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# E v o l D i r

March 1, 2016

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

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## 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](mailto:Golding@McMaster.CA).

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

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



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### Aber UK Genetics Apr5-7

Of course you are planning on coming to the 60th annual meeting of the Ecological Genetics Group, a special interest group of the Genetics Society and the British Ecological Society. The meeting is 5 - 7 April 2016. The meeting is preceded by a workshop on phenomics and genomics on the 4th of April, with a programme now available: <http://www.aber.ac.uk/en/ibers/events/egg2016/> The EGG meeting itself is an excellent and informal forum for presenting novel data. Talks from young scientists and PhD students are particularly welcome. There is also a poster session and opportunities to present a discussion topic.

Accommodation is in the old college and sea front halls in Aber, a smashing location.

Conference dinner will also be there and our now traditional EGG heads Pub Quiz. There will be also be a field visit to our nearby Upland research centre. Overall plenty of time for informal chats with all participants.

Please keep those offers of papers, posters and discussion topics coming in. <http://www.aber.ac.uk/en/ibers/-events/egg2016/> Hope to see you all in Aber in April.

Regards

John

Professor John Warren

Institute of Biological, Environmental & Rural Sciences (IBERS) Edward Llwyd Building Aberystwyth University Penglais Campus Aberystwyth Ceredigion SY23

3DA

Tel: 01970 621637

Sent by Kirsten Wolff

Newcastle University

Kirsten Wolff <kirsten.wolff@newcastle.ac.uk>

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### **Asilomar California LocalAdaptation Jul14-17**

EARLY BIRD REGISTRATION NOW! The American Genetic Association President's Symposium, "Local adaptation: from phenotype to genotype to fitness", will be held July 14-17, 2016, at beautiful Asilomar, CA (<http://www.visitasilomar.com/>). In the past, many studies dealt only with phenotypes/traits, but today the connection to genotype is becoming feasible for more and more organisms. Our speakers are a blend of established and new investigators, working on a variety of organisms, and who are taking diverse approaches to the question. The AGA will provide several travel awards to 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>

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 Illinois 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

Lynda Delph, AGA President

AGAJOH <AGAJOH@oregonstate.edu>

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### **AsilomarCA LocalAdaptation Jul14-17 Registration**

#### EARLY BIRD REGISTRATION NOW!

The American Genetic Association President's Symposium, 'Local adaptation: from phenotype to genotype to fitness', will be held July 14-17, 2016, at beautiful Asilomar, CA (<http://www.visitasilomar.com/>).

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Lynda Delph, AGA President

AGAJOH <AGAJOH@oregonstate.edu>

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## Austin Evolution Jun17-21 SpotlightPhylogenetics

We've extended the deadline for our spotlight session to March 19th, 2016.

Please send on your ideas!

——— Forwarded message ——— From: Erick Matsen <matsen@fredhutch.org> Date: Tue, Jan 26, 2016 at 10:13 AM Subject: Conference: Evolution 2016 Spotlight session on Next-generation phylogenetic inference To: evoldir <evoldir@evol.biology.mcmaster.ca>

This is a call for speakers for a Spotlight session devoted to next-generation phylogenetic inference at the 2016 Evolution Meetings in Austin. Spotlight sessions are a new type of session that differ from the traditional symposia at these meetings. For more information visit: <http://www.evolutionmeetings.org/instructions-for-presenters.html> Topic: Statistical phylogenetic inference methods, and in particular Bayesian methods, are reaching a hard limit on the number of taxa that can be used in an analysis. Although many interesting and worthwhile efforts have been made to increase the computational efficiency of these methods, it appears that existing inference strategies will simply not scale to orders of magnitude more taxa. In this session we will explore alternate strategies and algorithms for phylogenetic inference.

Organizer(s): Frederick Erick Matsen (Fred Hutchinson Cancer Research Center, matsen@fredhutch.org), Tracy Heath (Iowa State, phylo@iastate.edu), and Felipe Zapata (San Francisco State, felipe.zapata@brown.edu)

The spotlight session consists of one 28 min, four 13 min, and twelve 5 min (Lightning) talks. If you are interested in speaking in this session please submit an application to Erick Matsen at matsen@fredhutch.org. The application must include your: (1) Name; (2) Institution; (3) rank (e.g., student, postdoc, faculty); (4) names & institutions of co-authors on your talk; (5) a short abstract (max: 300 words); and (6) which talk type(s) 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 Feb. 21, 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 13 min. talk in a regular contributed session at the meeting even if you apply to participate in a Spotlight session. However, if you are selected to speak in the spotlight session, you will have to choose which talk slot to use as each conference attendee is allowed to give only one oral presentation. Applicants will be informed about the outcome of their application by late March.

Organized sessions are committed to representing diversity. All interested individuals are encouraged to apply.

Useful links: Evolution 2016 conference website: <http://www.evolutionmeetings.org/evolution-2016-austin-texas.html> Information for presenters, including Spotlight sessions: <http://www.evolutionmeetings.org/instructions-for-presenters.html> Frederick "Erick" Matsen, Associate Member Fred Hutchinson Cancer Research Center <http://matsen.fredhutch.org/> Erick Matsen <matsen@fredhutch.org>

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## Austin Evolution Jun17-21 Spotlights

### EVOLUTION2016 SPOTLIGHT SESSIONS

This year we are introducing a new way to give an oral presentation at the 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 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 this session 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 the 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 please 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.

The deadline for applications to all 3 Spotlight Sessions has been extended to Apr. 30 (coinciding with the end of early meeting registration).

This years 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:KatieWagner (U Wyoming) Applications to: cwagne22@uwo.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 this series please submit an application to the appropriate Spotlight Session 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 an 'open session' at the meetings even if you apply to participate in a Spotlight Session, and you should do so if you want to ensure that you can give a talk at the meeting. 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.

Organized sessions are committed to representing diversity. All interested individuals are encouraged to apply. [howard.rundle@uottawa.ca](mailto:howard.rundle@uottawa.ca)

## Austin Plant Speciation June 16-17

We are excited to announce that a Plant Speciation Mini-Conference will be held on June 16-17, 2016 at the University of Texas at Austin. This is an informal meeting with the goal of bringing together scientists interested in the process of Plant Speciation for discussions, sharing of ideas, and community building. The meeting will occur just prior to the International Evolution Meeting, which begins the evening of June 17 at the Palmer Convention Center in downtown Austin. The conference will be free of charge, but requires prior registration.

The meeting is open to students, postdocs, and faculty members who are interested in topics related to Plant Speciation. For more information and registration, see the conference link: <https://plantspeciation.wordpress.com>  
Rationale: Our understanding of plant speciation has greatly expanded ever since University of Texas Professor Verne Grant published his magnum opus *Plant Speciation* 45 years ago. From the quantification of reproductive isolating barriers, and the order in which they establish, to determining the genetic mechanisms underlying those barriers, major advances have been made in how new plant species originate. Simultaneously, the advances in molecular biology and phylogenetic methods have allowed the study of adaptive radiations, the identification of key innovations driving diversification, and the discovery of unsuspected links between geography and diversity. Despite this progress, a synthesis between the processes driving the evolution of plant populations with those contributing to patterns of biodiversity remains elusive. The time is ripe for a synthesis to integrate studies of reproductive isolation in plants with those revealing phylogenetic patterns of plant diversification.

The primary aim of the Plant Speciation Mini-Conference is to bring together researchers that work at the cutting edge of plant speciation at both the population and phylogenetic level. Of particular interest will be addressing the following fundamental questions about plant speciation: 1) Does ecology drive postzygotic isolation and if so, how? 2) How does geography interact with ecology to facilitate speciation? 3) What is the role of chromosomal rearrangements in reproductive isolation and how do those rearrangements become established? 4) How do abiotic and biotic factors contribute

independently and interactively to plant speciation? 5) Do hybrid incompatibilities snowball over time? 6) How does sexual selection contribute to plant speciation? 7) What is the role of genetic drift in plant speciation? 8) What reproductive barriers are most important early in plant speciation and what barriers evolve later to forever prevent hybridization between phylogenetic lineages into the future? Can these processes determine phylogenetic patterns of plant diversity? Answers to these and similar questions will pave the way for a new understanding of how processes responsible for population level divergence shape the tree of life.

Thank you for your interest,

The Organizers: David Lowry, Daniel Ortiz-Barrientos, Yaniv Brandvain

David B. Lowry Assistant Professor Plant Biology Department Michigan State University Plant Biology Laboratories Room 268 517-432-4882 <http://davidbryantlowry.wordpress.com/> David Lowry <dlowry@msu.edu>

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## Austin Texas SocStudyEvolution Jun 17-21

### SOCIETY FOR THE STUDY OF EVOLUTION

Get Ready for EVOLUTION 2016! Our annual meeting with SSB & ASN will be June 17-21, 2016 in Austin, TX. Registration will open in late Feb. or early March. In addition to the standard sessions and symposia, this year will see the introduction of spotlight sessions, organized by young leaders in the field. SSE's spotlight session, "Understanding history and process in rapid diversification with genomic data", is organized by Catherine Wagner (UWyo). The spotlight series consists of one 30 min, five 15 min, and twelve 5 min (lightning) talks. If you are interested in speaking in this series please submit an application to Catherine Wagner (catherine.wagner@uwyo.edu).

The application must include: (1) Name, (2) Institution, (3) rank (e.g., student, postdoc, faculty), (4) names & institutions of collaborators (5) a short abstract (max: 300 words), and (6) which talk types you are willing to give (30, 15, or 5; the more flexible you are the more likely you are to be selected). Applications must be received by February 28, 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 talk in an open session at the Evolution Meetings even if you apply to participate in a spotlight session. However, if you are selected to speak in the spotlight series, you will have to choose which talk slot to use as each attendee is allowed to give only one oral presentation.

**LIFE DISCOVERY CONFERENCE** The dynamic and changing worlds of biology and education are converging in the discovery, learning and practice of science. The Life Discovery - Doing Science Conference seeks to create connections that inspire Biology in Action. Now in its third year, the conference (sponsored by SSE and other scientific societies) offers more than 30 hands-on workshops and presentations, networking sessions and two keynotes by Andrew Martin from UC Boulder and Kevin Coyle from the National Wildlife Federation that share ideas and strategies to engage your students in discovering life on earth. Register by March 4th. Colleagues from all disciplines seeking to connect educational approaches with the rich advances of Biology are encouraged to attend.

We're anticipating 2000+ attendees, over 1000 talks, hundreds of posters, and a variety of workshops and other special events! Please visit the EVOLUTION 2016 site for further information about the meeting, field trips, and more.

**AWARD DEADLINES** The Theodosius Dobzhansky Prize is awarded annually by the Society for the Study of Evolution to recognize the accomplishments and future promise of an outstanding young evolutionary biologist. The Dobzhansky Prize is accompanied by a check for U.S. \$5000. The candidate must have a Ph.D. (or equivalent) awarded no earlier than May 2012 and no later than 1st February 2016, and must be actively involved in research in the field of evolutionary biology. Candidates may apply directly or may be nominated. The application/nomination materials must be sent as PDF e-mail attachments is 15 February 2016. All materials should be sent to the SSE Secretary (Cynthia Weinig) at [cweinig@uwyo.edu](mailto:cweinig@uwyo.edu).

The W.D. Hamilton Award for Outstanding Student Presentation will be given to a student who has presented an outstanding talk at the annual meeting. Finalists will present their papers during a day-long symposium of Hamilton Award candidate talks. This year, finalists will receive a \$500 travel stipend from the SSE to attend the Evolution meeting. Graduate students must indicate their interest to compete by checking a box for the Hamilton Award during meeting registration. Submit a 400-word abstract and talk title as part of the meeting registration process by 11:59 p.m. on APRIL 30. Finalists will be notified by May 15.



Thank you for your continued work and support of our mission. Best wishes, Kimberly Hughes, SSE President [3c37ac39-671f-40fb-aa19-f895fab2b20c.jpg] SSE Business Office PO Box 299 | St. Louis Missouri, 63166 314-577-9566 [www.evolutionsociety.org](http://www.evolutionsociety.org) friend on Facebook | forward to a friend Copyright © 2016 Society for the Study of Evolution, All rights reserved. You are receiving this communication as a member of the Society for the Study of Evolution. Our mailing address is: Society for the Study of Evolution PO Box 299 St Louis, MO 63166 Add us to your address book unsubscribe from this list | update subscription preferences

Society for the Study of Evolution  
hcacanindin@evolutionsociety.org>

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### **AustinTX UndergradTravelAward Jun17-21**

Travel Award - Undergraduate Diversity at Evolution 2016

We are pleased to announce an undergraduate travel award to bring talented and diverse undergraduates to the Evolution meetings this June 17-21 in Austin, TX ([www.evolutionmeetings.org](http://www.evolutionmeetings.org)).

For the 13th year we will fund a cohort of undergraduates from throughout the U.S. and Puerto Rico to (1) present a poster at the meetings, (2) receive mentoring from graduate students, postdocs and faculty, and (3) participate in a career-oriented 'Undergraduate Futures in Evolutionary Biology' panel and discussion. The program is sponsored by SSE/BEACON and covers the costs of travel, registration, food and accommodation at the meetings. The application deadline is Monday, April 18th, and decisions will be announced by Tuesday, April 26th.

Applications are welcomed from all undergraduates, and the admissions goal is to create a diverse pool of students. An overview of the program and the online application can be found at: <http://beacon-center.org/ude/>. Applications consist of a short statement of interest, a letter of recommendation, and the title and abstract of the poster to be presented.

