GEE is a large and collegial Department which embraces essentially all aspects of modern biology and has grown significantly over recent years. The UGI is a vibrant Institute which has been recently created as centre of excellence in medical, statistical and computational genetics.

This post is funded until 31st May 2019 in the first instance and is available now.

Key Requirements Applicants should possess a PhD or equivalent in statistical genetics, bioinformatics or a related subject. Applicants with a strong background in either discipline with the desire and ability to learn new skills are welcome to apply for this position. Previous experience in either quantitative genetic analysis or next-gen sequence analysis, including ability to program in languages such as R, C/C++, Perl, Python, HTML is essential. A research track record e.g. relevant publications in peer-reviewed journals is desirable. Experience with wheat or other plant genetics/genomics is desirable

but not essential; we would consider suitably qualified applicants without prior experience with plants. Further Details

A Job Description, Person Specification and application form can be accessed at <https://goo.gl/hWlq9> . For informal queries on the role please contact Richard Mott r.mott@ucl.ac.uk.

“Mott, Richard” <r.mott@ucl.ac.uk>

UCologne BioinformaticsPopGenet

A postdoctoral position to work on molecular population genetics of wild populations of *Danio rerio* is immediately available in the labs of Maria Leptin (http://www.embl.de/research/units/-directors_research/leptin/) and Thomas Wiehe (<http://www.bioinf-popgen.uni-koeln.de/>) at the Institute of Genetics, University of Cologne, Germany.

We are seeking a skilled bioinformatician or molecular biologist with expertise in the handling and analysis of NGS data, and who ideally has experience in evolutionary biology or immunology.

The aim of the project is to understand the evolutionary causes and mechanisms which have generated a large family of innate immune receptor genes (NLR family) in *Danio rerio* (<http://biorxiv.org/content/early/2015/07/07/022061.1>). An integral part of the project is to survey and analyze genetic diversity in these genes from several wild populations of *Danio* and to explore the link to ecological conditions. The project is part of a DFG-funded Priority Program to study processes of Rapid Evolutionary Adaptation (<https://dfg-spp1819.uni-hohenheim.de>).

The position is initially available for two years, with the perspective of prolongation, and is to be filled as soon as possible. The position is paid according to the German salary scale TVL E13, full time employment, and comes with the usual social benefit packages. Our research groups are part of the Institute of Genetics and are members of the Collaborative Research Center SFB680 (<http://www.sfb680.uni-koeln.de>), and of the Priority Programs SPP1590 (<http://www.dfg-spp1590.de>) and SPP1819 (<https://dfg-spp1819.uni-hohenheim.de>). Besides its excellent scientific environment, Cologne offers a wide range of cultural life and entertainment options.

For inquiries and further details please contact Thomas Wiehe at twiehe@uni-koeln.de. Applications should con-

tain a resumé with past and planned research, and the details of two reference addresses, and be sent as a single PDF file to the above address.

– Thomas Wiehe Universitaet zu Koeln Institut fuer Genetik Zuelpicher Stra3e 47a D-50674 Koeln Germany Tel 0049 221 470 1588

“twiehe@uni-koeln.de” <twiehe@uni-koeln.de>

sensitive: you must start by May 1, 2016, so contact me (David.Pollock at UCDenver dot edu) right away if interested. You also must be a US Citizen. Colorado is a great place to live.

David Pollock, Biochemistry and Molecular Genetics, Human Medical Genetics and Genomics, Computational Bioscience, University of Colorado School of Medicine.

“Pollock, David” <David.Pollock@ucdenver.edu>

UColorado Boulder Speciation

Postdoc Opportunity in Speciation and Evolutionary Genomics

National Science Foundation-funded Postdoctoral Researcher Opportunity available in Sam Flaxman’s lab at the University of Colorado Boulder, starting June 1st, 2016

As part of a very recently awarded NSF EAGER grant, the Flaxman lab at University of Colorado Boulder is currently searching for a postdoctoral researcher to work on developing and using simulation methods for population genomic inference. The grant is a two-year award that includes funding for a full-time postdoctoral researcher to assist in the goals of that project. The postdoc will be responsible for developing and testing theoretical predictions about the evolution of genomic divergence using both coalescent and forward-in-time based simulations, which will then be cross-validated using available empirical data. The intended start date of the position is June 1st, 2016.

For full details, please visit: <https://docs.google.com/document/d/127FBy9JFJSdRm2AOjPrGfTlGu7IURmBV2gWxwnjWTEY/edit?usp=sharing> or contact Samuel.Flaxman@colorado.edu

Samuel Melvin Flaxman
<Samuel.Flaxman@colorado.edu>

UExeter ViralEvolution

Dear all,

I have a postdoc position available in my lab looking at the evolutionary and mechanistic basis of virus host shifts. I am in the process of setting up a new group at the University of Exeter’s Cornwall campus, which is home to a range of researchers working on various aspects of evolution and ecology, including a large number of groups working on host-parasite interactions (see <http://biosciences.exeter.ac.uk/cec/research/>) .

Full details of the position can be found here: https://jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/run/ETREC107GF.open?VACANCY_ID=-443027EJmM&WVID=3817591jNg&LANG=USA As well as having suitable experience, the ideal candidate should be excited, passionate and enthusiastic about doing good science, and want to work in a friendly and sociable group.

Any further questions please get in touch.

Cheers,

Ben Longdon

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>

UColorado Denver MolecularEvolution

I have an opening for a postdoc in molecular evolution (see www.EvolutionaryGenomics.com to get an idea of the wide variety of things we work on). This is time

UFlorida Gainesville Systems Genetics

Postdoctoral fellowship in Systems Genetics:

An exciting dynamic project on the response of Maize to Ozone. We will be looking for splicing changes, allele specific expression differences, metabolic changes and changes in photosynthesis and yield due to the response to ozone in a diverse set of germplasm. Successful applicants should have enthusiasm for working on the cutting edge of data integration and experience in quantitative genetics or biostatistics with basic knowledge of genetics. Intellectual curiosity is necessary and teamwork is essential. The McIntyre Lab is at the forefront of the development of analytical methods using a systems genetics approach. There are opportunities to work with other systems and to interact with a dynamic set of collaborators. The group is small but extremely productive and very interactive. We are located at the University of Florida in Gainesville, Florida USA. Gainesville is a friendly college town in a diverse and welcoming community. The position is two years with possible extension to a third year. The starting date is flexible with a preference for Spring/Summer 2016. The University is an equal opportunity employer. Interested parties should send a CV and names of three references to Lauren McIntyre (mcintyre@ufl.edu).

mcintyre@ufl.edu

UFrancoisRabelais Tours SymbioticBacteria

Variation and transmission patterns of symbiotic microbial communities associated with wood-feeding insects

A 18-months postdoctoral position is available in the Insect Biology Research Institute at the University of France Rabelais in Tours (France). The postdoc fellow will participate to the Xylobiotic project funded by the *gignonCentreValdeLoire*. This project aims to investigate the role of symbiotic microbial communities in the invasion success and dynamics of wood-feeding insect species. The candidate

will work in close collaboration with several entomologists, evolutionary biologists and ecologists who are involved in this research project.

Scientific objectives

The specific aim of the postdoc is to investigate the evolutionary dynamics of the Symbiotic Microbial Communities (SMC) associated to the hindgut of subterranean termites and to the mycangia of ambrosia beetles. More specifically, this project aims: (i) to study the diversity and composition of the SMC associated to these insects, (ii) to analyze the intra and inter-population variations of the SMC, (iii) to determine the efficiency of vertical transmission of the symbionts (from parents to offspring), and (iv) to test the possibility that symbionts can be horizontally transferred between host species (host-switching events). This research will principally involve analyses of high-throughput sequencing of microbial barcoding regions (rRNA 16S for prokaryotes, 18S for protists, ITS for fungi) isolated from insect tissues.

Candidate profile

The postdoc fellow will be in charge to lead all the DNA metabarcoding data analyses. We therefore are looking for candidates with a background in evolutionary genomics and/or microbial ecology with a high skill level in bioinformatics. The ideal candidate will demonstrate the ability to analyze Illumina sequence data sets, and use high throughput sequencing data to characterize and interpret the diversity and structure of microbial communities. An experience in analyzing meta-genomes and/or transcriptomes will also be highly valuable.

Environment

Our Institute is a unit of the *Centre National de la Recherche Scientifique* that provides a stimulating environment, including a rich spectrum of research activities in life sciences related to the insects (<http://irbi.univ-tours.fr>). Tours is a mid-sized French city, well connected to Paris and Bordeaux and offering a broad range of cultural and recreational activities (<http://www.tours-tourism.co.uk>).

Schedule

The postdoc position ideally will start in September 2016, although some arrangements eventually could be made. Applications will contain a CV, a cover letter describing candidate background and interests, a description of previous research experiences, and contact names and emails for two letters of reference. Complete application files must be sent to Dr Franck Dedeine (franck.dedeine@univ-tours.fr) as soon as possible and before June 13th. Pre-selected candidates might then

be interviewed by a selection committee in June or July.
 Franck Dedeine Maître de conférences Institut de Recherche sur la Biologie de l'Insecte (IRBI) UMR CNRS 7261 - Université de Tours Equipe Ecologie Chimique et Evolutive des Insectes Sociaux Tél: 02 47 36 71 23 franck.dedeine@univ-tours.fr

Franck Dedeine <franck.dedeine@univ-tours.fr>

UHelsinki Evolutionary Genomics

Post-Doc in Evolutionary Analysis of Gene Regulation

We seek a highly motivated and creative individual to join our Bioinformatics for Molecular Biology and Genomics research group at Department of Biosciences, University of Helsinki, Finland.

*Project Description:

In this project, biological experimentation is combined with methods development to estimate conserved gene regulatory networks. Initial application area is evolution of leaf formation. Leaves are optimal for the purpose, since they are easy to quantify in large amounts with several replicates per individual, they vary between and within species, and there exists a large amount of publicly available gene expression data from leaf development in different species. In addition to public data, leaf formation is studied in a large birch population (family Betulaceae) which is characterised in a high-throughput plant phenotyping facility, followed by genomic and transcriptomic sequencing of selected phenotypes.

*Research Environment:

Research is carried out in Bioinformatics for Molecular Biology and Genomics research group headed by D.Sc Jarkko Salojärvi. The group is focusing on plant systems biology by combining different omics data to study the evolution and adaptation of gene regulation in plants.

The group is part of Finnish Center of Excellence in Molecular Biology of Primary Producers, and housed within the Viikki Biocentre campus of University of Helsinki. The campus has exceptional research facilities, including state-of-the-art core facilities such as next generation sequencing platforms (Illumina HiSeq, PacBio), plant growth chambers, greenhouses, and a high-throughput plant phenotyping facility.

*Required Qualifications and Application Instructions:

The candidate should have experience or necessary skills to learn machine learning or advanced statistics, and/or population genomics, and programming/scripting experience (preferably R). Previous background of working in a Linux environment with genomic and transcriptomic data analysis is needed. The working language of the group is English, and therefore excellent communication skills in English are imperative.

The position is for two years, and salary is according to the University salary system, which is based on qualifications and personal performance. A post-doctoral fellow will likely be at level 5 (salary before taxes 3100-3700 Euro/ month). Preferable starting time is August 2016, but is flexible.

To apply, please send a letter of motivation describing your reasons for applying to the position, CV, transcripts and contact details for at least two references.

All materials should be sent in English to jarkko.salojarvi@helsinki.fi. Review of applications will begin April 1 and will continue until a suitable candidate is found.

Jarkko Salojärvi, D.Sc (Tech) Bioinformatics for Molecular Biology and Genomics Department of Biosciences P.O.box 65 (Viikinkaari 1) FI-00014 University of Helsinki, Finland

E-Mail: jarkko.salojarvi@helsinki.fi SkypeID: jarkko.salojarvi

“jarkko.salojarvi@Helsinki.FI”
 <jarkko.salojarvi@Helsinki.FI>

ULausanne Comparative Genomics

Two postdoc positions in Comparative Genomics and Evolutionary Modeling

Job description

Two postdoctoral positions are available in my group in the Department of Ecology and Evolution of the University of Lausanne: - the first position aims at better understanding the genomic architectures involved in the adaptive radiations of clownfish - the second aims at developing and improving current methods to estimate the rates of evolution of phenotypic traits along phylogenetic trees.

Both positions are for up to two years and are part of a project funded by the Swiss National Science Founda-

tion. Interested candidates should apply by sending a letter describing your research motivation and experience, a detailed CV and contact details of three referees to Nicolas Salamin (see contact details below) directly.

Position 1: Genomics of adaptive radiations

The main objective of the first position is to analyse the genomic elements involved in the adaptive radiation of clownfish to better understand the genetic mechanisms that are responsible for the specialisation of this iconic group of organisms. In a second step, full genome and transcriptome data will be used jointly with the phylogenetic context to assess the presence of parallel patterns of genomic change that lead to phenotypic diversification of clownfishes. This will allow to assess if comparable mechanisms are at play between the micro- and macro-evolutionary scales.

Profile requirements: The ideal candidate should be an autonomous and ambitious person with enthusiasm for inter-disciplinary work, who will need to interact productively with evolutionary biologists, genome biologists and computer scientists, and read the corresponding range of scientific literature. Candidates must have completed their PhD degrees or equivalent in a relevant field.

The requirements include a strong bioinformatic background and deep interest in computational biology and theoretical aspects of evolutionary biology. Previous experience with evolutionary biology and/or computational biology is also expected.

*** Position 2: Evolutionary modeling***

The first objective of the second position is to develop a novel model testing framework to further understand the evolution of the variance in phenotypic traits within a macro-evolutionary framework. The second objective is to model the evolution of phenotypic traits across speciation events to better understand the relationship between macro-evolutionary models and micro-evolutionary processes.

Profile requirements: The ideal candidate should be an autonomous and ambitious person with enthusiasm for inter-disciplinary work, who will need to interact productively with evolutionary biologists, genome biologists and computer scientists, and read the corresponding range of scientific literature. Candidates must have completed their PhD degrees or equivalent in a relevant field.

The requirements include a strong mathematical or statistical and computer science background and deep interest in computational biology and theoretical aspects of evolutionary biology. Previous experience with evolutionary biology and/or computational biology is also expected.

lutionary biology and/or computational biology is also expected.

Working environment

The successful candidates will be part of the Department of Ecology and Evolution of the University of Lausanne as well as the Swiss Institute of Bioinformatics. The Department of Ecology and Evolution of the University of Lausanne offers a supportive and stimulating environment, with access to excellent computer and academic facilities.

Contact details

Do not hesitate to contact me for any information on these positions. To apply, please send by email i) a letter describing your research motivation and experience, ii) a detailed CV, iii) contact details of three referees. The application deadline is set to April 15th 2016 and the start date will be discussed with the candidates.

Nicolas Salamin nicolas.salamin@unil.ch www.unil.ch/-phylo www.isb-sib.ch/salamin-nicolas "nicolas.salamin@unil.ch" <nicolas.salamin@unil.ch>

ULausanne TheoEvolutionaryBiol

1 postdoctoral position in Lausanne: Theoretical evolutionary biology, social evolution, and human evolution

A theoretical evolutionary biology postdoctoral position for 1 year (extensible for 2 more years) is open in the research group of Laurent Lehmann at the Department of Ecology and Evolution of the University of Lausanne (<https://www.unil.ch/dee>). We study social evolution from a mathematical and computational point of view with a current focus on human evolution and address the following type of questions:

How did large-scale stratified human societies emerge from small-scale egalitarian societies? Is this the result of an increase in the technologies of production and exchange (invention of agriculture and trading) or in the technology of appropriation (intensification of warfare)? What are the selection pressures on increased lifespan and cognition in the human lineage? Is this the result of an ecological or a social pressure? How does the determinants of behavior evolve in social environments? Should behavior be genetically driven, acquired by social learning, or is free choice of actions delegated to the individual?

Applicants with a strong interest in these research ques-

tions are encouraged to apply. Applicants should have a Ph.D. in a relevant area (e.g. evolutionary biology, economics, anthropology, physics, or mathematics), with strong mathematical and computing skills, and a vivid interest in fundamental research.

Inquiries and applications should be sent to laurent.lehmann@unil.ch by April 31th. They should include a CV, a statement of research interests, and names of 2-3 referees. Only applications with all these information will be considered. Starting date is negotiable, from May 2016 onwards.

Laurent Lehmann <Laurent.Lehmann@unil.ch>

ULaval EvolutionGeneDuplicationNetworks

Postdoctoral position: evolution of gene duplication and protein networks

A postdoctoral position is available in the Landry Laboratory at Université Laval in Québec City under the Canada Research Chair in Evolutionary Cell and Systems Biology. The PDF will work on a project aimed at dissecting the role of gene duplication in the evolution of protein complexes and cellular complexity using yeast as a model system. The position is funded for up to three years with a competitive fellowship and several independent fellowship opportunities for both Canadian and foreign candidates.

The candidate is expected to have a PhD in biology or a related discipline, and a strong background in molecular and cell biology with basic skills in bioinformatics and statistics. The candidate should have strong leadership skills, motivation and creativity and be able to work in a team of collaborators.

The Landry lab is located at the Institut de Biologie Intégrative et des Systèmes (IBIS) of Université Laval and is part of the Québec Network for Research on Protein Function, Engineering, and Applications (PROTEO). IBIS and PROTEO offer very stimulating training environment and cutting edge technologies in genomics and proteomics. The Landry lab is an international team of 15 students, PDFs and research associates from different backgrounds (microbiology, biology, bioinformatics, biochemistry) addressing questions in evolutionary cell and systems biology.

The application package (1 single PDF file) should include a motivation letter demonstrating the interest of

the candidate for the field and his/her ability to perform this type of research, a short project proposal (half a page), reprints of the candidate's most important contributions, a CV and the contact information of three people who can provide letters of reference. The file should be sent to landrylaboratory@gmail.com

Starting date could be as early as June 2016 but could extend until the end of 2016. The competition will remain open until a candidate is selected.

For recent publications from the Landry lab, please visit:

<http://landrylab.ibis.ulaval.ca/> Christian Landry

Christian Landry, PhD Professeur agrégé Chaire de Recherche du Canada Biologie évolutive des systèmes cellulaires // Canada Research Chair Evolutionary Cell and Systems Biology Département de Biologie Institut de Biologie Intégrative et des Systèmes PROTEO Local 3106, Pavillon Charles-Eugène-Marchand 1030, Avenue de la Médecine Université Laval Québec (Québec) G1V 0A6 Canada <http://landrylab.ibis.ulaval.ca/> Téléphone: 418-656-3954 Télécopieur: 418-656-7176

Christian Landry <Christian.Landry@bio.ulaval.ca>

UNorthCarolina Charlotte PathogenEvolution

Post-doctoral positions in Molecular Epidemiology of Pathogens at UNC Charlotte.

Duties will include supporting projects through original research and publication, collaboration with other team members, and mentoring of students.

The successful candidates will also contribute to development of proposals for funding.

Applicants should have experience in programming, molecular systematics, biogeography, host-pathogen systems, and/or bioinformatics.