For inquires, please contact one of the organizers: Alexa Warwick - [awarwick@msu.edu](mailto:awarwick@msu.edu) Richard Kliman - [rmkliman@cedarcrest.edu](mailto:rmkliman@cedarcrest.edu) Scott Edwards - [sedwards@fas.harvard.edu](mailto:sedwards@fas.harvard.edu)

“[awarwick@msu.edu](mailto:awarwick@msu.edu)” <[awarwick@msu.edu](mailto:awarwick@msu.edu)>

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### **Boise Idaho InvasivePlants Oct17-20**

Plan to join us October 17-20, 2016 at the Boise Centre in Boise, ID for the 4th Conference - Invasive Plants in Natural Areas. This four day conference will feature presentations on the latest developments in invasive plant research and provide ample opportunity for managers and researchers to engage and identify creative new approaches to managing invasions. Join the discussion of possibilities and problems specific to the management of invasive plants in natural areas, and perhaps more importantly, contribute to solutions! More information about symposia topics (hopefully one about evolution in invasions!) will be provided soon! See [www.nripc.org](http://www.nripc.org) for more information

“Gaskin, John” <[John.Gaskin@ARS.USDA.GOV](mailto:John.Gaskin@ARS.USDA.GOV)>

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### **Bournemouth UK ProtistEvolution Apr6-8**

Early Bird Registration Deadline 20th March 2016

The Protistology-UK Spring Meeting 2016 will take place at Bournemouth University (Dorset), UK. Registration opens on the 10th February.

The meeting will incorporate three symposia:

Eukaryote taxonomy and diversity studies in an HTS era

The eukaryote genome

Protist ecology

The meeting will also host a half-day applied phy-cology session, sponsored by PHYCONET < <http://www.phyconet.org.uk/> > with 1-2 key-note speakers, as well as contributed talks and posters.

Invited speakers include John Day (SAMS), David Montagnes (Liverpool University), Saul Purton (UCL), Ross Waller (Cambridge University), Bryony Williams (Ex-eter University) and Tom Williams (Bristol University).

As in previous years, the Conference will offer sessions for posters, student talks and contributed talks. Bur-saries are available for presenting students. Prizes for

best student talks and posters will be awarded, including the Humphrey Smith Prize for best talk.

Martin Carr

Dr. Martin Carr <http://www.protistology.org.uk> mart-carr74@gmail.com

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## Edinburgh QuantGenetics Mar9

The 10th meeting of the Edinburgh Alliance for Complex Trait Genetics, sponsored by the Genetics Society, will take place on Wednesday 9th March 2016 from 13.00 to 18.30 at the Royal College of Physicians, 9 Queen Street, Edinburgh, EH2 1JQ.

All welcome.

If you want to attend, please sign up at <http://tinyurl.com/hwvc9gx> by Friday 4th March.

Josephine Pemberton & Chris Haley

### PROGRAMME

13.00 Arrival and registration

13.30 Session 1

13.30 Sophie Marion de Proce (Institute of Genetics and Molecular Medicine) Locally elevated mutation rates in mammalian promoters.

14.00 Charley Xia (Institute of Genetics and Molecular Medicine) Genetic analysis of obesity traits in Scotland.

14.30 Brian Charlesworth (Institute of Evolutionary Biology) Associative overdominance.

15.00 Michael Morgan (Department of Physiology, Anatomy and Genetics, Oxford) Teasing apart the genetic complexity of hair pigmentation in humans.

15.30 Tea

16.00 Session 2

16.00 Georgios Banos (SRUC Edinburgh) Genetic evaluations for bovine tuberculosis resistance in dairy cattle.

16.30 Jacob Moorad (Institute of Evolutionary Biology) Why are humans so long-lived? Selection for genes that promote late-life human lifespan.

17.00 Peter Joshi (Usher Institute for Population Health Sciences and Informatics) Genetic Architecture of Human Lifespan - UKBiobank GWAS results.

17.30 Discussion and refreshments

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

Josephine Pemberton <j.pemberton@ed.ac.uk>

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## Exeter BehaviourEvolution Jul28-Aug3

International Society for Behavioural Ecology Congress, Exeter, UK, 28 July - 3 August 2016

Abstract submission is now open. Go to [www.isbe2016.com](http://www.isbe2016.com) to submit an abstract for a poster or oral presentation. Deadline for consideration as an oral presentation is 31st March. Standard registration remains open until early June with discounts of over 30% still available for students and delegates from developing world countries

“alex.thornton@exeter.ac.uk”  
<alex.thornton@exeter.ac.uk>

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## Helsinki WildPlantPathosystems Aug29-31

Dear colleagues,

We are pleased to announce the 2nd international meeting on

### WILD PLANT PATHOSYSTEMS

29-31 August 2016, Helsinki

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

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



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

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

Conference website: <http://allaine.it.helsinki.fi/?p=244> Contact: [krista.raveala@helsinki.fi](mailto:krista.raveala@helsinki.fi) and [anna-liisa.laine@helsinki.fi](mailto:anna-liisa.laine@helsinki.fi)

– Professor Anna-Liisa Laine

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[helsinki.fi/science/metapop/](http://helsinki.fi/science/metapop/) twitter: @annaliisalaine

“[anna-liisa.laine@helsinki.fi](mailto:anna-liisa.laine@helsinki.fi)” <[anna-liisa.laine@helsinki.fi](mailto:anna-liisa.laine@helsinki.fi)>

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## Lyon Behaviour Evolution Jun27

We inform you that the twelfth edition of the “ECOLOG & BEHAVIOUR” meetings will occur this year in Lyon (France) between June 27th and July 1st 2016.

The “Ecology & Behaviour” conference is an international scientific congress in the themes of ecology, evolutionary biology, and animal behaviour that distinguishes itself by the will clearly displayed to favour the participation of PhD and Post-doctoral students.

Unlike most congresses and symposium, NO CHARGE is asked to PhD students and post-doctoral students (including accommodation and lunches) if they participate through the presentation of a poster or an oral communication (in English).

We are now accepting abstracts for graduate students and post-docs presentations in talk and poster formats.

Please visit our presentation registration page for more information on submission requirements and procedures: [eb2016.sciencesconf.org](http://eb2016.sciencesconf.org)

\*The deadline for abstract submissions is March 20th, 2016\*.

The E&B organization committee  
[eb2016.sciencesconf.org](http://eb2016.sciencesconf.org)

Christophe Plantamp <[cplantamp@gmail.com](mailto:cplantamp@gmail.com)>

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## Lyon Evolutionary Behaviour Jun27-Jul1

Conference : Ecology and Behaviour meeting - Lyon(France) - June 27th July 1st

>From the 27th of June to the 1st of July 2016, Lyon will host the twelfth edition of Ecology and Behaviour meetings. Since 2005, this scientific meeting about animal behavior, ecology and evolution is organized every year in a different French city. This year, for the second time in the history, this conference takes place in Lyon.

The Ecology and Behaviour meetings propose an uncommon format in the landscape of scientific conferences. They offer to young researchers a convivial atmosphere to present and exchange about their work in the presence of renowned specialists. Plus, no registration fee is asked for participants presenting either an oral communication or a poster.

Submissions are already possible and will run until March 20th on the website of the meeting [eb2016.sciencesconf.org](http://eb2016.sciencesconf.org), on the submit page.

Â

The organization committee

[eb2016@sciencconf.org](mailto:eb2016@sciencconf.org)

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## Orlando PopEvolQuantGenetics Jul13-17

The Allied Genetics Conference (TAGC) will include a new meeting on Population, Evolutionary and Quantitative Genetics organized by Mike Lynch

Although most of the central venues of TAGC revolve around the long-standing model-organism meetings, the broad and overlapping fields of population, evolutionary, and quantitative (PEQ) genetics span these systems and more. Thus, in the interest of developing a fully comprehensive genetics conference, the Genetics Society of America (GSA) will also convene the first joint meeting for researchers in the latter fields. Topics will range from population genomics to molecular evolution to the dissection of the determinants of quantitative-trait variation, with equal emphasis placed on both model and non-model organisms across the Tree of Life. PEQ has a long history of both applied and theoretical research, and both will be an integral part of this meeting.

The intention here is to promote a strong cross-disciplinary network of colleagues performing both theoretical and empirical work. The meeting will consist of a series of short talks, poster sessions, and plenary talks, and will be dovetailed with the model-organism venues to facilitate maximum interaction among those with similar conceptual interests. As many as 90 oral presentations will be delivered directly in the PEQ meeting, with dozens to hundreds of others with direct connections being given in the other model-organism sub-meetings. Time in the schedule will be set aside for the usual GSA-sponsored career-development workshops, including education-oriented, grant-writing, and networking sessions focused on strategies for building successful teaching methodologies and lasting collaborations.

GSA plans for PEQ to become the premier, regular gathering of graduate students, postdoctoral scholars, and established scientists in these central areas of genetics, ideally being established as another of the several periodic meetings sponsored and managed by the GSA. After nearly 100 years of research in population, evolutionary, and quantitative genetics, the time for holding such an exciting meeting is long overdue.

These topics will be featured at the conference and speakers will be selected from submitted abstracts in the following areas:

Population Genomics Experimental Evolution Genome Evolution Quantitative Traits Ecological Evolution Adaptation and Speciation Molecular Evolution

Abstract Submission and Registration Deadline March 23, 2016

[www.genetics2016.org/communities/peqg](http://www.genetics2016.org/communities/peqg) CONFERENCE ORGANIZERS

Kirsten Bomblies, Harvard University

Michael Lynch, Indiana University

Lauren McIntyre, University of Florida

Bret Payseur, University of Wisconsin

Dmitri Petrov, Stanford University

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

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

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## OxfordUK InsectSymbionts Mar15

Royal Entomological Society Special Interest Group on Insect Symbionts

15th March 2016 in Oxford, UK

Invited speaker: Prof Christoph Vorburger, EAWAG, Switzerland

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

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

[ailsa.mclean@gmail.com](mailto:ailsa.mclean@gmail.com)

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## OxfordUK ProbGen2016 Sep12-14

Dear Colleagues,

We are pleased to announce that the 2nd Probabilistic Modeling in Genomics Conference (ProbGen16), will be held at the Department of Statistics, University of Oxford, UK, from 12-14 Sept 2016. We would appreciate if you could circulate this announcement to your local colleagues and collaborators.

The conference will cover probabilistic models, algorithms, and statistical methods across a broad range of applications in genetics and genomics. We invite

abstract submissions on a range of topics including Population Genetics, Functional Genomics, Systems and Structural Biology, Methods for Genome-wide Association Studies, Causal inference in genetic studies, Assembly and Variant Identification, Phylogenetics, Natural Selection and Quantitative Genetics.

Alongside invited speakers, oral presentations will be selected from submitted abstracts. We particularly encourage abstract submissions for oral and/or poster presentations from junior investigators, including post-doctoral fellows and graduate students.

This is an annual meeting, held at Cold Spring Harbor in 2015 and which evolved from the success of previous similarly-themed workshops held at the HHMI Janelia Farm Research Campus (2013) and Merton College, Oxford (2014).

The conference talks will be held in the new Department of Statistics building in central Oxford, with accommodation across the road at Somerville College. The meeting will begin with an informal dinner on the evening of Sunday 11 September 2016. Talks will take place from Monday 12 September until lunchtime on Wednesday 14 September.

Registration will open soon. We have provisional capacity for ~130 participants; due to space limitations, registration will proceed on a first-come-first-served basis.

The registration and abstract submission deadline will be Friday 15 July 2016.

The conference webpage can be found at <http://www.stats.ox.ac.uk/events/probgen16> Please send enquiries to [probgen16@stats.ox.ac.uk](mailto:probgen16@stats.ox.ac.uk)

Organizers: Jonathan Marchini, University of Oxford, UK Simon Myers, University of Oxford, UK Jotun Hein, University of Oxford, UK Peter Ralph, University of Southern California, USA

“myers@stats.ox.ac.uk” <myers@stats.ox.ac.uk>

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**Roscoff France**  
**50yrsMolecularHistory May9-13**  
**Reminder3**

Dear Colleagues,

This is the last day for applying. In particular, we have a number of reserved places for PhD students.

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There is only one month left to apply to the Jacques Monod conference on molecular evolution in May 2016. We particularly encourage the application of PhD students. Note that the inscription fees listed below include board and lodging. Selected applicants will be expected to present a poster.

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

May 9-13 2016

It is with the popularization of molecular tools and the disclosure of genome sequences that evolutionary models have become decisive in biology, in part because this information is simply so abundant and so complex that only a comparative method could reveal its meaning. In 2016, it will be 50 years that Emile Zuckerkandl and Linus Pauling have laid the foundation of molecular phylogeny, and molecular evolution in general, in their seminal article entitled “Molecules as documents of evolutionary history”. The fundamental realization of this article was that DNA does not only encode the elementary functional elements of an organism, it also harbours abundant information on the evolutionary history and life history traits of its ancestors.

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

These recent years have seen tremendous developments in this direction, which we will attempt to review in this conference.