Ph.D. required in biology, computer science, or related fields.

send CV to unccpostdoc@gmail.com

Dan Janies <unccpostdoc@gmail.com>

UOslo Yersinia aDNA

CEES, Department of Biosciences Postdoctoral Research Fellow in Biology, Comparative Infection Biology and Ancient DNA

See also :

<http://uio.easycruit.com/vacancy/1597287/96871?iso=no> Position as Postdoctoral Research fellow available at the Department of Biosciences, Centre for Ecological and Evolutionary Synthesis (CEES)

The fellowship will be for a period of 2 years and 8 months. Starting date as soon as possible and preferably no later than 01.06.2016. No one can be appointed for more than one specified period at the same institution. Within the framework of the position duties may be assigned.

Job Description:

Main objective of the project Comparative Infection Biology (COMPI) is the genomic investigation of pathogenic species in the *Yersinia* genus using ancient DNA (aDNA) techniques, high-throughput sequencing methods and related bioinformatics. The *Yersinia* genus comprises an assemblage of diverse pathogens capable of infecting vertebrates in terrestrial and marine ecosystems. Nonetheless, the evolutionary and ecological processes underlying the epidemiology of these pathogens remain debated. The project includes investigations on *Y. pestis*, responsible for all known historic plague pandemics and *Y. ruckeri*, a marine pathogen affecting various fish species. Using a multidisciplinary approach, involving paleogenomics, climatological and ecological data we aim to understand spatial and temporal trajectories of *Yersinia* species in the past. A core component of the project is the aDNA analysis of ancient samples, including medieval human remains and historical fish collections, for identification and phylogenetic analysis of *Yersinia* (and other pathogens). Datasets from historic Atlantic cod specimens have been generated and are available for analysis. Comparative studies of population dynamics and pathogenicity factors of the bacteria will provide a better understanding of the biological processes underlying bacterial infection.

The successful candidate will work in close collaboration with a multi-disciplinary group of international recognized experts from the fields of microbiology, ecology, genomics and evolution from the teams of CEES (led by

Nils Chr Stenseth), COMPI (Dirk Linke, PI) and MedPlag (“MedPlag: The medieval plagues: ecology, transmission modalities and routes of the infections”, Advanced Grant funded by the European Research Council (ERC): Barbara Bramanti, PI).

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.

We search for an applicant who has completed a PhD degree (or other education equivalent to a Norwegian degree) of high quality in biology, evolutionary biology, bioinformatics or a field demonstrably relevant to the project description.

The applicant should have a strong publication record, and should be able to document extensive analytical skills, amongst others using bioinformatics applied to (ancient DNA) population genomics. The successful applicant is expected to work in the newly build aDNA laboratory at IBV for the generation of aDNA data.

The successful candidate will work in the ancient DNA environment at the CEES (Dr. Barbara Bramanti and Stephanie Hänsch) and closely collaborate with several researchers at the CEES (Prof Nils Chr. Stenseth and Dr Bastiaan Star) and IBV (Prof Dirk Linke) who have complementary skills, as well as with our international collaborators. We seek a highly motivated, enthusiastic person with the ambition to gain insight and publish papers in leading, international journals, in possession of good interpersonal skills and willing to collaborate with researchers across disciplines.

The main purpose of post-doctoral research fellowships is to qualify researchers for work in top academic positions within their disciplines.

Please also refer to the regulations pertaining to the conditions of employment for post-doctoral fellowship positions.

A good command of English is required.

Salary

Position code 1352, Pay grade: 57 - 65 (NOK 483 700 – 560 700 per year)

The application must include:

- Application letter including a statement of interest, summarizing your scientific work and interests and describing how you fit the description of the person we seek.
- CV (summarizing education, positions and academic work – scientific publications)
- Copies of educational

certificates, transcript of records and letters of recommendation - List of publications and academic work that the applicant wishes to be considered by the evaluation committee Names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number).

— / —

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>

UPotsdam EvolutionReproductiveBehaviour

POST DOC: Reproductive behaviours in a risky world: are mothers trading-off offspring safety for future fitness?

Background

Individuals do not only have to eat without been eaten, they also have to balance the risk of mortality with their investment into reproduction. We study trade-offs between reproductive and anti-predatory behaviours. Rodents are a suitable study system: they are highly depredated, have flexible mating system (i.e. can mate singly or multiply), and can potentially simultaneously invest into nestling litters (current investment) and pregnancy (future investment). This produces a conflict between caring for the current offspring, and leaving the offspring temporally behind for mating in order to be able to invest into future offspring. It further allows to separate the effects of predation risk on different stages in the life cycle on the trade-off between current reproductive investment (nest guarding) and future reproductive investment (mating behaviour). In our experiments individual variation in time allocation, physiological responses, space use and mating success will be monitored allowing quantifying both behavioural and fitness consequences. Experiments are conducted in different spatial and temporal scales: behavioural observations in the laboratory and automated telemetry observations in semi-natural enclosures, allowing for novel estimates of the general flexibility of reproductive behaviour and measuring life-history trade-offs of reproduction and mortality risk for individuals in semi-natural settings. Experimental data either already exists or has to be collected. The post-doc is expected to work with and publish this data.

Research Environment

Our (all female) research group “Animal Ecology” at the University of Potsdam consist of three scientists (Eccard and Dammhahn, Behavioural Ecology, Scheffler, Human Biology) and two technicians. We run large outdoor facilities with enclosures and automated telemetry and a behavioural research facility. We part of the Potsdam/Berlin research Area with several universities and research institutions. Currently we supervise 8 PhD projects in Behavior/Evolution/Conservation (see our homepage). Our strengths are experimental approaches and statistical modelling. Potsdam is a beautiful town 20km southwest of Berlin and great to live and work in.

For more information on our projects and the group: <http://www.uni-potsdam.de/en/ibb/researchgroups/-fullprofessors/animal-ecology/forschung/research-animal-ecology.html>

How to apply: Your application should include a cover letter, C.V., papers, and contact information of two referee. The position is available until a suitable candidate is found. Please send your application to Maria Thrun (mthrun@uni-potsdam.de)

Tierökologie - Prof. Dr. Jana Eccard Institut für Biochemie und Biologie Mat.-Nat. Fakultät - Universität Potsdam Maulbeerallee 1 14469 Potsdam Telefon: 0331 9771923 Telefax: 0331 9771948 Email: eccard@uni-potsdam.de

Jana Eccard <eccard@uni-potsdam.de>

UZurich EvolutionMulticellularity

Postdoc position in Evolutionary Ecology at the University of Zurich, Switzerland

A postdoctoral position in evolutionary ecology, of 18 months duration, is available at the University of Zurich working with Prof Hanna Kokko and her international team www.kokkonuts.org. This research group is also part of a Centre of Excellence in Biological Interactions, which will bring the postdoc in contact with Universities of Helsinki and Jyväskylä in Finland (<https://www.jyu.fi/bioenv/en/divisions/coe-interactions>). The research involves theoretical studies related to life history questions in modular organisms, a question that can be framed within the general context of the evolution of multicellularity. There is also potential to collaborate with Will Ratcliff’s group at Georgia Tech

(<http://www.ratcliffab.biology.gatech.edu/>).

We are a team that places a lot of emphasis on creating theoretical work that integrates well with empirical findings. The most up to date version of our current interests can be best described by the list of journal club articles that we discuss each week (www.kokkonuts.org, click on 'journal club'). We are looking for a researcher who combines a broad interest in the research areas described there, with a specific interest of developing theory for life histories of organisms that do not fit the classical assumptions of much of modelling (such as discrete generations, clear distinction between germ line and soma, clear boundaries between individuals). Applicants should come with a strong set of theoretical skills. Applicants who are adept at generating research ideas - as long as they fall within the broad scope of our focal topics as implicitly defined by the journal club - are preferred over those who expect a clearly delineated project to be given to them.

The working language in the group is English (German

skills are not essential). The position is available from mid-year 2016. The target application date is March 31, 2016, but open until a suitable candidate has been found.

Applicants should send a cover letter with a

- statement of their research interests, especially in relation to the journal club articles as mentioned above
- C.V. (including publication list), and
- the names and contact details of at least one referee.

Applications should form a single pdf file and this should be sent to: hanna.kokko@ieu.uzh.ch

Prof. Hanna Kokko Department of Evolutionary Biology and Environmental Studies University of Zurich, Winterthurerstrasse 190 CH-8057 Zurich, Switzerland tel +41 (0)44 635 47 40 www.kokkonuts.org hanna.kokko@ieu.uzh.ch

Hanna Kokko <hanna.kokko@ieu.uzh.ch>

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Boston Plant microMORPH

Reminder! Applications due March 15.

Due to overwhelming interest, plant 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, Pamela” <pamela.diggle@uconn.edu>

cE3c Portugal 2 EvolBiol

Subject: Portugal-cE3c-Course: two advanced courses with deadlines March-April 2016

cE3c Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the two with closer deadlines.

Additional informations at:

<http://ce3c.ciencias.ulisboa.pt/training/?cat=1> cE3c Centre for Ecology, Evolution and Environmental Changes Advanced Course Molecular Evolution

organized by Rita Ponce and Teresa Nogueira | 18-22 April 2016 @ Lisbon, Portugal

Objectives: In this course we will explore evolutionary change at the molecular level. We will focus on the origin of genomic variability and the forces that drive the evolutionary process at molecular level, as well as origin of novel gene functions and genome organization. We will integrate the knowledge from molecular evolution to other levels, such as cell biology, physiology and the relationship of genotype to phenotype and will address several applications. Part of the course will involve the discussion of both classical and recent papers and hand-on analysis of case studies.

Course instructors

Rita Ponce (anaritaponce@gmail.com)

(<https://www.linkedin.com/in/rita-ponce-7189283b>)

Teresa Nogueira (teresainogueira@gmail.com)

cE3c collaborator (<http://ce3c.ciencias.ulisboa.pt/teams/user/?id=285>)

Intended audience

This five days intensive course will be open to a maximum number of 20 participants, being directed to PhD or MSc students in Biology, Evolution, Genetics or related areas, and postdocs and other professionals working in related topics.

Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of

fees for other participants see the programme details (access link below)

Deadline for applications: March 18th, 2016

Candidates should send a short CV and motivation letter to Rita Ponce (anaritaponce@gmail.com)

For additional details about the course and to know how to register, click here:

<http://ce3c.ciencias.ulisboa.pt/training/ver.php?id> For more information about the course, please contact by email:

Rita Ponce (anaritaponce@gmail.com) or Teresa Nogueira (teresainogueira@gmail.com)

cE3c Centre for Ecology, Evolution and Environmental Changes Advanced Course EvoS-2

organized by Filipa Vala | May 2-20 2016 @ Lisbon, Portugal

Objectives: Evolutionary theory provides a framework for understanding all living systems. Nevertheless, throughout the 20th century, with a few exceptions, evolutionary biologists have avoided using evolution to address problems related to our own species. EvoS is a program created by David Sloan Wilson, and aims at turning evolutionary theory into a common language to all areas that pertain to the natural world, including human affairs. This advanced course is part of the initiatives of EvoS at the University of Lisbon.

Course instructor

Filipa Vala (fdvala@fc.ul.pt)

Post-Doc at the Centre for Ecology, Evolution and Environmental Changes (cE3c), Faculty of Sciences of the University of Lisbon (<http://ce3c.ciencias.ulisboa.pt/-teams/user/?id=111>)

Intended audience

This course will be open to a maximum number of 15 participants, being directed to PhD or MSc students in Biology, Evolution, Ecology or related areas, and post-docs and other professionals working in related topics.

Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below)

Deadline for applications: April 15th, 2016

Candidates should send a short CV and motivation

letter to Filipa Vala (fdvala@fc.ul.pt)

For additional details about the course and to know how to register, click here:

<http://ce3c.ciencias.ulisboa.pt/training/ver.php?id> For more information about the course, please contact by email:

Filipa Vala (fdvala@fc.ul.pt)

Margarida Matos <mmmatos@fc.ul.pt>

Chicago TreeGeneConservation May16-19

The following announcement is about an exciting and unique forest gene conservation workshop to be held in Chicago in May. Please pass on to interested colleagues and students! Abstract submission is closed but registration is OPEN.

There will be a National workshop on Gene Conservation of Tree Species, May 16 - 19, 2016 in Chicago, Illinois. The USDA Forest Service is a main sponsor of this event. For more details on this meeting, visit: <http://www.fs.fed.us/about-agency/gene-conservation-workshop> About the Workshop

The purpose of the workshop is to facilitate the exchange of the latest information, research, and action on genetic conservation of tree species, especially those species at risk from stressors such as insects, diseases, drought, and development. The workshop will highlight risk assessments that help to inform genetic conservation strategies as well as major actions taken by organizations for long-term conservation of tree genetic material. Using this information, participants will develop a set of actions during the meeting that can be used to form and strengthen partnerships, and foster collaboration to accelerate genetic conservation efforts.

Who Should Attend

This workshop is open to individuals and organizations with interest in tree genetic conservation, including state and federal resource managers, conservation groups, botanic gardens, forest industry and scientists from public and private institutions. This workshop will bring together a mix of land managers, conservation and restoration practitioners, researchers, and non-governmental organizations who share the goal of conserving tree species. In addition, to foster collaboration and networking, time has been built into the agenda and space

will be available for affiliated groups/chapters to hold meetings and/or promote their work.

Plenary Speakers

Tom Tidwell (Welcome Address), Chief, USDA Forest Service, Washington DC Rob Mangold Pacific Northwest Research Station Director, USDA Forest Service, Portland, OR Kayri Havens Director, Plant Science and Conservation, Chicago Botanic Garden, Glencoe, IL Paul Smith Secretary General, Botanic Gardens Conservation International, London, UK Christopher Richards Research Plant Geneticist, USDA Agricultural Research Service, Fort Collins, CO Hosny El-Lakany Director, International Forestry Program, University of British Columbia, Vancouver, BC, Canada Sir Peter Crane (Banquet Speaker, "The Future of Trees") Dean, School of Forestry & Environmental Studies, Yale University, New Haven, CT

Workshop Topics The workshop will address the following topics:

In- Situ Conservation Ex-Situ Conservation Identification of ecosystems/species to be conserved Restoration of species/ecosystems of conservation concern Tools and techniques for Tree Genetic Conservation

For more details on this meeting, visit: <http://www.fs.fed.us/about-agency/gene-conservation-workshop> "shoban@alumni.nd.edu" <shoban@alumni.nd.edu>

CIBIO Portugal Morphology

The objectives of this short course are to provide students the basic principles of functional morphology, biomechanics and movement analyses that may allow them to use these to study whole-animal performance in an ecological and evolutionary context.

Click here to see the PROGRAMME for the course.

COURSE INSTRUCTORS

Anthony Herrel, C.N.R.S/M.N.H.N. Paris, D????partement d'Ecologie et de Gestion de la Biodiversit????, Paris, France

Arie van der Meijden, CIBIO-InBIO, University of Porto, Porto, Portugal

Antigoni Kaliontzopoulou, CIBIO-InBIO, University of Porto, Porto, Portugal

INTENDED AUDIENCE This course will be open to a

maximum number of 20 participants.

Priority will be given to:

???? 1st year PhD students attending the BIODIV Doctoral Programme;

???? other BIODIV PhD students;

???? PhD students attending other courses;

???? other post-graduate students and researchers.

REGISTRATION Registration deadline: March 31, 2016.

Participation is free of charge for BIODIV students | Registration fee for other participants: 100,00. To register, please send an e-mail accompanied by your short CV to Maria Sant'Ana at post.graduation@cibio.up.pt. Please refer your status (PhD student, MSc Student, Other) and the University to which you are affiliated.

For more information about the course, please contact: post.graduation@cibio.up.pt.

CIBIO - Centro de Investiga????????o em Biodiversidade e Recursos Gen????ticos

InBIO Laborat????rio Associado, Universidade do Porto

Campus Agr????rio de Vair????o

Rua Padre Armando Quintas

4485-661 Vair????o

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t: +351 252 660 411 Ext. 285

f: +351 252 661 780

e: divulgacao@cibio.up.pt

w: <http://cibio.up.pt> | <http://inbio.pt>

f: <https://www.facebook.com/cibio.inbio> CIBIO-InBIO Divulga????o

Faro Portugal MarineGenomics Sep14-16

WEBSITE: http://att.ccmr.ualg.pt/-marine_genomics_2016 WORKSHOP IN MARINE

GENOMICS - Guest speaker J. Mark Cock (Roscoff Marine Station). Mark obtained his PhD from Leeds University in 1985 and worked during his early career on several aspects of terrestrial plant biology including nitrogen metabolism, nodulation

and self-incompatibility. In 2002, Mark moved to the Station Biologique de Roscoff (France) where he initiated a project aimed at developing the filamentous brown alga *Ectocarpus siliculosus* as a genetic model species for the phaeophyceae. Mark applies genetic and genomic approaches to identify key regulators of developmental processes, such as life cycle regulation and sex determination, and to dissect the regulatory pathways.

DESCRIPTION: Learn the theory and practice of Marine Genomics through specialist tuition and hands-on practical exercises. The course details all aspects of the genomic analysis of marine organisms, and requires no previous specialist knowledge. Participants will take part in seminar-style sessions, with theory interspersed with computational exercises and one-to-one tuition. See the programme below for details.

VENUE: Centre of Marine Sciences, University of the Algarve, Faro, Portugal. <http://ccmar.ualg.pt> - Google maps: <https://goo.gl/cM78fp>

DATE: 14th-15th-16th September 2016

FORMAT: 3-day workshop consisting of lectures, and hands-on practical sessions on computers. Participants will use computational equipment provided by the workshop, but may also wish to bring laptops. The course is equivalent to 3 European ECTS credits.

INTENDED AUDIENCE: PhD students, post-doctoral and advanced researchers (but no formal restriction)

REGISTRATION FEE: Early-bird 200 euro (only 5 places available) thereafter 270 euro. Registration includes cost of Welcoming Buffet and Closing Gala Dinner. Registration does not include travel and lodging. Faro has an international airport located 4 km from the Gambelas Campus of the University of the Algarve where the course will take place.

HOW TO APPLY: Applications in the form of a CV should be sent to ccmaratt@ualg.pt no later than 31st July 2016. Applicants will be selected on a first-come-first-served basis.

SCHOLARSHIPS: At least 2 scholarships to cover registration fees will be awarded to PhD students; applicants should send a motivational letter and proof of student status.

ACCOMMODATION: Recommended: Hotel Aeromar at the Faro beach has temporarily reserved 8 double rooms that must be reserved by May 31 at the latest - after that date they will not save the rooms. These 8 rooms cost 62,5 euros (single occupancy) or 80 euros (double occupancy), including breakfast. Special price for CCMAR-UAlg. Additional accommodation

is available at the beach and in Faro city centre. A workshop-provided minibus service will run between the beach, Faro city centre, and campus.

CONTACTS: Gareth Pearson - Research Associate, CCMAR - gpearson@ualg.pt Cymon J. Cox - FCT Coordinating Researcher, CCMAR - cymon@ualg.pt

Advanced Technologies and Training programme @ CCMAR 2016 ccmaratt@ccmar.ualg.pt, att.ccmarmar.ualg.pt

PROGRAMME:

Wednesday 14th September

9:00-10:15 Introduction to Marine Genomics

Tutor: Mark Cock

10:30-13:00 Experimental design - marine genomic pipelines

Tutors: Nadège Zaghdoudi and Gareth Pearson

This session will introduce the student to some of the possible experimental workflows for marine genomics through interactive, hands-on exercises. Students will learn the details of a model genomics information pipeline from sample extraction all the way through data analysis. We will focus on the use of RNA-seq analyses in phylogenomics studies but the analytical strategy is broadly applicable to various data types used to answer a variety of questions. The student will be introduced to a basic workflow framework to which additional tools and analytical details will be added during the course. By the end of the course, it is expected that the students will have a thorough understanding of the types of genomics tools available, and how and when to properly apply them to questions in marine genomics.

14:00-18:30 Introduction to bioinformatic techniques

Tutors: Pedro Fernandes and Daniel Sobral

Basic bioinformatic concepts and practices will be introduced. This session will teach the following topics: bioinformatics in biological research; the need to adopting Linux platforms; Linux command line; Linux file system navigation; installing software in Linux systems; biological databases, interoperability, and file formats; sequence alignments (global, local algorithms); the concept of "database search" in molecular biological data; speeding-up: the BLAST family of programs, interpretation of results; changing parameters in BLAST searches; concepts and methods of maintaining reproducibility in bioinformatics.

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Glasgow DNAtaxonomy Aug8-11

“Advances in DNA taxonomy”

Instructors - Prof. Ziheng Yang and Dr. Diego Fontaneto

This course will run from 8th - 11th August 2016 at SCENE Field Station, Loch Lomond national park, Scotland

<http://prstatistics.com/course/advances-in-dna-taxonomy-dntx/> Course content is as follows

Day 1

- Introduction to DNA taxonomy
- The applied ecological approach and the theoretical evolutionary approach.
- What is needed to perform DNA taxonomy.
- How to get data.
- Phylogenetic reconstruction using distance-based and parsimony methods.
- Introduction on NJ, UPGMA, parsimony; when and why they can be used for DNA taxonomy.
- Computer practical.

Day 2

- Phylogenetic reconstructions
- Using Maximum Likelihood with computer practical on Maximum Likelihood.
- Using Bayesian Inference with computer practical on Bayesian Inference.

Day 3

- Single-locus DNA taxonomy.
- Most commonly used methods Rationale and use for fixed threshold, ABGD, K/theta, PTP, GMYC with computer practicals.
- Other methods, Haplowebs, bGMYC, etc. with computer practicals

Day 4

- Multi-locus DNA taxonomy with computer practicals

Please email any inquiries to oliverhooker@prstatistics.com or visit our website

www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

Upcoming courses - email for details oliverhooker@prstatistics.com

ADVANCING IN STATISTICAL MODELLING USING R (May)

TIME SERIES MODELS FOR ECOLOGISTS AND CLIMATOLOGISTS USING R (May)

INTRODUCTION TO PYTHON FOR BIOLOGISTS (May)

GENETIC DATA ANALYSIS USING R (August)

INTRODUCTION TO BAYESIAN HIERARCHICAL MODELLING (August)

MODEL BASED MULTIVARIATE ANALYSIS OF ECOLOGICAL DATA USING R (October)

LANDSCAPE (POPULATION) GENETIC DATA ANALYSIS USING R (October)

APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS (October)

Dates still to be confirmed - email for details oliverhooker@prstatistics.com

STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR USING R

INTRODUCTION TO R AND STATISTICS FOR BIOLOGISTS

Oliver Hooker

PR Statistics

“oliverhooker@prstatistics.co.uk”

<oliverhooker@prstatistics.co.uk>

Glasgow Linux workflows Aug15-19

Glasgow.LINUXworkflows.Aug15-19

Course: Introduction to LINUX workflows for biologists

Instructor: Dr. Martin Jones

This course will run from 15th - 19th August 2016 at SCENE (the Scottish Centre for Ecology and the Natural Environment), Loch Lomond National Park, Glasgow.

Course overview: Most high-throughput bioinformatics work these days takes place on the Linux command line.

The programs which do the majority of the computational heavy lifting — genome assemblers, read mappers, and annotation tools — are designed to work best when used with a command-line interface. Because the command line can be an intimidating environment, many biologists learn the bare minimum needed to get their analysis tools working. This means that they miss out on the power of Linux to customize their environment and automate many parts of the bioinformatics workflow. This course will introduce the Linux command line environment from scratch and teach students how to make the most of its tools to achieve a high level of productivity when working with biological data.

Availability: 15 places total.

Course programme

Monday 15th - Classes from 09:00 to 17:00 (approximately)

— Session 1 - The design of Linux

In the first session we briefly cover the design of Linux: how is it different from Windows/OSX and how is it best used? We'll then jump straight onto the command line and learn about the layout of the Linux filesystem and how to navigate it. We'll describe Linux's file permission system (which often trips up beginners), how paths work, and how we actually run programs on the command line. We'll learn a few tricks for using the command line more efficiently, and how to deal with programs that are misbehaving. We'll finish this session by looking at the built in help system and how to read and interpret manual pages.

— Session 2 - System management

We'll first look at a few command line tools for monitoring the status of the system and keeping track of what's happening to processor power, memory, and disk space. We'll go over the process of installing new software from the built in repositories (which is easy) and from source code downloads (which is trickier). We'll also introduce some tools for benchmarking software (measuring the time/memory requirements of processing large datasets).

Tuesday 16th - Classes from 09:00 to 17:00 (approximately)

— Session 3 - Manipulating tabular data

Many data types we want to work with in bioinformatics are stored as tabular plain text files, and here we learn all about manipulating tabular data on the command line. We'll start with simple things like extracting columns, filtering and sorting, searching for text before moving on to more complex tasks like searching for duplicated values, summarizing large files, and combining

simple tools into long commands.

— Session 4 - Constructing pipelines

In this session we will look at the various tools Linux has for constructing pipelines out of individual commands. Aliases, shell redirection, pipes, and shell scripting will all be introduced here. We'll also look at a couple of specific tools to help with running tools on multiple processors, and for monitoring the progress of long running tasks.

Wednesday 17th - Classes from 09:00 to 17:00 (approximately)

— Session 5 - EMBOSS

EMBOSS is a suite of bioinformatics command-line tools explicitly designed to work in the Linux paradigm. We'll get an overview of the different sequence data formats that we might expect to work with, and put what we learned about shell scripting to biological use by building a pipeline to compare codon usage across two collections of DNA sequences.

— Session 6 - Using a Linux server

Often in bioinformatics we'll be working on a Linux server rather than our own computer — typically because we need access to more computing power, or to specialized tools and datasets. In this session we'll learn how to connect to a Linux server and how to manage sessions. We'll also consider the various ways of moving data to and from a server from your own computer, and finish with a discussion of the considerations we have to make when working on a shared computer.

Thursday 18th - Classes from 09:00 to 17:00 (approximately)

— Session 7 - Combining methods

In the next two sessions — i.e. one full day — we'll put everything we have learned together and implement a workflow for next-gen sequence analysis. In this first session we'll carry out quality control on some paired-end Illumina data and map these reads to a reference genome. We'll then look at various approaches to automating this pipeline, allowing us to quickly do the same for a second dataset.

— Session 8 - Combining methods

The second part of the next-gen workflow is to call variants to identify SNPs between our two samples and the reference genome. We'll look at the VCF file format and figure out how to filter SNPs for read coverage and quality. By counting the number of SNPs between each

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To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

Glasgow ViralBioinformatics Aug1-5

The deadline for applications to the course is Friday 18th March 2016.

Training course on Viral Bioinformatics and Genomics
Glasgow, United Kingdom

Course Dates: Monday 1st - Friday 5th August 2016
Course Cost: £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@glasgow.ac.uk”
<Richard.Orton@glasgow.ac.uk>

Hinxton Cambridge CancerEvolution Jul11-15

Wellcome Genome Campus Advanced Courses and Scientific Conferences

EVOLUTIONARY BIOLOGY AND ECOLOGY OF
CANCER 11-15 July 2016 Wellcome Genome Campus,
Hinxton, Cambridge, UK

Save the Date: <https://-registration.hinxton.wellcome.ac.uk/events/-item.aspx?e=597>

We are pleased to announce a new course focusing on Evolutionary Biology and Ecology of Cancer. Knowledge of evolution and ecology is important to understand and clinically control cancer. Unfortunately, there are few cancer biologists trained in evolution and ecology, and few evolutionary biologists and ecologists work in cancer research.

The aim of this new course is to cross-train evolutionary biologists and ecologists in cancer, and to train cancer biologists in the relevant evolutionary biology and ecology to facilitate cross fertilization of ideas and forge active collaborations. For example, in the areas of evolutionary modelling and 'steering' in vitro, in determinants of convergent evolution, and in predictive parameters for evolutionary progression.

Course topics -The dynamics of somatic evolution - Cancer phylogenetics -Ecological theory -Cooperation and cheating between neoplastic cells -Ecology of cell-type interactions -Ecological interactions with the microbiome -Ecology of inflammation in tumours -Ecological measurements -Acquired therapeutic resistance and adaptive therapy

This course is aimed at researchers currently working in cancer and/or evolution and ecology. It is particularly suited to evolutionary biologists and ecologists interested in moving into cancer research, and to cancer biologists and oncologists who lack formal training in evolutionary biology. Applications are invited

from early career scientists, including post-graduate students, postdoctoral fellows and new principle investigators. For further information, please visit the course website: <https://registration.hinxton.wellcome.ac.uk/events/item.aspx?e=597> Course instructors Athena Aktipis (Arizona State University, USA & Institute of Cancer Research, UK) Mel Greaves (Institute of Cancer Research, UK) Carlo Maley (Arizona State University, USA & Institute of Cancer Research, UK)

A list of confirmed tutors will be available shortly. To register your interest in this course, please contact scientificconferences@wellcomegenomecamous.org.