Invited speakers (provisional titles)

ABBYSophie (Paris, France) Evolution playing a molecular building set: origins and distribution of bacterial secretion systems

ACHTMANMark (Warwick, United Kingdom) Ages of bacterial pathogens

ALMERic (Cambridge, USA) Driving forces of microbiome evolution

DURETLaurent (Lyon, France) Biased gene conversion as a 4th evolutionary force

FARIANuno (Oxford, United Kingdom) Viral evolution

GALTIERNicolas (Montpellier, France) Population ge-

nomics of non model animals: genetic diversity, adaptive rate and effective population size

GILBERT Thomas (Copenhagen, Denmark) Ancient DNA, ancient genomes, and the hype of de-extinction

GOGARTEN Peter (Storrs, USA) Horizontal gene transfer: the pan-genome as shared genetic resource of a lineage

GRAUR Dan (Houston, USA) The vocabulary of molecular evolution and the transgressions of functional genomics: a rose by any other name would be misleading

GRIBALDO Simonetta (Paris, France) Phylogenomics and the tree of life

HEATH Tracy (Ames, USA) Molecular, morphological, and macroevolutionary models for dating species divergence times

KATZ Laura (Northampton, USA) The eukaryotic phylogeny

KOSIOL Carolin (Vienna, Austria) Polymorphism-aware phylogenetic models for species trees

LAGERGREN Jens (Stockholm, Sweden) Generative models of gene family evolution

LÁPEZ-GARCÍA Purificación (Orsay, France) Diversity of microbial life

McLYSAGHT Aoife (Dublin, Ireland) Whole genome duplication

MORAN Nancy (Austin, USA) Symbiosis in evolution

PAGEL Mark (Reading, United Kingdom) Beyond molecular data: information and evolution in the cultural realm

PHILIPPE Hervé (Moulis, France) Models of sequence evolution

SANMARTIN Isabel (Madrid, Spain) Spatiotemporal evolution of lineages and biotas using Bayesian approaches

SEMON Marie (Lyon, France) Insights into making different types of the same organ using developmental transcriptomes as molecular microscopes

STADLER Tanja (Zürich, Switzerland) Modelling and inference of species diversification

SZÁLLÁSI Gergely (Budapest, Hungary) Genomescale reconstruction of phylogenies

TELFORD Maximilian J. (London, United Kingdom) The new animal phylogeny

WARNOW Tandy (Urbana, USA) New coalescent-based species tree estimation methods

Deadline for application: February 1st, 2016

Registration fee (including board and lodging)

\$430 for PhD students \$625 for other participants

Application for registration The total number of participants is limited to 115 and all participants are expected to attend for the whole duration of the conference. Selection is made on the basis of the affinity of potential participants with the topics of the conference. Scientists and PhD Students interested in the meetings should send:

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

to the Chairperson of the conference (vincent.daubin@univ-lyon1.fr) before the deadline. After it, the organizers will select the participants. Except in some particular cases approved by the Chairperson, it is recommended that all selected

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

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**San Antonio TX**  
**SMBE Satellite Genetics Admixed Pop**  
**May 18-20**

Conference Announcement: SMBE Satellite Meeting on the Genetics of Admixed Populations May 18-20, 2016 San Antonio TX

Early Registration deadline: February 15, 2016 Final Registration deadline: March 15, 2016

Studies of admixed populations and the admixture process touch on topics central to evolutionary and molecular biology, including the dynamics of gene flow and hybridization, population expansions, and adaptation. Admixed populations have been leveraged to detect disease and phenotypic associations, elucidate mechanisms and timescales of speciation, and infer regions under selection. Acting as a natural experiment, admixed populations provide insight into unique adaptations of their parental populations, and evolutionary processes in related populations more generally. Admixture is also intimately linked with the recombination process, which shuffles segments of different ancestry, and is proven to vary in rate and location based on ancestry.

The primary goal of this satellite meeting is to emphasize the common theoretical and empirical underpinnings of the study of admixed human populations with the study of hybridization in other animals and even plants, opening up methods and study design from a specific organism to a wider audience. We hope to bridge theoretical and data-driven approaches, starting a discussion on the suitability of methods to various systems and open questions that may be better resolved using an interdisciplinary approach, as well as considering ethical concerns associated with these studies.

Workshop sessions include: Admixture as a dynamic process Novel Methods to Untangle Admixture Empirical Studies of Population History Admixture as a Mechanism for and Against Speciation Admixture and Selection: Phenotypic and Medical Implications Panel Discussion: Ethical considerations and Sampling Schemes

For a full list of confirmed speakers and information on local arrangements, please visit: <http://anthgen.org/-smbe2016> Please direct all questions to the conference organizers at [smbe2016admix@gmail.com](mailto:smbe2016admix@gmail.com)

Conference Organizers:

Amy Goldberg: [agoldb@stanford.edu](mailto:agoldb@stanford.edu) Ellen Quillen: [EQuillen@txbiomed.org](mailto:EQuillen@txbiomed.org) Heather Norton: [heather.norton@uc.edu](mailto:heather.norton@uc.edu) Abigail Bigham [awbigham@umich.edu](mailto:awbigham@umich.edu) Joanna Malukiewicz: [jmalukie@gmail.com](mailto:jmalukie@gmail.com) Anne Stone: [acstone@asu.edu](mailto:acstone@asu.edu)

Heather L. Norton Assistant Professor Department of Anthropology 446 Braunstein Hall PO Box 210380 University of Cincinnati Cincinnati, OH 45221-0380 Office: 513-556-3594 [heather.norton@uc.edu](mailto:heather.norton@uc.edu) <http://homepages.uc.edu/~nortonhr/MoCHA/Home.html> "Norton, Heather (nortonhr)" <[nortonhr@UCMAIL.UC.EDU](mailto:nortonhr@UCMAIL.UC.EDU)>

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## 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](http://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](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](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](mailto: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](mailto:aksakai@uci.edu)), Anna Monfils ([monf1ak@cmich.edu](mailto:monf1ak@cmich.edu)), or Heather Cacanindin ([hcacanindin@botany.org](mailto:hcacanindin@botany.org)).

"[aksakai@uci.edu](mailto:aksakai@uci.edu)" <[aksakai@uci.edu](mailto:aksakai@uci.edu)>



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## Seville EvolEcol Jan31-Feb4

Dear colleagues,

Please find included the second circular and call for symposium proposals of the XIV MEDECOS & XIII AEET meeting (deadline: March 31th, 2016). All information can be found at the following link: <http://www.medecos-aet-meeting2017.es/> We would appreciate if you can circulate this announcement to your colleagues and networks. Apologies for cross-posting.

Looking forward to meet you in Seville next year,

Leyre Jiménez-Eguizábal Administración AEET tel.: 34 91 4887329 <http://www.aet.org> Twitter: @AEET\_ Facebook: Asociación Española de Ecología Terrestre

Dr. Juan Arroyo [arroyo@us.es](mailto:arroyo@us.es) Departamento de Biología Vegetal y Ecología. Dept. of Plant Biology and Ecology Universidad de Sevilla Apartado 1095 - E41080 Sevilla, Spain phone: desk office: +34 954 557 058 lab: +34 955 420 845 fax: +34 954 557 059 Research group: <http://grupo.us.es/grnm210/> [https://www.researchgate.net/profile/Juan\\_Arroyo3/](https://www.researchgate.net/profile/Juan_Arroyo3/) Juan Arroyo <[arroyo@us.es](mailto:arroyo@us.es)>

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## Smithsonian Biodiversity Nov9-11

The Smithsonian Institute for Biodiversity Genomics (SIBG) and BGI are co-organizing the inaugural Global Biodiversity Genomics Conference to be held in Washington, D.C. USA from November 9-11, 2016 at the Smithsonian Institution's National Museum of Natural History. The conference will have sessions focusing on a broad array of relevant topics, including presentations and discussions of critical technological and analytical tools and sessions oriented around broad taxonomic groups (e.g. plants, vertebrates, invertebrates, and microbes) planned in conjunction with groups such as G10K ([genome10k.soe.ucsc.edu](http://genome10k.soe.ucsc.edu)), GIGA ([giga-cos.org](http://giga-cos.org)), and i5K ([arthropodgenomes.org/wiki/i5K](http://arthropodgenomes.org/wiki/i5K)). Sessions are planned to include invited speakers as well as selected talks and posters from applicants, including students. Attendees will be limited to 450 people. Further announcements providing details of additional sponsors,

activities, and registration procedures will be forthcoming. Please hold the dates and address questions to Warren Johnson at: [contactbiogenomics@si.edu](mailto:contactbiogenomics@si.edu)

“JohnsonWE@si.edu” <[JohnsonWE@si.edu](mailto:JohnsonWE@si.edu)>

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## Switzerland GenomicBasisEcoEvolutionaryChange Jun5-9

Conference reminder: Genomic basis of eco-evolutionary change, Location: Ascona, Switzerland. Date: June 5th-9th 2016 Deadline for applications: 21st February 2016

Dear all,

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

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

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

Confirmed speakers:

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

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

Please send your application, all in one PDF, by the



21st of February to monte-verita@env.ethz.ch.

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

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

The organising committee

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

Dr. James Buckley Adaptation to Changing Environments (ACE) postdoctoral fellow Institute of Integrative Biology, ETH Universitätstrasse 16 CHN G 35.2 8092 Zürich 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>

## TexasAMU EvolutionaryBiology Mar31-Apr1

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

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

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

We are now accepting \*abstracts for student presenta-

tions in talk and poster formats\*. Both graduate and undergraduate students are encouraged to present original research during the student research symposium on Friday, April 1. Please visit our presentation registration page for more information on submission requirements and procedures:

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

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

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

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

Regards,

2016 Ecological Integration Symposium Committee

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

Danielle Macedo <[dcdmacedo@gmail.com](mailto:dcdmacedo@gmail.com)>

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## Tuscany Speciation Feb19-24

We are pleased to announce SPECIATION 2017, a Gordon Research Conference (GRC) dedicated exclusively to speciation research. The conference — the world's largest of its kind — will be held at the Renaissance Tuscany Il Ciocco Resort & Spa in Italy during the week of February 19-24, 2017. Invited presentations and discussion sessions will cover a broad array of timely topics in speciation research.

The conference will be directly preceded by a two-day Gordon Research Seminar (GRS), co-chaired by Amanda Hund and Laurel Symes, that offers opportunities for early-career scientists to get involved at the forefronts of modern speciation research. Participants will engage in scientific discussions on salient topics of interest, thereby gaining knowledge and confidence for their participation in SPECIATION 2017.

The GRC conferences on speciation raise to a trans-Atlantic level a tradition of international conferences on speciation research that was initiated by the European Research Networking Programme 'Frontiers of Speciation Research'. The three conferences held thus far, in 2010, 2013, and 2015, have helped facilitate bridge-building between disparate approaches to speciation research and have attracted hundreds of participants from all facets of speciation research.

Registration for SPECIATION 2017 is open at

<https://www.grc.org/programs.aspx?id=16903> and will continue until the venue's capacity is filled.

A preliminary conference program with list of session titles will be available on April 1 and the full conference program will be finalized by early autumn.

With many thanks and best wishes,

Åke Brännström & Rebecca Safran

Rebecca J Safran <[rebecca.safran@colorado.edu](mailto:rebecca.safran@colorado.edu)>

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## UCambridge EvolutionaryGenetics Mar15 Deadline

Evolutionary Genetics and Genomics Symposium (Abstract Submission Deadline Approaching)

Please note that the deadline for the abstract submission for Evolutionary Genetics and Genomics Symposium 2016 is approaching (February 22).

The annual Evolutionary Genetics and Genomics Symposium (EGGS) will take place on Tuesday 15th March 2016 at the University of Cambridge.

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

Abstract submission is now open. If you would be interested in presenting a talk please submit your abstract via this link: <https://docs.google.com/forms/d/1W2BMTt268.q4XEYv0IVwSiwnVmVIPs2KRYsXd.lJrNk/-viewform> We will also have talks by four invited speakers:

- Mary J. OConnell, University of Leeds
- Magnus Nordborg, Gregor Mendel Institute of Molecular Plant Biology, Vienna
- Federica Di Palma, TGAC
- Eric Miska, Wellcome Trust Sanger Institute, University of Cambridge

For more information, please visit <http://www.evolutionarygenetics.group.cam.ac.uk/eggs/> or email [eggs.symp@gmail.com](mailto:eggs.symp@gmail.com)

With best wishes,

The organising committee

[cc625@cam.ac.uk](mailto:cc625@cam.ac.uk)

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## UMichigan CommunityEvolution Mar12

REGISTER NOW: <http://sites.lsa.umich.edu/ecss/register/> We are pleased to announce this year's Early

Career Scientist Symposium,\* Frontiers in Community Assembly\*, to be held Saturday, March 12, 2016 in the Chemistry Building on the campus of the University of Michigan, Ann Arbor. The symposium will focus on the integration of evolutionary and ecological perspectives to understand community assembly.

Our outstanding lineup of keynote speakers and emerging leaders will present a diverse array of integrative advances in our understanding of community assembly. These topics include new conceptualizations of the species pool for community ecology, the genomic processes underlying species coexistence, phylogenetic models of community composition, insights from paleocommunities, and coevolutionary networks.

We are delighted to announce our keynote speakers: Rosemary Gillespie, professor and Schlinger Chair in Systematic Entomology, Department of Environmental Science and Essig Museum of Entomology, University of California, Berkeley, and Tadashi Fukami, associate professor, Department of Biology, Stanford University. You can read more about them and our early career speakers and their presentations under the speakers tab on our website. Early career scientists are considered senior graduate students, postdoctoral researchers, and first- or second-year faculty.

Registration is free of charge but we strongly encourage you to register so we may provide adequate food and refreshment.

Graduate students from all universities and all disciplines are invited to present their work during a lunchtime poster session, and can indicate so when they register. Poster specifications: <http://sites.lsa.umich.edu/ecss/promotional-materials/grad-student-posters/> Lunch will be provided at the poster session and a reception will follow the symposium.