Dates for your diary Application deadline: 10 May

View Full Details: <https://registration.hinxton.wellcome.ac.uk/events/item.aspx?e=597> Please feel free to forward this information to your colleagues.

Treasa Creavin <treasa.creavin@wellcomegenomecampus.org>

Hinxton UK HumGenomeAnalysis Jul20-26 DeadlineApr8

Human Genome Analysis: Genetic Analysis of Multifactorial Diseases 20-26 July 2016, Wellcome Genome Campus, Hinxton UK Application and Bursary Deadline: 8 April

Summary: This intensive, computational course is aimed at scientists actively involved in genetic analysis of multifactorial traits. The programme provides a comprehensive overview of the statistical methods currently used to map disease susceptibility genes in human populations.

Bursaries: Limited bursaries are available (up to 50% of the course fee) and are awarded on merit. URL: <https://registration.hinxton.wellcome.ac.uk/events/item.aspx?e=3D566> COURSE INSTRUCTORS

Daniel Weeks (University of Pittsburgh, USA) Heather Cordell (Newcastle University, UK) Simon Heath (Centre Nacional d'Anàlisi Genòmica (CNAG), Barcelona, Spain) Janet Sinsheimer (UCLA, USA) Eric Sobel (UCLA, USA) Joe Terwilliger (Columbia University, USA)

GUEST SPEAKERS for 2016

Richard Duerr (University of Pittsburgh, USA) Andrew Morris (University of Liverpool, UK) Nicole Soranzo (Wellcome Trust Sanger Institute, UK) Timothy Thorn-

ton (University of Washington, USA) Chris Wallace (University of Cambridge, UK)

Full details at: www.welcomegenomecampus.org/coursesandconferences "JanetS@mednet.ucla.edu" <JanetS@mednet.ucla.edu>

Kunming Metabarcoding Aug22-26

Dear Colleagues,

We are please to announce that this year the sixth DNA Metabarcoding Spring School will held in Kunming (China) and will be organized in collaboration with Doug Yu and Xin Zhou.

Please take care than this year the registration period will end by May the 15th, 2016.

<http://metabarcoding.org/spip.php?article76> Best regards

Eric Coissac

Dr Eric Coissac Associate professor Laboratoire d'Ecologie Alpine UMR UGA-USMB-CNRS 5553 Université Grenoble Alpes CS 40700 38058 Grenoble cedex 9 -France

The sixth DNA metabarcoding Spring School at Kunming

FROM AUGUST 22TH TO 26TH, 2016

DNA metabarcoding is a rapidly evolving method for assessing biodiversity from environmental DNA and bulk samples. It has a wide range of applications: biodiversity monitoring, animal diet assessment, reconstruction of paleo communities, among others. DNA metabarcoding uses molecular techniques such as PCR and next generation sequencing, and integrates skills in bioinformatics and biostatistics with classical ecological knowledge.

The DNA metabarcoding spring school is now in its sixth edition, and this year it is co-organized by the metabarcoding.org team and the Kunming Institute of Zoology, with support from the Chinese Academy of Sciences, Yunnan.

The DNA metabarcoding spring school will be held from August 22 to 26, 2016

The school will be divided in two parts:

- Two days of lectures (22nd, 23rd) - Three days of practicals

All the lectures and the practicals will be taught in English

The number of participants in the lecture portion is not limited, but registration is mandatory.

The number of participants in the practical portion is limited to 24.

Candidates can apply for the school by sending an email to the following address :

kunming2016@metabarcoding.org

The email must contain a brief curriculum vitae and a short letter of motivation. For applicants wishing to participate in the practical sessions, we request a more complete letter indicating how your research will benefit from DNA metabarcoding and what you are hoping to learn from this school. As part of the course, each participant in the practical portion will give a flash talk (5 minutes) about your research and how it is related to DNA metabarcoding.

Registration deadline is 15 May 2016

Main lecturers - Xin Zhou (BGI, China) - Douglas Yu (KIZ, China; University of East Anglia, UK) - Frédéric Boyer (LECA, CNRS, France) - Antony Chariton (CSIRO, Australia) - Eric Coissac (LECA, UGA, France) - Pierre Taberlet (LECA, CNRS, France) - Lucie Zinger (EDB, CNRS, France) - Kristine Bohmann (Geogenetic center - Danemark)

Course Schedule

The lectures will cover different aspects of DNA metabarcoding. The bioinformatics practicals will introduce data analysis from raw sequences to basic ecological conclusions. The molecular ecology practical will present basic techniques for DNA extraction in the field and DNA amplification by PCR. After the course formally ends on 26 August, many of the lecturers will remain in Kunming to allow for one-on-one interaction and consultation.

Travel and accommodation

Flights to Kunming To get to Kunming (KMG), the best way is to fly. If travelling from Europe, there is a direct flight from Paris-CDG to KMG, on China Eastern Airlines (MU). Arrival should be by Sunday 21 August. Another good flight from Europe is the KLM AMS-CTU flight (KL891 and KL892), then flying by China Eastern from CTU to Kunming (MU).

Please feel free to consult with us over the best flight.

China requires an entry visa, arranged before travel. Chinese visa details link The visa type is F, and you need an invitation letter from KIZ. We will provide this

upon email request. Please give us your this information to include on the letter:

1) full name as stated on the passport 2) gender 3) date of birth 4) planned arrival and departure dates

Accommodation and Meals Students are responsible for their own hotel costs and meals. A shared room will cost approximately RMB 250 (~35euro) per night (i.e. RMB 125 per student-night), and the hotels are close to the course venue. We will provide box lunches on 22-26 August.

Eric Coissac <eric.coissac@inria.fr>

LakeBalaton Hungary ConservationGenetics May30-Jun10 Deadline

SHORT TITLE

Registration Deadline - CONGEN2016 Lake Balaton Hungary

LONG TITLE

Deadline approaching - Recent Advances in Conservation Genetics Course (ConGen2016)at Lake Balaton, HUNGARY www.congen2016.com Dear Conservation Genetics Community:

Please note that the Registration deadline for ConGen2016 is approaching (April 15).

The 2016 Recent Advances in Conservation Genetics Short Course (ConGen2016) will be held at Balaton Limnological Institute of the Hungarian Academy of Sciences near Budapest, Hungary over May 30-June 10, 2016. The course will host 25-30 students dedicated to conservation and about 20-25 faculty from around the world.

The course will be directed by Dr. Stephen J. O'Brien, and taught by renowned scientists in methods, interpretation, and applications of molecular genetic analyses for conservation of endangered species, who will also share a variety of their personal experiences in this important field. ConGen2016 faculty (<http://congen2016.com/home/congen2016-faculty/>) is an amazing group of people who come from all around the world and will be teaching, sharing their conservation stories and interacting with students during the course.

For the first time in its ore than 25 year history Congen is coming to Europe. The 2016 course will be organized

in collaboration with the Balaton Limnological Institute on the shores of this charming freshwater lake in Hungary. It is one of the largest freshwater lakes, and one of the region's foremost tourist destinations. The mountainous region of the northern shore is known both for its historic character and as a major wine region, while the flat southern shore is known for its resort towns. Due in no small way to the scientific efforts of the Balaton Institute researchers, Lake Balaton is today one of the most intensively studied lakes of the world.

Who should apply?

Applicants should be conservation-minded scientists (advanced graduate students, post-docs, teachers, and researchers with advanced degrees) from academia, government, NGOs, or industry who are studying the genetics of endangered species and who will apply the knowledge gained from this course to the conservation of such species.

Please submit your registration here: <http://congen2016.com/home/registration/> Registration Cost:

Early Registration - paid before March 1, 2016: The cost per participant will be US\$2,150 and will include your accommodation, all meals and travel from and to the airport.

Late Registration - paid after March 1 and before April 25, 2016: The cost of late registration per participant will be US\$2,350 and will include your accommodation, all meals and travel from and to the airport.

Application forms: Please complete the application form below and submit together with a CV. Successful applicants will be notified via email and will be sent additional course information and they must ensure that they check the following list. Payment must be made in full using the PayPal link that will only be made available to the successful applicants have been notified or by direct bank deposit (SWIFT).

Scholarships:

Partial or full scholarships may be awarded to registered students, subject to availability. The scholarship application is a separate process and will be coordinated with our sponsors. To be eligible for a scholarship, please apply on this page <http://congen2016.com/home/registration/scholarship-application/> . Please note: Scholarships will be allocated based on need, scholastic potential, likelihood of conservation translation, the applicant's CV, and other information contained in the application form. Scholarships will be awarded as a complete or partial refund of the tuition for those applicants who have already submitted their deposit.

Course Faculty

- Stephen J. O'Brien: Chief Scientific Officer at the Theodosius Dobzhansky Center for Genome Bioinformatics, St. Petersburg State University, RUSSIA
- Scott Baker: Professor and Associate Director, Marine Mammal Institute, Oregon State University, OREGON, USA
- Oliver Ryder: Director of Genetics and Kleberg Chair of San Diego Zoo's Institute for Conservation Research, CALIFORNIA, USA
- Joan Pontius: Senior Bioinformatics Scientist at ESAC Inc, Rockville MARYLAND, USA
- Harris Lewin: Vice chancellor for research at the University of California, Davis, CALIFORNIA, USA
- Dennis Larkin: Reader in Comparative Genomics Veterinary College, London, ENGLAND, UK
- Bridget von Holdt: Assistant Professor, Ecology and Evolution, Princeton University, NEW JERSEY, USA
- Augustinho Antunes: CIMAR, Centro Interdisciplinar de Investiga  o Marinha e Ambiental, Laboratory of Ecotoxicology,

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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>

Leipzig Germany Biodiversity Jun19-25

iDiv Summer School 2016 "Biodiversity Synthesis and Integration"

19-25 June 2016, Leipzig Germany Open to PhD students and advanced master's students

summerschool.idiv.de

The German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, a global hub for biodiversity science, invites graduate students to apply to its second summer school taking place in Leipzig, Germany, from 19 to 25 June, 2016.