Looking forward to your participation,

2016 Early Career Scientists Symposium organizing committee

“marschmi@umich.edu” <marschmi@umich.edu>

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## Vairao Portugal Congenomics2016 May3-6

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

ABSTRACT SUBMISSION DEADLINE APPROACHING! - 21 February

TRAVEL GRANTS AVAILABLE FOR STUDENTS: We encourage student participation by providing travel grants (priority will be given to students from member countries of the ConGenOmics network\*). Check conditions for application at <http://congenomics2016.com/-submissions/>. Any kind of presentation may be eligible, including early stage of scientific or academic projects. These travel grants will cover registration fee, lodgement at selected hostels and travel expenses up to 500 EUR. Decisions will be made on time before the early registration fee deadline.

CONFIRMED INVITED SPEAKERS: Fred Allendorf (University of Montana) Mike Bruford (Cardiff University) Lisette Waits (University of Idaho) Natasha de Vere (National Botanic Garden of Wales) Emma Teeling (University College Dublin) Kerry Naish (University of Washington)

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

ABOUT: This conference aims to gather the best research currently being performed on Genomics and its applications to Conservation. The program includes six invited plenary lectures, submitted oral communications (regular and flash) and poster sessions, covering the state of art on conservation genomics. The following main subjects will be addressed, emphasizing their applied nature: - Demographic inference and population history;  $\hat{A}$ '- Adaptive genetic variation (including quantitative traits and epigenetics);  $\hat{A}$ '- Population viability;  $\hat{A}$ '- Taxonomic identification (using whole genome, mitogenome, metabarcoding);  $\hat{A}$ '- Environmental DNA.

The conference is organized by ConGen (Conservation genetics and wildlife management) research group and hosted in CIBIO/InBIO Associate Laboratory (<http://cibio.up.pt/>) and the University of Porto facilities in Vairao, Portugal, and the ConGenOmics Research Networking Programme\*.

(\*) ConGenOmics is an ESF Research Networking Programme that aims to bring together European and pan-Å' European specialists on conservation genomics, to develop and improve the knowledge transfer of the technical advances and challenges in conservation genomics, focusing specifically on the application of genomic techniques. ConGenOmics programme organizes workshops, summer schools, collaborative expert meetings and an exchange program at pan-Å'European level, to further develop the field of conservation genomics and to aid in the knowledge transfer of the technological advances and challenges among European research groups focusing specifically on applications of genomic technologies in conservation biology. More details in <http://www.ru.nl/congenomics> ORGANIZING AND SCIENTIFIC COMMITTEE: Paulo Célio Alves (University of Porto) Ricardo Jorge Lopes (University of Porto) José Melo-Ferreira (University of Porto) Raquel Godinho (University of Porto)

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

Questions? Contact us by email (info@congenomics2016.com) or on Facebook/twitter jmeloferreira@cibio.up.pt

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## Vairao Portugal ConservationGenetics May3-6

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

**NEW ABSTRACT SUBMISSION DEADLINE! - 1 MARCH**

**TRAVEL GRANTS AVAILABLE:** ConGenOmics\* will fund the participation of early career researchers with travel grants. These grants are available for graduate students (priority to PhD students) and post-Å'docs (maximum 2 years after PhD) that will present their work. We encourage any kind of presentation, including early stages of scientific or academic projects. Priority will also be given to students and post-docs from ConGenOmics member countries. Check conditions for application at <http://congenomics2016.com/submissions/>.  
**INVITED SPEAKERS:** Fred Allendorf (University of Montana) Mike Bruford (Cardiff University) Lisette

Waits (University of Idaho) Natasha de Vere (National Botanic Garden of Wales) Emma Teeling (University College Dublin) Kerry Naish (University of Washington)

**IMPORTANT DATES:** 1 March: Submit your abstract online. 18 March. Abstract acceptance notification. Decision on travel grant applications. 31 March: Early registration fees: 250 EUR (standard), 100 EUR (students).

**ABOUT:** This conference aims to gather the best research currently being performed on Genomics and its applications to Conservation. The program includes six invited plenary lectures, submitted oral communications (regular and flash) and poster sessions, covering the state of art on conservation genomics. The following main subjects will be addressed, emphasizing their applied nature: - Demographic inference and population history; - Adaptive genetic variation (including quantitative traits and epigenetics); - Population viability; - Taxonomic identification (using whole genome, mitogenome, metabarcoding); - Environmental DNA.

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Questions? Contact us by email (info@congenomics2016.com) or on Facebook/twitter.

jmeloferreira@cibio.up.pt

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## Valencia RNAmodification Evolution Mar1 LastCall

\*SMBE Satellite Meeting. Valencia, Spain - Last Call\*

This is the last call to submit your abstract to the SMBE Satellite Meeting on RNA modification and its implication on adaptation and evolution.

Abstract deadline: March 1, 2016. More information about the meeting can be found at: <http://smbeed2016.cibiv.univie.ac.at/> Confirmed invited speakers: Jianzhi Zhang. University of Michigan, USA Jin Billy Li. Stanford University, USA Gideon Rechavi. Tel Aviv University, Israel Josh Rosenthal. Institute of Neurobiology, University of Puerto Rico Ann Ehrenhofer-Murray. Humboldt University, Berlin, Germany Ayelet Lamm. Technion - Israel Institute of Technology, Israel Yi Tao Yu. University of Rochester, USA Susana Rodriguez. Centro de Investigacion Principe Felipe, Spain Thorsten Stafforst. Tubingen University, Germany Nina Papavasiliou. The Rockefeller University, USA Pablo Vera. Instituto de Biologia Molecular y Celular de Plantas - IBMCP/CSIC, Spain Miguel Gallach <miguel.gallach@univie.ac.at> Arndt von Haeseler <arndt.von.haeseler@univie.ac.at> Michael Jantsch <Michael.Jantsch@univie.ac.at>

Miguel Gallach Center for Integrative Bioinformatics Vienna (CIBIV) Max F. Perutz Laboratories(MFPL) Telf: +43 1 4277 74330 Postal Address: Ebene 1 Campus Vienna Biocenter 5 CIBIV, MFPL 1030 Vienna Austria e-mail: miguel.gallach@univie.ac.at migaca2001@gmail.com <http://www.cibiv.at/~mgallach/> <https://scholar.google.at/citations?user=3DRNeD2AAAAAJ&hl=3Den> SMBE Satellite Meeting in VALENCIA <http://smbeed2016.cibiv.univie.ac.at/> Miguel Gallach <miguel.gallach@univie.ac.at>

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## YosemiteNatIPark Symbiosis May6-8

ADVANCED REGISTRATION EXTENDED TO MARCH 8th

Dear Colleagues,

The Sixth annual Symbiosis Workshop will take place on May 6th-8th, 2016 at the Sierra Nevada Research Station, Yosemite National Park. This has become a great venue for a diversity of symbiosis researchers, so we hope to continue to attract a diverse group:

Keynote speaker 2016: Dr. Betsy Arnold from the University of Arizona.

Information about our meeting:

**Why:** Our goal is to better integrate scientists that focus on symbiosis research. We plan to continue annual workshops at Yosemite as this site is both beautiful and secluded. This will be our 6th annual meeting and we have been attracting scientists from all over the country and overseas.

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

**When:** The talks and formal meeting will be held May 7-8, 2016, though we make accommodation arrangements available for attendees to arrive on Friday the 6th to provide opportunities to enjoy the park. Since time at the conference is limited, we ask attendees to submit an abstract and a preference (talk versus poster). Priority will be given to those presenting.

Abstract and early bird registration are due on March 8th, 2016.

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

Link to meeting information: <http://www.sachslab.com/symbiosis-2015.php> The registration form for the 2016 Symbiosis Workshop is active: <http://snri.ucmerced.edu/symbiosis> Payments should be made at: <https://intelforms.ucmerced.edu/Form/Symbiosis> Please direct any questions to the organizers:

Joel Sachs joels@ucr.edu

A. Carolin Frank cfrank3@ucmerced.edu

Joel Lawrence Sachs <joel.sachs@ucr.edu>



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## GradStudentPositions

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### Barcelona 15 SingleCellGenomics

15 PhD/Research positions on Promoting Single Cell Genomics to explore the ecology and evolution of hidden microeukaryotes (H2020-MSCA-ITN SINGEK)

Microbial eukaryotes cover the widest phylogenetic diversity in the eukaryotic tree of life and are essential components of all Earth's ecosystems. Paradoxically, they remain largely unknown, hiding a wealth of genes and genomes that are key to understand the ecology and evolution of microbial ecosystems. SINGEK is a H2020 Marie-Skłodowska-Curie Innovative Training Network (MSCA-ITN) project aimed at providing a unique and structured training programme to 15 Early Stage Researchers (ESRs) to study microeukaryotes at the single-cell level. ESRs will be trained in the use of an array of laboratory methods (cell sorting and molecular tools for nucleic acid amplification and high throughput sequencing), bioinformatic techniques (genome and tran-

scriptome assembly and functional gene annotations), and will work on scientific questions in the fields of microbial ecology and evolution in order to investigate microeukaryotes in unparalleled detail. The training structure is a central part of SINGEK project and will include: local and network-wide activities, secondments to other network laboratories and workshops in transferable skills essential for successful career development.

All positions are for 3-years contracts starting in October 1st, 2016, most of them leading to a PhD degree. Specific conditions may apply to individual positions depending on local regulations.

Top-level graduates in biology, bioinformatics, microbial ecology, molecular biology, evolutionary biology, biodiversity, biotechnology, physics, nanoscience, engineering or computer science are encouraged to apply. No discrimination will be made on the basis of nationality, gender, race, religion or disability.

H2020 EU funding imposes strict eligibility criteria: At the time of recruitment the researcher must not have resided or carried out his/her main activity (work, studies, etcâ) in the country of the host institute for more



than 12 months in the 3 years immediately prior to his/her recruitment under the project. The researcher should also be in the first four years of their research careers at the time of recruitment by the host organisation and have not been awarded a doctoral degree.

Candidates may apply through the SINGEK applications system ([www.singek.eu/call-for-positions/](http://www.singek.eu/call-for-positions/)), which will request the following information: 1. An application form, including a CV overview, ESRs' positions of interest (up to 3), and a statement of their motivation for applying. 2. A full CV. 3. An academic record, with a scan of the degree qualifications. 4. Two recommendation letters.

Each project supervisor will revise the candidates' documentation and, on the basis of the completeness and adequacy of the requested material and quick eligibility check, will score candidates based on: (1) academic profile; (2) personal motivation; (3) scientific skills and relevant experience; and (4) English proficiency. Shortlisted candidates will be invited to teleconference interviews with the relevant project supervisor(s).

Application deadline: 17:00 GMT on the 15th April 2016

More information: [www.singek.eu](http://www.singek.eu) Candidates are invited to contact potential supervisors to get more details.

List of 15 ESR projects

ESR 1 - Genome basis for ecological differentiation among related uncultured lineages Supervisor: Ramon Massana Host institution: Institute of Marine Sciences (ICM-CSIC), Barcelona, Spain

ESR 2 - Next steps towards systems biology: disentangling complex ecological networks in marine microbes Supervisor: Ramiro Logares Host institution: Institute of Marine Sciences (ICM-CSIC), Barcelona, Spain

ESR 3 - Uncultured opisthokonts and the origin of metazoan multicellularity Supervisor: Iñaki Ruiz-Trillo Host institution: Institute of Evolutionary Biology (CSIC-UPF), Barcelona, Spain

ESR 4 - Single cell transcriptomics for ecological and metabolic niche-mapping of uncultured microeukaryotes Supervisor: Stefan Bertilsson Host institution: Uppsala University (UU), Uppsala, Sweden

ESR 5 - Disentangling the origin of eukaryotes using phylogenomics and comparative genomics approaches Supervisor: Thijs Ettema Host institution: Uppsala University (UU), Uppsala, Sweden

ESR 6 - Development of methodology for single cell organism genome analysis Supervisor: Ivo Gut Host institution: National Centre for Genomic Analysis (CNAG-

CRG), Barcelona, Spain

ESR 7 - Deep eukaryotic phylogenomics Supervisor: Purificación López-García Host institution: Unité Ecologie Systematique Evolution (Univ. Paris-Sud-CNRS-AgroParisTech), Paris, France

ESR 8 - From single-cells to global oceans: using single-cell genomes/transcriptomes to reconstruct and interpret worldwide meta-omics

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## BielefeldU MarineMammal EvolutionaryGenomics

Graduate position: Early stage fellowship in Marine population genomics PhD studentship in marine mammal evolutionary genomics

Funding is available for an early stage researcher (ESR) as part of a Marie Curie Initial Training Network. The researcher will be based in the Hoffman lab at Bielefeld University ([www.thehoffmanlab.com](http://www.thehoffmanlab.com)) and will also go on secondment to the Harper Lab at Cambridge University ([www.cai.cam.ac.uk/people/liz-harper](http://www.cai.cam.ac.uk/people/liz-harper)). This position provides an excellent opportunity for the candidate to obtain experience of diverse methodologies, from next generation sequencing to geometric morphometrics and scanning electron microscopy.

There is mounting concern over the acidification of the Worlds oceans. In the 250 years since the onset of the industrial revolution, atmospheric CO<sub>2</sub> levels have risen from 280 to 381 parts per million and average ocean pH has fallen from 8.16 to 8.05. Human-driven emissions of CO<sub>2</sub> continue to rise and have begun to outstrip even the most pessimistic of IPCC model scenarios. How will life in the oceans adapt to this changing environment? Particular concern has been expressed over organisms with heavily calcified shells such as molluscs, as their ability to extract carbonate ions from seawater and incorporate these into their skeletons may be compromised.

This position forms part of a Marie Curie Initial Training Network entitled CACHE: Calcium in a Changing Environment, funded by the EU (ref: 605051) and coordinated by the British Antarctic Survey. The aim

of this network is to take a coordinated multidisciplinary approach to understanding calcium regulation and shell production in four commercially important shellfish species, the king scallop (*Pecten maximus*), the Pacific oyster, (*Crassostrea gigas*), the blue mussel (*Mytilus edulis*) and the soft shell clam (*Mya arenaria*). The network comprises 10 partners from 6 European countries, including research institutes, universities and commercial enterprises. Full details of the network can be found at [www.cache-ITN.eu](http://www.cache-ITN.eu). The ESR will be expected to work with two other ESRs based in Bielefeld and Cambridge respectively. He or she will be involved in projects using population genomic approaches to (i) conduct a comparative analysis of the population structure of the four species along a European latitudinal cline; (ii) explore how stocking practices, hybridization, oceanographic barriers and life-history interact to shape population structure; (iii) determine the relative contributions of genotype and phenotypic plasticity to shell morphology and ultrastructure; (iv) test for signatures of selection at candidate genes involved in calcium regulation and deposition. There will also be scope for the ESR to explore their own related interests within the framework of this project.

We seek a bright and highly motivated candidate who holds a B.Sc. or equivalent in a relevant topic (e.g. marine biology, population or evolutionary genetics, bioinformatics). An M.Sc. would also be advantageous but is not necessary. The ideal candidate will have some practical experience of working in a genetics lab and / or strong quantitative skills including experience of working in R. Experience of next generation sequencing approaches is desirable although training can be provided. The candidate should also be able to work both independently and as part of a multidisciplinary team. A high standard of spoken and written English is required.

The ESR will join the Hoffman lab, a young and dynamic group comprising five PhD students and a postdoc. They will be based at the Department of Animal Behaviour at Bielefeld University ([www.uni-bielefeld.de/biologie/animalbehaviour/home.html](http://www.uni-bielefeld.de/biologie/animalbehaviour/home.html)). The department currently hosts six principal investigators, seven postdocs and over thirty PhD students. It offers a stimulating international environment and an excellent research infrastructure including brand new molecular laboratories and computing facilities. The working language of the Department is English. Bielefeld is a city of 325,000 inhabitants with an attractive historical centre and easy access to the Teutoberger Wald for hiking and other outdoor pursuits. It offers a very high standard of living and is well connected to most major European cities.

This position offers a generous stipend of at least

euro3700 per month, including a mobility allowance, for a period of up to 18 months. Funding is also available for the fellow to attend at least one meeting in Portugal, and there may be opportunities for fieldwork in other European countries.

To apply for the position, please provide: (i) a letter of motivation including a maximum 2-page statement of your research interests,

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## CharlesU Prague SexChromosomeEvolution

CharlesU\_Prague.SexChromosomeEvolution

PhD position in Evolution of sex chromosomes in squamate reptiles

A position for a PhD candidate is currently open in the laboratory of Dr. Lukas Kratochvil, Department of Ecology, Charles University in Prague, Czech Republic. The successful PhD candidate will join our current projects on the study of the evolution of sex chromosomes in squamate reptiles with molecular and cytogenetic methods.

Project description: The aim of the project is to examine the evolution of sex chromosome and their homology based on gene content in selected lineages of squamate reptiles (eg. lizards and snakes). Squamate reptiles possess lineages with either XX/XY, ZZ/ZW or temperature-dependent sex determination systems. Despite the recent advantages in the field, our knowledge about the sex determination systems and sex chromosome homology is limited only to few groups of reptiles (eg. iguanas, advanced snakes), while the majority of reptilian lineages remain unstudied. The successful candidate will collaborate with the other team members and will study the evolution of sex chromosomes in a multidirectional approach, involving cytogenetics (eg. FISH, chromosome painting), molecular genetics (eg. qPCR) and bioinformatics (eg. transcriptomics). More information about our current research activity can be found in the following publications:

<http://www.ncbi.nlm.nih.gov/pubmed/26702042>

<http://www.ncbi.nlm.nih.gov/pubmed/25424152>

<http://www.ncbi.nlm.nih.gov/pubmed/24433436>

Qualifications: The applicant should possess Master degree (or equivalent title) and has a proven expertise in a related field of biology: evolutionary biology, cytogenetics, phylogenetics, genomics and/or bioinformatics. Previous experience in herpetology is not necessary. The ideal candidate should be scientifically motivated, able to work both independently and as a part of the team and should have a publication record. High standard of spoken and written English is required.

Application: The applicant should send a letter explaining your background and motivation, a full CV and contact information for two references to: [lukas.kratochvil@natur.cuni.cz](mailto:lukas.kratochvil@natur.cuni.cz); [michail.rovatsos@natur.cuni.cz](mailto:michail.rovatsos@natur.cuni.cz).

The deadline for submission of applications is March 31, 2016.

Lukas Kratochvil

Associate Professor Department of Ecology Charles University in Prague Faculty of Science Vinicn?? 7, 128 43 Praha 2 [www.natur.cuni.cz/en](http://www.natur.cuni.cz/en) Tel.: +420 221 95 1745 e-mail: [lukas.kratochvil@natur.cuni.cz](mailto:lukas.kratochvil@natur.cuni.cz)

“Michail Rovatsos,  
<[michail.rovatsos@natur.cuni.cz](mailto:michail.rovatsos@natur.cuni.cz)>

Ph.D.”

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## Essen Metabarcoding

The University of Duisburg-Essen (Campus Essen) Centre for Water and Environmental Research (ZWU) Aquatic Ecosystem Research Group (Leese-Lab) offers 1 PhD position (Part-time 55%; salary equivalent TV-L 13) in Genetic Monitoring / Metabarcoding (BMBF German Barcode of Life 2 subproject)

The group of Prof. Florian Leese is interested in developing new molecular approaches to assess the ecological status of aquatic ecosystems. Specifically, we develop and apply DNA metabarcoding to monitor changes in stream communities under environmental stressors. Furthermore, we utilize genome-wide markers and perform transcriptional profiling to understand population and organismal responses to multiple stressors. As part of a recently granted subproject within the large collaborative German Barcode of Life Project (GBOL2, funded by the Federal Ministry of Education and Research, BMBF), we want to bring DNA metabarcoding of freshwater invertebrates to the application stage. In cooper-

ation with our collaborators at the Zoological Research Museum Alexander Koenig (Bonn, Germany), the candidate will collect samples, perform experiments, generate and analyse next-generation sequencing data on whole communities (amplicon sequencing). Further reading: Elbrecht & Leese, PLoS ONE 2015, DOI: 10.1371/journal.pone.0130324; Macher, Salis et al., Ecological Indicators, 2016.

The successful candidate (f/m) will hold a Master in Biology, Chemistry or Bioinformatics and has good experience in molecular lab work. Furthermore, he/she has experience and strong interest in a programming or scripting language (e.g. R, C, Python). Candidates will benefit from the international and interdisciplinary research environment at the research group, the GBOL2 project and the ZWU. Excellent high-throughput genomics and bioinformatics equipment are available in the newly equipped labs.

The position will start as soon as possible initially for 2,5 years (will be extended). Deadline: 29. February 2016

For more information please visit: <http://udue.de/-leeselab> <https://www.uni-due.de/zwu/> <https://www.bolgermany.de> Please send applications as a single pdf file with reference code 42-16 to [miriam.schmidt@uni-due.de](mailto:miriam.schmidt@uni-due.de). For questions please contact [florian.leese@uni-due.de](mailto:florian.leese@uni-due.de).

We are one of the youngest universities in Germany and think in terms of possibilities, not limitations. In the heart of the Ruhrregion, we develop ideas of the future at our 11 faculties. We are strong in research and teaching, live diversity, support potential and are highly committed to an educational equality that has earned this name.

The University Duisburg-Essen aims at promoting the diversity of its members (see <http://www.uni-due.de/diversity/international.shtml>). Applications from disabled persons or equivalents according to Â§2 Abs. 3 SGB IX are encouraged.

The University Duisburg-Essen has been awarded for its effort to promote gender equality with the “Total-E- Quality-Award”. It aims at increasing the share of women in the scientific personnel and therefore explicitly encourages women to apply. Women will be preferentially considered when equally qualified according to the state equality law.

Link to original job offer: URL: <http://tinyurl.com/-jd8ta6x> Prof. Dr. Florian Leese University of Duisburg-Essen Faculty of Biology Aquatic Ecosystem Research Universitaetsstrasse 5 D-45141 Essen, Germany

Email: [florian.leese@uni-due.de](mailto:florian.leese@uni-due.de) +49 201.183-4053 | Bielefeld.DE>  
 @leeselab <http://udue.de/leeselab> [florian.leese@uni-due.de](mailto:florian.leese@uni-due.de)

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## GermanCanadian 6 Bioinformatics

The International DFG Research Training Group

“Computational Methods for the Analysis of the Diversity and Dynamics of Genomes”

at Bielefeld University, Germany, offers 6 PhD positions starting October 2016.

Research will focus on the development of methods of high importance for the practical comparative analysis of genomes, in particular in view of both the variation between individuals (diversity) and the change in populations over time (dynamics). Our program aims at training specialists in handling big data related to genomics and molecular biology.

PhD students will hold 3-year positions, payed according to German TV-L 13 table, i.e., a monthly gross salary of approximately 3200 Euros. This international graduate program is a close cooperation with Simon Fraser University (SFU), Vancouver, Canada ([www.sfu.ca/~madd-gen](http://www.sfu.ca/~madd-gen)). It involves a six-months research stay at SFU or one of the other partner institutions in Vancouver. (Funds to support parents and handicapped persons are available.)

Candidates should hold an excellent Master degree (or equivalent) in bioinformatics, computer science, mathematics, or a related area. They have to demonstrate broad background in the interdisciplinary field of bioinformatics in general, with a focus on computer science and deep knowledge in the area they apply for. As students must be able to communicate their work in the research training group, and have to quickly integrate into both the Bielefeld and Vancouver environment, good communication skills are demanded. Knowledge of the English language is required, whereas German is not necessary.

Application deadline: May 8, 2016

For further information and application instructions, see our website:

[www.didy.uni-bielefeld.de](http://www.didy.uni-bielefeld.de) DiDy-students mailing list [DiDy-students@cebitec.uni-bielefeld.de](mailto:DiDy-students@cebitec.uni-bielefeld.de) <https://mail.cebitec.uni-bielefeld.de/mailman/listinfo/didy-students> Georges Hattab <[ghattab@CeBiTec.Uni-](mailto:ghattab@CeBiTec.Uni-)

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## Ghent GenomeAnnotation

PhD student - New tools for genome annotation in unknown microeukaryote lineages

In the framework of a H2020 Marie-Skłodowska-Curie Innovative Training Network on Promoting Single Cell Genomics to explore the ecology and evolution of hidden microeukaryotes (SINGEK), we have a position open for a \*PhD student in Bioinformatics\*, with a strong focus on tool development and data visualization.

Specifically, we are looking for: -Master in computational sciences, preferably with some experience in biological data analysis -Experience with Unix and command-line usage -Good programming skills (Python, or Java/C++) -Experience with relational databases (mySQL), PHP and webdesign/JavaScript is a plus -Excellent English communication skills -A passion for science and driven to decode the mysteries of life.

Need more info? Contact Prof. K. Vandepoele ([klaas.vandepoele@psb.vib-ugent.be](mailto:klaas.vandepoele@psb.vib-ugent.be)).

Want to apply? Find the application form here: <http://www.singek.eu/esr-10-new-tools-for-genome-annotation-in-unknown-microeukaryote-lineages/> .  
 “[klaas.vandepoele@psb.vib-ugent.be](mailto:klaas.vandepoele@psb.vib-ugent.be)”

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## IBDM Marseille EvolutionWingPigmentation

PhD position available in the Prud'homme lab (Marseille, France)

Evolution of the gene network controlling wing pigmentation in *Drosophila*

We are looking for a PhD student to study the evolution of the gene regulatory network controlling the formation of a wing pigmentation pattern in *Drosophila* species. This wing spot has emerged from a spot-less ancestor, around 15 millions years ago, and then diversified in shape, color and intensity between species.

The goal of the project is to peer into the genomic changes responsible for these different evolutionary tran-



sitions. The student will use comparative functional genomics across species to identify candidate genes and cis-regulatory sequences associated with these transitions. These candidates will be further validated in vivo by functional manipulations using genome editing approaches.

Ultimately, these results will help to better understand how a gene regulatory network emerge during evolution and give rise to a novel morphological trait, and how alterations of this network underlie morphological diversification of a morphological trait.

Candidates (from any nationality, with no requirement to understand French) are expected to have a background in developmental biology, genetics, and a strong interest in evolution.

Please send a CV, a motivation letter, a description of research experience and interests and e-mail contact for 2-3 references to [benjamin.prudhomme@univ-amu.fr](mailto:benjamin.prudhomme@univ-amu.fr)

The position is funded for 3 years by an ERC grant and must start before July 1st 2016.

Our lab is part of the Institute of Developmental Biology of Marseille (IBDM), an interdisciplinary research center studying developmental biology and neurobiology. More information about the lab and the institute can be found here: [www.prudhommelab.com](http://www.prudhommelab.com) & [www.ibdm.univ-mrs.fr](http://www.ibdm.univ-mrs.fr) Benjamin Prud'homme <[benjamin.prudhomme@univ-amu.fr](mailto:benjamin.prudhomme@univ-amu.fr)>

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## IowaStateU ConservationGenetics

M.S. Graduate Assistantship V Conservation/Population genetics at Iowa State University. STARTING DATE: Fall 2016 (option to start earlier in the summer) CLOSING DATE: Position is open until filled. DESCRIPTION: The Roe Lab at Iowa State University (<http://www.nrem.iastate.edu/research/roe/>) is searching for an MS student to study conservation/populations genetics of one of a variety of freshwater organisms including mussels, fishes and shrimps. The position can involve a combination of laboratory, and fieldwork. The student will work with the PI to develop an original thesis project or build off of existing research tracks in the lab. QUALIFICATIONS: B.S. in biology, genetics, fisheries, wildlife, biology, or related field. Minimum GPA of 3.25 and combined quantitative/verbal GRE scores of 300. Previous laboratory experience with PCR and computer and/or bioinformatics skills is preferred.