The summer school mingles 20 promising young researchers and experienced researchers in a relaxed and constructive atmosphere. The overarching aim of the

summer school is that students and researchers benefit from their common work by publishing together the results of their research project. The programme will consist of daily plenaries on integrative biodiversity study, launching the day with a methodological talk and finishing with a keynote lecture. The greatest part of the programme will be dedicated to research projects, designed by in-house researchers of iDiv to be completed by 3-6 students, with objectives of article submission. Opportunities will also be available to encounter and chat with the local researchers.

The summer school is aimed mainly at PhD students working on biodiversity topics, but applications from advanced master's level students will be considered. Travel grants are also available, based on quality and resources of the applicants, covering part or all travel and accommodation costs.

For more details, please consult our webpage summer-school.idiv.de. The deadline for application to the summer school is Sunday, 03 April 2016.

“ulrike.schmidt@idiv.de” <ulrike.schmidt@idiv.de>

MBL WoodsHole MolecularEvolution ApplDueApr4

Applications for the Workshop on Molecular Evolution at the MBL in Woods Hole are due April 4th, 2016. The application materials can be found at <http://www.mbl.edu/education/special-topics-courses/workshop-on-molecular-evolution/>. See https://molevol.mbl.edu/index.php/Main_Page for information about the workshop.

“Hillis, David” <dhillis@austin.utexas.edu>

MichiganStateU Avida-ED Jun9-11

*The application deadline has been extended, so we're sending the announcement again.

*

***2nd Active LENS Workshop: June 2016*

The 2nd annual Avida-ED Active LENS Workshop will be held at Michigan State University June 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/>. *We have extended the application deadline; applications will be considered on a rolling basis through March 31, 2016*. If you have any questions or difficulties with the application, contact Michael Wiser (mwiser@msu.edu).

“mwiser@msu.edu” <mwiser@msu.edu>

Naples NGSVariantCalling May02-06

* ELIXIR-ITA, in collaboration with the Institute of Genetics and Biophysics is pleased to inform you that the applications for the upcoming training course on “NGS for evolutionary biologists: from basic scripting to variant calling” are now open.

**

IMPORTANT DATES for this Course*:* * Deadline for applications: 30/03/2016 * Latest notification of acceptance: 10/04/2016 Course date: 2-6/05/2016 * *Venue: Biblioteca, Consiglio Nazionale delle Ricerche, via P. Castellino 111, 80131 Naples, Italy *

* *A maximum of 20 candidates will be selected based on their research profile. Notifications of acceptance will be sent shortly after the closing date of registration.*

Priority will be given to candidates from ELIXIR-ITA institutions and other ELIXIR nodes. Should you have any question, do not hesitate to contact the ELIXIR-ITA training coordinator, Dr Allegra Via, at a.via@ibbe.cnr.it or elixir.ita.training@gmail.com

** Full details, including the course programme and the application form, at: <http://-bioinformaticstraining.pythonanywhere.com/course/5/> Instructors*:* Chiara Batini (University of Leicester, UK) Vincenza Colonna (CNR, Napoli, IT) Allegra Via (CNR, Bari, IT)

Course description * This course will provide an introduction to next generation sequencing platforms, data analysis and tools for data quality control, including alignment to a reference sequence, data handling and visualisation, and variant calling and filtering (single

nucleotide polymorphisms and structural variants). The course will be delivered using a mixture of lectures and computer based hands-on practical sessions, including mini-projects to be completed by the participants using the knowledge gained at the course. Projects will cover the general topics of population structure and admixture, demographic changes and natural selection. * This course is aimed at PhD students and post-doctoral researchers who are applying, or will apply in the near future, high throughput sequencing technologies and the related bioinformatics tools in their research. Participants with limited UNIX/Linux and R/Bioconductor experience will be provided with basic understanding of the command-line operations and the foundations of the R programming language on the first day of the course.

Thank you for your interest,

The Organisers

Chiara Batini (University of Leicester, UK) Vincenza Colonna (CNR, Napoli, IT) Allegra Via (CNR, Bari, IT) *

“cb334@leicester.ac.uk” <cb334@leicester.ac.uk>

Roscoff MarineEvolGenomics Jun13-24 DeadlineMar31

12th Summer Course on

Marine Ecological & Evolutionary Genomics

Applications have to be completed before Thursday, March 31st 2016 - 8.00am CET. No application will be considered after this deadline.

Aims

Marine genomics knowledge is crucial for understanding the marine environment and for an efficient use of its resources. State of the art NGS methods have revolutionized the field, spawning applications in basic research and environmental management. The course will give insight into population, environmental, biodiversity, comparative, evolutionary and functional genomics through lectures, case studies and computer labs.

Target group

Advanced PhD students (at least in their second year) and junior postdocs with a solid knowledge in marine ecological and environmental genomics, phylogenetics and/or population genetics.

Context

The 12th edition of the MEEG Summer Course is sponsored by EuroMarine, the European marine science network (www.euromarinenetwork.eu) and EMBRC-France (www.embrc-france.fr/fr), the French node of the European Marine Bioresources Center (www.embrc.eu).

Application To apply, please click on How to apply on the left menu and read the instructions carefully. Do not forget to submit your Curriculum vitae (2 pages), a cover letter (1 page) and a support letter before March 31st 2016. 18 participants will be selected according to the following criteria:

1. Relevance of the course for their PhD or post-doc project
2. Background and experience of applicant
3. Diversity; we aim for participants with different research backgrounds (only one person per institute will be considered) and equal gender balance among participants.

The selected candidates will be notified by April 7th 2016 and are requested confirm their attendance within seven days. We will have a waiting list in case of non-confirmations and cancellations.

Matthias Obst <matthias.obst@marine.gu.se>

SanJuan PR PCM Workshop Reminder Jun28-Jul1

This is just a reminder that the deadline to apply for our workshop on phylogenetic comparative methods is the 1st of April, 2016. We cannot guarantee that applications received after the deadline will be considered. // Este anuncio es un aviso que la fecha para entregar una aplicación por nuestro taller en métodos comparados en Puerto Rico es el 1 de abril de 2016. No podemos garantizar que aplicaciones recibidas después de esta fecha van a estar evaluadas.

The following is an announcement for a workshop we will offer on phylogenetic comparative methods in San Juan, Puerto Rico from June 28 - July 1, 2016. The course is free of cost, and there are various stipends to partially or fully cover travel and lodging expenses. A Spanish version of the announcement can also be seen below.

El siguiente es un anuncio por un taller sobre métodos comparativos filogenéticos que ofreceremos en San Juan, Puerto Rico desde el 28 de junio hasta el 1 de julio, 2016. El curso es libre de costos, y hay varios estipendios disponibles para minimizar o cubrir los gastos de

viaje y alojamiento en San Juan. Versión en español abajo.

Intensive short course on macroevolution and phylogenetic comparative methods in R

We are pleased to announce a new graduate-level intensive short course on the use of R for phylogenetic comparative analysis and downstream implementation in macroevolutionary studies. The course will be four days in length and will take place at the Hyatt House Hotel of San Juan from the 28th of June to the 1st of July, 2016. This course is partially funded by the National Science Foundation, with additional support from the University of Massachusetts Boston and the University of Puerto Rico, Río Piedras. There are a number of full stipends available to cover the cost of travel, room and board for qualified students and post-docs. Applicants are welcome from any country; however, we expect that most admitted students will come from the Caribbean region and Latin America. Accepted students from further afield may be offered only partial funding for their travel expenses. Topics covered will include: an introduction to the R scientific computing environment, tree manipulation, independent contrasts and phylogenetic generalized least squares, ancestral state reconstruction, models of character evolution, diversification analysis, and visualization methods for phylogenies and comparative data. Course instructors will include Dr. Liam Revell (University of Massachusetts Boston), Dr. Luke Harmon (University of Idaho), Dr. Mike Alfaro (University of California, Los Angeles), and Dr. Ricardo Betancur (University of Puerto Rico).

Instruction in the course will be primarily in English; however some of the instructors and TAs of the course are competent or fluent in Spanish and English. Discussion, exercises, and activities will be conducted in both languages.

To apply for the course, please submit your CV along with a short (1 page) description of your research interests, background, and reasons for taking the course. Admission is competitive, and preference will go towards students with background in phylogenetics and a compelling motivation for taking the course. In your application please indicate your preferred travel airport, if appropriate. Applications should be submitted by email to pr.phylogenetics.course@gmail.com by April 1st, 2016. Applications may be written in English or Spanish; however all students must have a basic working knowledge of scientific English. Questions can be directed to liam.revell@umb.edu.

Curso de macroevolución y uso de métodos filogenéticos comparativos en R

Nos complace anunciar un nuevo curso intensivo tipo taller para estudiantes graduados/posgrado sobre el uso de R en métodos filogenéticos comparativos con enfoque a estudios sobre macroevolución. El curso tendrá una duración de cuatro días y se llevará a cabo en el Hyatt House Hotel de San Juan, Puerto Rico, entre el 28 de junio y el 1 de julio de 2016. Este curso estará parcialmente financiado por la National Science Foundation (Estados Unidos), con apoyo adicional de University of Massachusetts Boston y la Universidad de Puerto Rico, Río Piedras. Hay varios estipendios completos disponibles para cubrir los costos de tiquetes de avión y alojamiento para estudiantes e investigadores postdoctorales calificados. Solicitudes de cualquier país serán recibidas; sin embargo, anticipamos que la mayoría de los estudiantes admitidos serán de la región Caribe y otros países latinoamericanos. Estudiantes provenientes de países más lejanos que resulten elegidos tendrán la posibilidad de recibir únicamente apoyo parcial para costear sus gastos del viaje. Los temas que serán

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Seoul ViralBioinformaticsEvolution Aug14-19

DEADLINE EXTENDED TO 15 MARCH 2016

“21st International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology”

Korea University College of Medicine, Seoul, Republic of Korea Sunday, August 14 - Friday, August 19, 2016

Dear colleague,

The 21st International Workshop on Virus Evolution and Molecular Epidemiology (VEME) will be hosted by the Korea University College of Medicine, Seoul, Republic of Korea during August 14-19, 2016.