STIPEND: \$19,848/year. CONTACT: Interested individuals should send a letter of interest, CV, unofficial copy of transcripts and GRE scores to Dr. Kevin J. Roe ([kjroe@iastate.edu](mailto:kjroe@iastate.edu)).

Kevin J. Roe Natural Resource Ecology & Management  
339 Science II Iowa State University Ames, IA 50014

[kjroe@iastate.edu](mailto:kjroe@iastate.edu)

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## KielU 3 Celegans

Kiel University, Germany

1 Postdoc + 3 PhD positions on the evolution and genetics of *C. elegans*-microbiota interactions

The positions are funded within a larger research initiative on host-microbiota interactions at Kiel University (Collaborative Research Center CRC1182 "Origin and function of metaorganisms").

The postdoc and one PhD position are supervised by Hinrich Schulenburg (projects A1.1 and A4.3) and address the evolutionary dynamics and genomics of *C. elegans* microbiota interactions, based on evolution experiments and genome sequencing (Schulenburg group).

The second PhD project (project A1.2) is supervised by Katja Dierking (Schulenburg lab) and looks at the transcriptomic and also genetic basis of the interaction, using RNASeq and functional genetic analysis.

The third PhD project (project A1.3) is supervised by Matthias Leippe and assesses the involvement of antimicrobial peptides and proteins in shaping *C. elegans*-bacteria interactions using biochemical and functional genetic approaches (Leippe group).

For further information, please check the webpage of the Collaborative Research Center (<http://www.metaorganism-research.com/>) or the Schulenburg group (which includes Katja Dierking; <http://www.uni-kiel.de/zoologie/evocogen/>) or the Leippe group (<http://www.uni-kiel.de/zoologie/zoophysiologie/>).

Application procedures are described on the webpage of the Collaborative Research Center (see above link; then under Jobs). Deadline for applications is 29 February 2016. If you have questions, then please contact either Hinrich Schulenburg ([hschulenburg@zoologie.uni-kiel.de](mailto:hschulenburg@zoologie.uni-kiel.de)), Katja Dierking ([kdierking@zoologie.uni-kiel.de](mailto:kdierking@zoologie.uni-kiel.de)), or Matthias Leippe ([mleippe@zoologie.uni-kiel.de](mailto:mleippe@zoologie.uni-kiel.de)).

Link: themeData Link: colorSchemeMapping

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](mailto:hschulenburg@zoologie.uni-kiel.de) Web: [www.uni-kiel.de/zoologie/evocogen/](http://www.uni-kiel.de/zoologie/evocogen/) Hinrich Schulenburg <[hschulenburg@zoologie.uni-kiel.de](mailto:hschulenburg@zoologie.uni-kiel.de)>

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### LinköpingU Sweden EvolutionaryGeneticsAgeing

PhD-position available on the evolutionary genetics of ageing at Linköping University, Sweden.

Ageing, the gradual deterioration of bodily functions that results in reduced reproductive capacity and increased probability of death, is something virtually all organisms experience. Already many decades ago evolutionary theory provided a robust general explanation for this phenomenon, yet most aspects of ageing are still far from understood today and many exciting discoveries lie ahead. The aim of the current project is to improve our understanding of the type of mutations that contribute to ageing, how genetic quality influences ageing and how this relates to the commonly observed sex differences in lifespan.

The project entails work on experimentally evolved populations (already established one year ago), assays of genetic variation in life history traits and, most likely, transcriptome analyses. All work will be conducted using the model organism *Drosophila melanogaster*. The successful candidate is expected to work closely with other members of the lab, whose work largely revolves around similar questions while taking a wider view of the genetics of sex differences in general (see postdoc position advertised at EvolDir).

We seek a bright, highly motivated, and enthusiastic person who is able to work both as part of a team and independently. The ideal candidate has a Master's degree in evolutionary biology or genetics, with a good background in bioinformatics and a documented interest in statistics. Experience in laboratory work with *Drosophila*, or another lab model insect, is beneficial. The working language at the department and lab is English. A high standard of spoken and written English is required. The successful candidate will join a research group led by Urban Friberg (see [https://](https://www.liu.se/forskning/foass/urban-friberg?l=en)

[/www.liu.se/forskning/foass/urban-friberg?l=en](https://www.liu.se/forskning/foass/urban-friberg?l=en)) and will receive her/his postgraduate training within IFM Biology at Linköping University. This position is financed for four full years, and may involve teaching to up to 20% (which will then prolong the position accordingly). For a very promising candidate, who does not fully meet the above criteria, a short term position may be offered aimed to help acquire the required experience needed to start the PhD position.

Applications should be written in English and include i) a cover letter with information on your background, research interests and experiences, and your motivation to work on this project (max 3 pages), ii) complete CV, iii) a description of undergraduate training and a copy of your transcripts, iv) the names and email addresses of 2-3 referees. Applications should be sent as one PDF to [urban.friberg@liu.se](mailto:urban.friberg@liu.se). The position is open until filled, and applications will be reviewed continuously, but for full consideration please apply by March 1. The preliminary starting date is May 1 2016, but is flexible.

“[urban.friberg@liu.se](mailto:urban.friberg@liu.se)” <[urban.friberg@liu.se](mailto:urban.friberg@liu.se)>

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### LinköpingU Sweden EvolutionAvianCognition

PhD-position available on the evolution of individual variation in animal cognition at Linköping University, Sweden.

Job description A fully funded 4-year PhD position is offered in the subject of ethology, in the research group of Hanne LÄvlie, Linköping University (IFM Biology). The job description entails to conduct research on the causes and consequences of variation in animal cognition, and we are particularly interested in links with animal personality. Cognitive processes are fundamental, but explanations to individual variation are still poorly explored. Animal personality (i.e. consistent individual behavioural responses), has recently experienced considerable research attention. Despite so, fundamental questions remain unanswered, such as why does variation in personality arise, and how is polymorphism maintained? Personality and cognition are predicted to be linked, but the causality and consequences of this relationship are still unknown. We have demonstrated individual variation in various cognitive tasks and observe links between learning speed and personality, in our model species the red junglefowl (*Gallus gallus*).



The aim of the proposed project is to improve our understanding of individual variation in animal cognition, by using the red junglefowl as model. The fowl is a particularly suitable species for research on this due to the possibility of combining our extensive understanding of behaviour, physiology and genetics in chickens, to apply a strong experimental design while examining behaviours under natural conditions or in the lab. The advertised position can be combined with a teaching assistantship of up to 20% within the biology undergraduate program, which will extend the position accordingly.

**Requirements** The successful applicant will be a highly motivated and talented candidate with a MSc-degree in biology (or equivalent), with a specialization in ethology, behavioural ecology, evolutionary biology, neurobiology or similar. Research experience in experimental animal behaviour, sound statistical knowledge and analytical abilities are merits, as is 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. The successful candidate should be enthusiastic about animal behaviour and handling birds.

What we offer Linköping University is a modern, innovative university with over 27000 students and 3900 employees. Biology at Linköping University offers excellent molecular facilities and exceptional avian housing facilities. The successful candidate will be part of the AVIAN behavioural genomics and physiology group (which currently has around 25 group members, including 10 PhD students), and part of the Centre of Excellence for Animal Welfare Science (in collaboration with SLU Uppsala).

Linköping is a popular university city, and is the fifth largest city in Sweden. It is located in central Sweden, just two hours by train from Stockholm, and offers proximity to the beautiful nature of Åstergötland, including the great lake Vättern, as well as both recent and pre-historic history, and cultural attractions.

**Equal opportunity** Linköping University continues to develop as an attractive and creative work place characterized by equal opportunities, which works actively to promote diversity and gender equality.

**Starting date** The position is available immediately, and will be set according to agreement.

**Salary** According to present rates at the university (starting at 25 000 SEK per month), including health insurance and other benefits, for 4 full years. A short-term position may be offered to a very promising candidate to ensure that the required experiences are acquired prior

to start.

**More information** Contact Hanne LÅvlie (hanne.lovlie@liu.se), tel +46 (0) 13-286681.

**Application procedure** The application should include a 1-2 page cover letter describing your research experience and interests, and your interest in this project, and a full CV (including name and contact details of 2 references who are willing to provide letters of support). Transcript of grades and copy of a relevant publication may be required at a later stage. Application should be sent as one PDF to hanne.lovlie@liu.se. The position is open until filled, and applications will be reviewed continuously, but for full consideration please apply by 31st of March 2016.

Hanne Lovlie <hanne.lovlie@liu.se>

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## Lund CyanobacteriaPopulationGenomics

PhD position at Lund University, Sweden

A 4-year doctoral position on cyanobacterial population genomics

**Project description**

Aquatic environments are of enormous importance as natural resources of drinking water, fish production, and recreation. However, surface waters worldwide are threatened by toxic cyanobacterial algal blooms, which have detrimental effects on human health and aquatic biota. One of the most important toxic cyanobacteria in Swedish freshwater is the genus *Microcystis*. We know which species may be harmful, but cannot predict where and when blooms will be toxic due to inter-population and strain variation. The aim of the project is to understand temporal and spatial prevalence, and the underlying function of toxicity. The overarching hypothesis is that toxic and non-toxic populations have emerged as a result of ecological differentiation. The approach is whole genome sequencing followed by population genetic analyses of toxic and non-toxic strains. The PhD students project will consist of designing and performing field sampling, formulating hypotheses, laboratory work, genome sequencing, genome analyses, and population genetic analyses.

**Required qualifications**

The successful candidate is required to hold a Masters degree or equivalent in biology with a specialization on

evolution and ecology. The candidate should have good knowledge and practical experience of laboratory work, especially molecular techniques. A basic understanding of aquatic ecosystems and microbial ecology are desired qualifications, and experience of work with microalgal culture, DNA sequence analysis and programming (within bioinformatics) are an additional merit. It is a requirement that the candidate should be able to read and write in English on a daily basis. Important personal qualities are to be creative, good at problem-solving, a team-worker, independent, resilient, and structured. At times the studies will require long workdays during field sampling, as well as trips with overnight stays within and outside Sweden. A drivers license is required. The application should include a curriculum vitae, copies of degrees and transcripts of academic letters, a personal letter stating your interest for the project and doctoral studies as well as any relevant experience for the project, contact information (phone, email) of two personal references. Relevant publications, including accepted academic papers or research thesis can also be enclosed.

#### Eligibility

Students with basic eligibility for third-cycle studies are those who: have completed a second-cycle degree. Have completed courses of at least 240 credits V of with at least 60 credits are from second-cycle courses, or have acquired largely equivalent knowledge in some other way, in Sweden or abroad.

The employment of doctoral students is regulated in the Swedish Code of Statutes 1998:80. Only those who are or have been admitted to PhD-studies may be appointed to doctoral studentships. When an appointment to a doctoral studentship is made, the ability of the student to benefit from PhD-studies shall primarily be taken into account. In addition to devoting themselves to their studies, those appointed to doctoral studentships may be required to work with educational tasks, research and administration, in accordance with specific regulations in the ordinance.

Last application date 07.Mar.2016 11:59 PM CET

Apply on: <https://lu.mynetworkglobal.com/en/what:job/jobID:89904/> Contact person: Karin Rengefors, [karin.rengefors@biol.lu.se](mailto:karin.rengefors@biol.lu.se)

Karin Rengefors, PhD Professor in Limnology Aquatic Ecology, Department of Biology Lund University Ecology Building 22362 Lund, Sweden e-mail: [karin.rengefors@biol.lu.se](mailto:karin.rengefors@biol.lu.se) phone: + 46462228427

URL: <http://biology.lu.se/karin-rengefors> Lab website: <http://rengeforslab.org/> See our EMBO-EMBL Symposium 2016 on aquatic microeukaryotes!

<http://www.embo-embl-symposia.org/symposia/-2016/EES16-01/index.html>

Karin Rengefors  
<[karin.rengefors@biol.lu.se](mailto:karin.rengefors@biol.lu.se)>

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## MaxPlanckEvolBio HostMicrobiomeEvolution

Max-Planck-Institute for Evolutionary Biology, Ploen, Germany

2 PhD positions on the evolutionary genetics of host-microbiota interactions in mice and humans

The positions are available in the lab of John Baines as part of a new Collaborative Research Center, "Origin and Function of Metaorganisms", funded by the German Science Foundation (DFG):

<http://www.metaorganism-research.com> The first project will apply a "systems genetic" approach (QTL mapping, transcriptomics, metagenomics) to understanding the evolution of host-microbial homeostasis in the intestine using the house mouse system (for background see Wang et al. 2015, Nat Commun 6: 6440).

The second project will focus on fine-scale analysis of intestinal bacteria (cultivation, single-cell genomics and metagenomics) that display host genetic associations in mice and humans.

For more information about the Max-Planck Institute for Evolutionary Biology and ongoing projects in the Baines lab, see:

<http://www.evolbio.mpg.de/2169/en> <http://web.evolbio.mpg.de/evolgenomics/> The application deadline is February 29, 2016. For further details and instructions for the application procedure, please see:

<http://www.metaorganism-research.com/jobs/> John Baines

Institute for Experimental Medicine Christian-Albrechts-University of Kiel Arnold-Heller-Str. 3 24105 Kiel Germany & Max-Planck-Institute for Evolutionary Biology August-Thienemann-Str. 2 24306 Ploen Germany Tel: +49-431-597-1921, +49-4522-763-367 Fax: +49-4522-763-281 Email: [baines@evolbio.mpg.de](mailto:baines@evolbio.mpg.de) Web: <http://web.evolbio.mpg.de/evolgenomics/> "baines@evolbio.mpg.de" <[baines@evolbio.mpg.de](mailto:baines@evolbio.mpg.de)>

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## MPIO Seewiesen EvolutionCognition

### MASTER PROJECT/INTERNSHIP OPPORTUNITIES - PARROT COGNITION (TENERIFE)

Comparative Cognition Research Group, Max-Planck Institute for Ornithology, Tenerife, Spain

The Max-Planck Comparative Cognition Research Group, a part of collaboration between the Max-Planck Institute for Ornithology, Seewiesen, Germany, and the Loro Parque Fundación (LPF), Tenerife, Spain is currently accepting applications for Spring/Summer term 2016 as part of research projects on social cognition in parrots (social learning capacity and cooperation) and a comparative study on physical cognition and problem solving abilities of parrots. CCRG invites applications for master thesis projects in a dynamic, international research environment. Successful applicants can expect to gain a solid insight in the field of Animal Cognition/Experimental Psychology and gain experience with working on parrots. The research is carried out on captive parrots of the LPF, which holds the largest parrot collection and gene reserve in the world (ca. 350 subspecies) for conservation and research purposes.

Possible research topics:

The social learning project is to study the social learning capacity of young individuals of slowly maturing, long-lived and large-brained psittacid species, as well as revealing potential underlying social learning mechanisms, with particular focus on imitation ability. Parrots, as plastic vocal learners, good vocal imitators and flexible, innovative species that probably exhibit life-long learning, represent interesting study candidates for testing their ability to copy novel behaviour from others. The aim of the cooperation project is to study prosocial tendencies and perspective taking in a cooperative context in parrots of different social and mating systems. The physical cognition project focuses on flexibility and innovative problems solving skills and underlying cognitive mechanisms across different parrots species.

Logistics:

Internship start and end dates are flexible but preference will be given to students that can start in February/March 2016. The position requires a minimum of 3-4 months, but ideally 6 months, continuous commitment at the research station in Tenerife, Spain. The

position is not paid but free accommodation in a shared student apartment can be provided. It requires a contribution to the running costs (electricity, water and internet) of ca. 50 Euro per month. Successful applicants will be responsible for their own transportation expenses to and from the research centre (Puerto de la Cruz, Tenerife, Spain).

Important skills/qualifications:

Applicants should be registered at a European University and look for a Master project or for an internship that counts towards their degree. Previous research experience is advantageous. Successful candidates will have:

a strong interest in comparative cognition and ambition to pursue a scientific career high motivation and commitment to the project reliability and an ability to work independently confidence to interact with animals good verbal and writing English skills an ability to work in an organised and reliable manner and to manage a variable and demanding workload initiative to develop the project good team work attitude and social skills (shared accommodation between 3 students)

To apply:

Please send your CV and a cover letter reporting any relevant experience you have and motivation to participate in the project to Dr. Auguste von Bayern (avbayern@orn.mpg.de) or Dr. Anastasia Krasheninnikova (anastacia.k@web.de). Contact details of 2 referees may be requested.

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

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## OklahomaStateU GrassGenetics

Oklahoma State University, Stillwater, Oklahoma

Ph.D. or masters positions in the genetic regulation of tillering in grasses, combining phenotypic, genetic, and molecular approaches

Research focus: We are seeking highly motivated doctoral or masters students to conduct research on image analysis and genetics of branching in the grass *Setaria* (foxtail millet/green foxtail), as part of an NSF Plant Genome grant focused on tillering in panicoid grasses. The primary objective of this research is to identify components of the gene regulatory network controlling branching in *Setaria* and their responses to environmental stimuli such as shading; combining QTL mapping with expres-

sion QTL studies, mutant analysis, and image analysis. There is considerable flexibility for graduate projects within this broad theme, and results will be of broad interest to maize, sorghum, and other grass researchers.

Essential qualifications include masters degree (for PhD) or experience in plant biology, genetics and/or molecular biology, and writing skills. Desirable qualifications include experience in growing plants, molecular lab techniques including working with RNA, quantitative genetics or statistics, and programming.

Salary: Stipend will be \$21,504 per calendar year plus tuition and health benefits.

Application deadline: As soon as possible, although positions will remain open until filled.

Application materials: Please send a brief cover letter, resume, transcripts, GRE scores, and contact information for two references to [andrew.doust@okstate.edu](mailto:andrew.doust@okstate.edu) to be considered for these positions.

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

Phone: 405-744-9559 Email: [andrew.doust@okstate.edu](mailto:andrew.doust@okstate.edu)

Websites: [http://botany.okstate.edu/people\\_research/Doust/index.html](http://botany.okstate.edu/people_research/Doust/index.html) <http://tillering.okstate.edu/>  
<http://osubioret.okstate.edu/> "Doust, Andrew"  
 <[andrew.doust@okstate.edu](mailto:andrew.doust@okstate.edu)>

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### PortlandStateU REUinPlantGenomics

NSF Research Experience for Undergraduates (REU) in Plant Ecology and Genomics

We are looking for two enthusiastic students interested in enhancing their research skills and experience in plant ecology, genomics, and bioinformatics in the Cruzan lab at Portland State University in Portland, Oregon.

Successful applicants will become part of a research team working on dispersal and gene flow in upland prairie plants in Oregon and Washington under pressure from climate change. Dispersal is critical for colonization, gene flow, and range expansion, and it is one of the most important but least understood aspects of the ecology of plants. Our research utilizes genomic techniques to detect the effects of dispersal over different spatial scales. This is an integrative research program that includes field work, wet lab preparation of genomic DNA for

next-generation sequencing, bioinformatics processing of sequence data, and analysis of patterns of gene flow using GIS and landscape genetic methods. Students will be exposed to a wide range of methods and are expected to develop an independent research project within the scope of the larger research program. More information on our research is posted on our lab web site: <http://web.pdx.edu/~cruzan/index.html>. Students will be fully supported for 10 to 12 weeks during the summer of 2016. Funding is provided from an REU supplement to our National Science Foundation Macrosystems Biology grant. Housing will be provided on campus along with a daily allowance for food and a \$500 weekly stipend.

The start of the REU is negotiable with optimal start dates between May 1 and June 17. To apply please email us an updated copy of your CV (including GPA) and a short (one page) statement of your research interests and experience, as well as goals for your education and career. Students with experience in computer programming and/or bioinformatics are encouraged to apply.

Application deadline is 29 February 2016. Feel free to email us with questions.

Send complete applications to: Pam Thompson, Postdoctoral Research Associate: [thompson@pdx.edu](mailto:thompson@pdx.edu) Mitch Cruzan, Principle Investigator: [cruzan@pdx.edu](mailto:cruzan@pdx.edu)

Mitch Cruzan Professor of Biology Portland State University PO Box 751 Portland, OR 97207 USA Web: <http://web.pdx.edu/~cruzan/> Pamela G. Thompson Postdoctoral Researcher Portland State University Department of Biology, SRTC rm 246 Portland, OR 97201 503-725-9503

Pamela Thompson <[thompson@pdx.edu](mailto:thompson@pdx.edu)>

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### QueenMaryULondon BayesianPhylogenetics

PhD position available in Mario dos Reis lab, Queen Mary University of London, UK.

Integrating fossils and genomes to elucidate the evolutionary history of species through time

The genomes of organisms bear the footprint of their evolutionary history. By combining information from molecular sequences (genomes) with information from the fossil record, inferences about this evolutionary history can be obtained and placed in the right geological context. However, the fossil record is notoriously incom-



plete, and patterns of genome evolution vary substantially among species, providing important challenges to the study of ancient evolutionary events. Recent advances in Bayesian statistics allow probabilistic modelling of the uncertainties in fossils and genomic evolutionary rates, so that robust inferences about species divergence times, that integrate these sources of uncertainty, can now be made. The Bayesian method is now being used to study controversial topics such as the pattern of diversification of birds and mammals relative to the End-Cretaceous mass extinction, or the elucidation of the time of origin of animals over 540 million years ago in the pre-Cambrian. In this project the student will work in the application and/or development of Bayesian MCMC statistical methods to study species divergences through time. The project will include the collection of genomic and fossil data from online databases, and the use of computer software for analysis. Experience in the use of statistical packages (such as R) and computer programming would be an advantage. The project is suitable for students interested in genomics, palaeontology and Bayesian statistics. Students with backgrounds in the life sciences, earth sciences, physics, computing or maths are welcomed to apply.

Deadline: 31st of March 2016. Interviews are expected to take place at the end of April or beginning of May.

Eligibility: open to UK and European students.

Funding: The studentship will cover tuition fees and provide an annual tax-free maintenance allowance for 3 years at Research Councils UK rates (pounds 16,057 in 2015/16).

Reference: dos Reis et al. (2016) Bayesian molecular clock dating of species divergences in the genomics era. *Nature Reviews Genetics*, 17: 71-80.

More info and application form: [bit.ly/dosreislab-phd](http://bit.ly/dosreislab-phd)

Enquiries: [m.dosreisbarros@qmul.ac.uk](mailto:m.dosreisbarros@qmul.ac.uk).

Mario dos Reis

School of Biological and Chemical Sciences Queen Mary University of London London E1 4NS

[mariodosreis.wordpress.com](http://mariodosreis.wordpress.com)

[mariodosreis@gmail.com](mailto:mariodosreis@gmail.com)

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## RoyalBotanicGardens AlpinePlantEvolution

Harding Alpine Plant and Fungal Research Programme PhD Fellowships The Royal Botanic Gardens, Kew seeks applications from promising and enthusiastic graduated students to join Kew's science and conduct a PhD project focusing on the evolution and ecology of alpine plants and fungi. The fellowship will provide you with the opportunity to gain essential research skills to successfully complete a PhD project. At the end of the fellowship you will be a fully minted PhD, hence enabling you to secure postdoctoral employment, and establish yourself as future researcher in science.

Hours of work : Full time Number of posts : 2 Contract Type : Fixed Term, 3 years Contract start date : 01/05/2016 (negotiable) Salary : GBP 16,057 Location : Kew Gardens, Richmond, United Kingdom Other Location : Queen Mary University of London / Reading University Closing Date : 21/03/2016

Two research fellowships are available, one in each of the following research projects:

1. Integrated monography of the genus *Saxifraga* L. as a window on the evolution of the European Alpine flora This project aims to use the species-rich, predominantly alpine genus *Saxifraga* (ca. 440 spp.) as a model to elucidate the eco-evolutionary assembly of mountain floras, with emphasis on the European Alps. We will conduct an extensive field campaign covering all parts of the Alps in order to comprehensively sample the diversity of European Alpine *Saxifraga*. Together with RBG Kew's outstanding collections and material obtained from collaborators, those samples will allow us to generate a densely sampled species-level phylogeny of the genus using state-of-the-art phylogenomics. This phylogenetic tree will serve as an essential framework for understanding the geographic and ecological origins of alpine *Saxifraga* diversity, in Europe and globally. We will gather complementary datasets on the geographic occurrence and traits of *Saxifraga* species, and integrate all three sources of information using niche modelling and phylogenetic, comparative approaches. This will allow us to test specific hypotheses regarding the evolution of alpine *Saxifraga* diversity, addressing the frequency of fundamental processes, and the role of traits in causing or inhibiting these processes. We will also use our data to gauge the future of *Saxifraga* diversity



worldwide and in the Alps, by assessing Global Change-related threats and quantifying to what extent species diversity, functional diversity and evolutionary heritage are at risk. Finally, we will also use the newly produced phylogenetic evidence to re-evaluate the higher level systematics of the genus. Taken together, those studies will form a modern integrated monographic account of *Saxifraga*. Contact person: Wolf Eiserhardt, W.Eiserhardt“at”kew.org

2. Evolution of Asteraceae in the European Alps: This project is aimed at better understanding the role of polyploidy and chromosomal rearrangements as evolutionary drivers in alpine ecosystems. We seek delivering critical knowledge on plant speciation in high mountain ecosystems, bringing robust evidence and new insights on the pivotal role that genomic mechanisms play in enabling adaptation to environmental stress. Taking the Asteraceae as a model system, the project research is summarised in three main work packages: (i) Assembly of a new phylogenetic backbone of alpine Asteraceae flora using NGS and complemented with loci-based phylogenies through a supertree approach. Chromosome and cytogenetic data, ecological variables and phenotypic traits will be gathered and integrated with the phylogenomic approach to enable detection of key factors and interactions involved in diversification processes in the Alps. (ii) The spatial distribution of different ploidy levels will be assessed in selected genera through a population-based approach. Those populations where multiple cytotypes coexist will be invaluable as they will provide the opportunity to model and predict how climate change will affect community assemblages, identifying which cytotypes will be favoured and those that will be at higher risk in the face of global warming. (iii) Pollinator communities and flower visit frequency will be assessed in relation to variation in ploidy levels and accounting for altitude. Pollinator monitoring will be carried out using motion detection devices. This will provide insights into whether different cytotypes are characterized by different pollinators and its potential link to shifts nectar chemistry. Contact person: Jaume Pellicer, J.Pellicer“at”kew.org Further information, including instructions on how to apply, is available from <https://careers.kew.org/-vacancy/harding-alpine-plant-and-fungal-research-programme-phd-fellowships-254393.html> Jurriaan de Vos <J.deVos@kew.org>

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## Simon Fraser U Social Evolutionary Genetics

MSc or PhD positions in social-evolutionary genetics at Simon Fraser University

One or more graduate student positions are now available for study of the roles of intragenomic conflict in human cognition and behavior. Research will focus on the genetics and epigenetics of human brain-expressed genomically-imprinted genes, to ascertain their roles in mediating variation in human psychological phenotypes.