The 'Phylogenetic Inference' module offers a theoretical background and hands-on experience in phylogenetic analysis for those who have little or no prior expertise in sequence analysis. An 'Evolutionary Hypothesis Testing'

is targeting participants who are well familiar with alignments and phylogenetic trees, and would like to extend their expertise to likelihood and Bayesian inference in phylogenetics, coalescent and phylogeographic analyses ('phylogenomics'). A 'Large Dataset Analysis' module will cover the more complex analysis of full genomes, huge datasets of pathogens including Next Generation Sequencing data, and combined analyses of pathogen and host.

Practical sessions in these modules will involve software such as, PHYLIP, PAUP*, DAMBE, PHYML, MEGA, PAML, HYPHY, IQ-TREE, TREE-PUZZLE, Consel, RAxML, Fasttree, SplitsTree, BEAST1, BEAST2, Mr-Bayes, Clusterpicker, PhyloPart, Phylotype, LASSO, bowtie, bcftools, PLINK, QuRe, Velvet, SPAdes, MEGAN, UGENE, Simplot, RDP3, Figtree, R package.

We recommend participants to buy The Phylogenetic Handbook as a guide during the workshop, and to bring their own data set.

The abstract and application deadline is extended to March 15th Selections will be made by the beginning of April.

The registration fee of 900 Euro covers attendance, lunches and coffee breaks. Participation is limited to 30 scientists in each module and is dependent on a selection procedure based on the submitted abstract and statement of motivation. A limited number of grants are available for scientists who experience difficulties to attend because of financial reasons.

Selection criteria: (in order of importance)

Quality of the abstract: abstracts will be reviewed and priority will be given to applicants who are first author on the abstract. Letter of motivation: how urgent/important is your need for training? Each module is preferably restricted to 1 participant from the same lab. We strive for participation from diverse countries.

Grant criteria: (in order of importance) Priority to countries with limited resources. Ranking according to the abstract quality.

Additional information and application forms are available on our website: <http://www.rega.kuleuven.be/cev/-veme-workshop/2016>

We are confident that this course meets the needs of many molecular virologists and epidemiologists, and hope we can assist you in your search for training in Bioinformatics methods.

Yours sincerely,

Prof. Dr. Man-Seong Park, Dr. Soo-Yon Rhee and Prof. Dr. Anne-Mieke Vandamme Organizers of the

workshop

Contact: veme2016@rega.kuleuven.be

heiko.schmidt@univie.ac.at

ShoalsMarineLab
MarineVertebrateEvol Jul25-Aug8

Shoals Marine Laboratory “summer college courses”
Anatomy & Function of Marine Vertebrates

Join us in Maine for a 2-week credit course in Anatomy & Function of Marine Vertebrates (BioSM 3210/MEFB 754) this summer! <http://www.shoalsmarinelaboratory.org/course/anatomy-and-function-marine-vertebrates> COURSE DESCRIPTION:

The course covers comparative anatomy and function of vertebrates, with a strong emphasis on marine species (e.g., sharks, bony fishes, marine birds, sea turtles, seals, and cetaceans). We combine studies of structure, evolution, physiology, and biomechanics to provide an integrative framework for understanding how animals use anatomy to interface with the marine environment. Laboratory and field activities include dissections of sharks and other fishes, marine mammal necropsies, trawling, whale watching, trips to the intertidal, and visits to nearby seal and seabird colonies. Each student will complete an independent research project on a topic within the field of anatomy and function. DATES: July 25 - August 8, 2016

CREDITS: 4 undergraduate credits from the Univ. of New Hampshire awarded upon completion

FACULTY: Dr. Stacy C. Farina (Postdoctoral Fellow, Harvard University) and Dr. Malcolm Gordon (Professor, UCLA)

PREREQUISITE: One semester of college-level biology or equivalent.

LOCATION: Shoals Marine Laboratory, Appledore Island, Isles of Shoals, Maine

APPLY ONLINE (no application fee!): <http://www.shoalsmarinelaboratory.org/admissions> For more information about the Shoals Marine Laboratory: www.shoalsmarinelaboratory.org Shoals Marine Laboratory (SML) on Appledore Island, Isles of Shoals, Maine is dedicated to undergraduate education and research in marine science. SML is a residential island campus

run by the University of New Hampshire and Cornell University since 1966. This summer will be the lab’s 50th Anniversary Year. SML offers students a unique opportunity to study marine science in the field with exceptional faculty from institutions throughout North America. The island field station supports research, sustainability, and fieldwork experience that a traditional campus setting cannot duplicate. Explore the blue while living green at the Shoals Marine Laboratory this summer!

stacy.farina@gmail.com

**TGAC Norwich UK RADseq and
Stacks May23-27**

Hi All,

We will be hosting a RAD sequencing and analysis course in June at TGAC in the UK.

http://www.tgac.ac.uk/361_Division/training-programme/courses-workshops/tgac-events/genotyping-by-sequencing-2016/ This course will discuss the RAD molecular protocol and the computational analysis of RAD data. We will start from the beginning in presenting analysis techniques, providing participants with a solid base of UNIX before we move on to analyzing data with Stacks.

- We will analyze data with and without a reference genome, focusing on analyzing data to look for population structure in the de novo case, and doing Fst genome scans in the reference genome case. We will also analyze RAD data to produce phylogenetic trees.

- We will have two guest speakers who will present their RAD analyses, including population structure in right whales and the effects of toxins on populations of brown trout.

- Students will have an opportunity to interact with the instructors, guest speakers, and fellow attendees giving lots of time to talk strategy and research tactics.

The course will run from May 23 through the 27th at The Genome Analysis Centre (TGAC) in Norwich, UK.

Please forward this message on to any local mailing lists if you think there may be interest.

Thanks and best wishes,

julian

Julian M Catchen, Ph.D. Assistant Professor Department of Animal Biology University of Illinois, Urbana-Champaign

jcachen@illinois.edu; @jcachen

"jcachen@illinois.edu" <jcachen@illinois.edu>

Toulouse Evolution May30-31 Registration

Dear colleagues,

Registration for the 4th Toulouse Economics and Biology Workshop, May 30-31, is now open: www.iast.fr/conference/4th-toulouse-economics-and-biology-workshop Please note the deadline for posters' submission is March 31, in two weeks. Submissions (abstract + C.V.) should be sent to econbio_poster@iast.fr. A limited number of travel grants will be available. To apply, please join a cover letter explaining why you are applying for a grant and why you are interested in attending the workshop.

The theme of the workshop this year is "Evolution: transmission mechanisms and population structure". The speakers are: Yann Algan, Sciences Po, Paris Carl Bergstrom, University of Washington Alberto Bisin, New York University Jean Clobert, Station d'Ecologie Théorique et Expérimentale du CNRS à Moulis Gabriella Conti, University College London Mats Gyllenberg, University of Helsinki Barry Hewlett, Washington State University, Vancouver Sarah Mathew, Arizona State University, Tempe Hisashi Ohtsuki, The Graduate University for Advanced Studies, Hayama David Queller, Washington University, St Louis Paul Seabright, Institute for Advanced Study in Toulouse, Toulouse School of Economics Joan Strassmann, Washington University, St Louis

The workshop will take place at the Institute for Advanced Study in Toulouse, Manufacture des Tabacs, 21 Allée de Brienne, 31015 Toulouse, France.

We look forward to welcoming you!

Organizers: Ingela Alger and Jörgen Weibull Co-organizers: Jeanne Bovet and Arnaud Tognetti

For any information please contact us at econbio@iast.fr

Arnaud gmail <arnaud.tognetti@gmail.com>

Vairao Portugal EvolutionFunctionalMorphology Apr18-20

The objectives of this short course are to provide students the basic principles of functional morphology, biomechanics and movement analyses that may allow them to use these to study whole-animal performance in an ecological and evolutionary context.

Click here to see the PROGRAMME for the course.

COURSE INSTRUCTORS

Anthony Herrel, C.N.R.S/M.N.H.N. Paris, DAA@partement d'Ecologie et de Gestion de la BiodiversitAA©, Paris, France

Arie van der Meijden, CIBIO-InBIO, University of Porto, Porto, Portugal

Antigoni Kaliontzopoulou, CIBIO-InBIO, University of Porto, Porto, Portugal

INTENDED AUDIENCE This course will be open to a maximum number of 20 participants.

Priority will be given to:

- 1st year PhD students attending the BIODIV Doctoral Programme;
- other BIODIV PhD students;
- PhD students attending other courses;
- other post-graduate students and researchers.

REGISTRATION Registration deadline: March 18, 2016.

Participation is free of charge for BIODIV students | Registration fee for other participants: euro 100,00.

To register, please send an e-mail accompanied by your short CV to Maria Sant'Ana at post.graduation@cibio.up.pt. Please refer your status (PhD student, MSc Student, Other) and the University to which you are affiliated.

For more information about the course, please contact: post.graduation@cibio.up.pt.

CIBIO - Centro de InvestigaAA§AA£o em Biodiversidade e Recursos GenAA©ticos

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Divulgaçã

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 notification 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 formatted) the message will be sent 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 preformatting 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 L^AT_EX do not try to embed L^AT_EX or T_EX in your message (or other formats) since my program will strip these from the message.