Imprinted genes are expressed from either the copy from the mother, or the copy from the father, in every individual. These genes are subject to within-genome conflict between the mother's and father's copies, which influences brain development, psychological and psychiatric variation, and behavior. However, the roles of brain-expressed imprinted genes in normal human populations are virtually unstudied.

See <http://www.sfu.ca/biology/faculty/crespi/publicationsrr.html> (especially paper #s 115, 117, 135, 144, 155, 169, 173, and/or 177) for examples of representative publications in this general area from the Crespi lab.

The successful candidate will have interests and/or background in evolutionary biology, genetics, and psychology. They will join the Crespi lab (<http://www.sfu.ca/biology/faculty/crespi/>), the Evolutionary Biology group ([www.sfu.ca/~fabstar/](http://www.sfu.ca/~fabstar/)) and the Human Evolutionary Studies Program ([hesp.irmacs.sfu.ca/](http://hesp.irmacs.sfu.ca/)) at Simon Fraser University, in beautiful Vancouver, Canada.

Application information:

Funding is available for Canadian students, though preference may be given to students with sources of external support such as NSERC Postgraduate Scholarships. International students are also very welcome to apply, but may be considered subject to access to funding from their home country. Formal application information is available at [http://www.sfu.ca/dean-gradstudies/future-academicprograms/faculty\\_of\\_science/biology.html](http://www.sfu.ca/dean-gradstudies/future-academicprograms/faculty_of_science/biology.html) If you wish to apply, please send a Curriculum Vitae, a copy of your academic transcripts (unofficial is acceptable), contact names and emails for two letters of reference, and a one-paragraph cover letter describing

your background and interests, to:

crespi@sfu.ca

Dr. Bernard Crespi, FRSC Professor, Department of Biological Sciences 8888 University Drive Burnaby, British Columbia, Canada V5A 1S6

Review of applications will begin March 28, 2016.

Informal inquiries are also welcome.

Possible start dates would include September 2016, January 2017, or May 2017.

Bernard Crespi <crespi@sfu.ca>

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## Southampton UK Empathy Cooperation Evolution

Modelling the effect of empathy and emotion on the evolution of strategies in two-player games

PhD position at the University of Southampton, UK

\*Deadline: February 18 2016\*

Project Description

This project involves mathematical modelling of experimental psychology data in order to explore the role of emotional states in the development of cooperation strategies in two-player social dilemma games. The aim is to understand better the role of empathy and emotional states in the evolution of cooperation in social groups.

A social dilemma arises when an individual's selfish interest diverges from that of the social group of which they are a part and on which they rely. A key question is why people seem to have evolved to cooperate in such situations when it appears to be to their individual disadvantage. A social dilemma game, such as the famous Prisoner's Dilemma, is a mathematical construct in economic game theory that aims to model social dilemmas. Social dilemma games can also literally be played as games, for example in psychology experiments that aim to discover how people really behave when presented with these stylised dilemmas. We aim to shed light on why people are typically more cooperative when playing such games than would be expected on purely rational grounds by investigating how the communication of emotional states between players might influence their behaviour. The PhD student on this project will analyse data from social dilemma game experiments

where players receive facial feedback that gives an impression of their opponent's emotional state. There may also be the opportunity to help run additional experiments. The student will further use the data and insight from the experiments to construct mathematical models of the evolution of player strategies in response to emotional feedback.

Applicants should have a first class degree in mathematics or a related discipline with a large quantitative component such as physics or statistics. An interest in psychology is essential and previous study of it will be an advantage. The project will be co-supervised between the Departments of Mathematical Sciences and Psychology and so applicants must have strong interest in and motivation for interdisciplinary research. The ability to communicate effectively across discipline boundaries is essential.

Funding Notes

Prospective candidates are required to apply for this studentship by applying for the MPhil/PhD in Mathematics using the University of Southampton on-line application system. A copy of the on-line application form and guidance notes can be found at the following website: <http://www.southampton.ac.uk/courses/how-to-apply/postgraduate-applications.page> The studentship will cover tuition fees and stipend for UK/EU applicants. Partial funding may be available for overseas applicants.

Links to supervisor webpages:

<http://www.southampton.ac.uk/maths/about/-staff/rbh2c14.page> <http://www.southampton.ac.uk/psychology/about/staff/he4g14.page>

Further information

<https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=690> R.B.Hoyle@soton.ac.uk

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## U Akron Ohio Wetland Evolution

MS STUDENT POSITION with TA support at the University of Akron for student to study ecology/evolution of organisms in temporary wetlands with Dr. Stephen Weeks and Dr. Randy Mitchell. TA accompanied with \$14,550 nine month stipend and full tuition remission. Applications and further information are available at <http://www.uakron.edu/biology/academics/ms-program/index.dot> The University of Akron is a state university located in the heart of Akron, Ohio, next

to the scenic Cuyahoga Valley National Park (CVNP). The Biology Department emphasizes collaborative and integrative research, including a PhD program in Integrated Bioscience. Facilities include a live animal research center, 400 acre field station, and greenhouse. We have excellent relations with the CVNP and local metroparks, which provide access to over 40,000 acres of potential field sites within 40 miles. Our graduate students have been successful in finding employment in their specialties, including work as professors, consultants, field technicians, government agents (e.g., EPA, department of natural resources), park naturalists, and many others.

The Department has a strong program in Ecology and Evolutionary Biology. Areas of interest for graduate research include: life history evolution, mating systems, aquatic ecology, pollination biology, wetland ecology, conservation biology, physiological ecology, isotope ecology, behavioral evolution, spider biology, and evolutionary biomechanics.

Akron is a great place to live, with a high quality of life. There are abundant natural amenities, including nearby metroparks and the CVNP, and ready access to many diverse cultural events in Akron and nearby Cleveland, including sports, several symphony orchestras, excellent museums, and the Blossom outdoor auditorium.

For more information, contact Steve Weeks (scw@uakron.edu) and Randy Mitchell (rjm2@uakron.edu)

“Mitchell,Randall J” <rjm2@uakron.edu>

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## UAuckland VineyardStatistics

I do understand that the position does not seem to have a lot of evolutionary relevance on the surface, but the shape of the data and the design make it advantageous to get a student who has skills in evolutionary biology, and is interested in working with molecular data from a wide variety of organisms. Since our project will sample over six years, three times each year, and we are also investigating microorganisms, there is a distinct evolutionary/developmental note in the project.

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PhD Scholarship in Modelling and Inference of a resilient vineyard ecology Applications are invited for a three year (full-time) PhD scholarship at the University of Auckland within an interdisciplinary project across the

Department of Statistics, School of Biological Sciences, the School of Chemical Sciences, and Plant and Food Crown Research Institute. The scholarship is funded by an MBIE Partnership programme with the NZ Winegrowers.

**Project Summary:** In our 7-year project we will investigate the ecosystem of several vineyards across New Zealand to study the impact of organic management techniques on longevity and sustainability of NZ vineyards. Data generated within the project will come from several sources, including microbiology and chemistry over multiple vintages. To get control of the data and identify interesting, evolutionary and functional, relationships within organisms, between organisms and chemistry, and the impact of vineyard management on these relationships, and ultimately the health and productivity of the vineyard, many challenges need to be addressed: How to reliably explore the data for causal relationships? How to model the interactions between organisms and environment? What statistical method best accommodates the complexity of this experiment?

We are looking for a motivated PhD student interested in undertaking research into data-driven model and method development to answer these questions. Ideally, the student has fundamental knowledge in multivariate data analysis, and a basic knowledge of statistical computing and database management. The student will be part of an interdisciplinary group of statisticians, biologists, and chemists, so the ability and willingness to communicate results across disciplines will be essential.

**Funding:** The scholarship includes a tax-free stipend of NZ\$25,000 per year for three years.

**How to Apply:** Applicants should have an Honours in Statistics, Bioinformatics (or equivalent), strong research potential, and able to commence by June 2016. Applications, including a curriculum vitae, academic transcripts, covering letter and contact details of two referees should be sent to Dr Steffen Klaere, by email to s.klaere@auckland.ac.nz. All applications received by 29 Feb 2016 will be considered.

Steffen Klaere <s.klaere@auckland.ac.nz>

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## UBayreuth Germany SpermMicrobeInteractions

\*\*\*DISENTANGLING HOST-PARASITE AND MALE-FEMALE COEVOLUTIONARY EFFECTS ON HOST

FITNESS\*\*\*

I am looking for an ambitious PhD-candidate interested in 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=en>) 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](mailto:oliver.otti@uni-bayreuth.de)

web: [https://www.bayceer.uni-bayreuth.de/toek1/en/mitarbeiter/mitarbeiter\\_detail.php?id\\_obj=106154](https://www.bayceer.uni-bayreuth.de/toek1/en/mitarbeiter/mitarbeiter_detail.php?id_obj=106154)

Oliver Otti <[oliver.otti@uni-bayreuth.de](mailto:oliver.otti@uni-bayreuth.de)>

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## UDuisburgEssen DNAMetabarcoding

We are one of the youngest universities in Germany and think in terms of possibilities, not limitations. In the heart of the Ruhrregion, we develop ideas of the future at our 11 faculties. We are strong in research and teaching, live diversity, support potential and are highly committed to an educational equality that has earned this name. The University of Duisburg-Essen (Campus Essen) Centre for Water and Environmental Research (ZWU) Aquatic Ecosystem Research Group (AG Leese) offers

1 PhD position, Doktorandenstelle (f/m) (Part-time 55%; salary equivalent TV-L 13) in Genetic Monitoring / Metabarcoding (BMBF German Barcode of Life 2 subproject)

The group of Prof. Florian Leese is interested in developing new molecular approaches to assess the ecological status of aquatic ecosystems. Specifically, we develop and apply DNA metabarcoding to monitor changes in stream communities under environmental stressors. Furthermore, we utilize genomewide markers and perform transcriptional profiling to understand population and organismal responses to multiple stressors. As part of a recently granted subproject within the large collaborative German Barcode of Life Project (GBOL2, funded by the Federal Ministry of Education and Research, BMBF), we want to bring DNA metabarcoding of freshwater invertebrates to the application stage. In cooperation with our collaborators at the Zoological Research Museum Alexander Koenig (Bonn, Germany), the candidate will conduct collect samples, perform experiments, generate and analyse next-generation sequencing data on whole communities (amplicon sequencing). Further reading: Elbrecht & Leese, PLoS ONE 2015; Macher et al., Ecological Indicators, 2016.

The successful candidate (f/m) will hold a Master in Biology, Chemistry or Bioinformatics and has good experience in molecular lab work. Furthermore, he/she has experience and strong interest in a programming or scripting language (e.g. R, C, Python). Candidates



will benefit from the international and interdisciplinary research environment at the research group, the GBOL2 project and the ZWU. Excellent high-throughput genomics and bioinformatics equipment are available in the newly equipped labs.

The position will start as soon as possible initially for 2,5 years. Deadline: 29. February 2016 Please send applications as a single pdf file with reference code 42-16 to miriam.schmidt@uni-due.de. For questions please contact florian.leese@uni-due.de.

The University Duisburg-Essen aims at promoting the diversity of its members. Applications from disabled or equivalent according to §2 Abs. 3 SGB IX are encouraged. The University Duisburg-Essen has been awarded for its effort to promote gender equality with the "Total-EQuality-Award". It aims at increasing the share of women in the scientific personnel and therefore explicitly encourages women to apply. Women will be preferentially considered when equally qualified according to the state equality law.

Vasco Elbrecht <luckylion07@googlemail.com>

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## UEastAnglia PopulationGenomics

What: FULLY FUNDED PHD STUDENTSHIP - Population demography and thermal adaptation in a model pest insect, supervised by Dr Lewis Spurgin and Professor Matt Gage

Where: University of East Anglia, Norwich, UK

Details:

Whats the project and why is it important?

Climate change is causing substantial shifts in the range and abundance of crop pests and pathogens, with potentially disastrous consequences for food security. Studying adaptation to climate in an evolutionary framework is a powerful way for identifying how, when and where pests will respond to climate change. However, our understanding of how natural selection enables individuals and populations to adapt to climate change, and the specific traits or genes responsible, is limited.

This PhD studentship will use experimental evolution and novel genomic approaches to understand how insect pests adapt to challenging environments. Specifically, we will use ongoing and new experiments of the pest beetle *Tribolium castaneum* to test how changes in demography (e.g. population size and migration) affect

adaptation to changing temperatures. There will also be an opportunity to use genome sequencing to identify the genetic basis of adaptation to climate. We expect the project to significantly advance our understanding of how populations, individuals and genomes adapt to novel climates, and identify the impacts of demography and adaptation on natural and pest populations. The project therefore addresses both a fundamental question in biology and a key societal challenge.

What other training is involved?

The student will receive training in ecology, evolutionary genetics and bioinformatics. UEA has an excellent training service for PhD students, equipping them for a wide range of careers within or outside of academia. Just round the corner, The Genome Analysis Centre has an excellent training programme for genomics and bioinformatics. The student will also be encouraged to attend external training courses, and national and international conferences.

Why work with us?

1. Great supervision. The student will be supervised by Dr Lewis Spurgin and Prof Matt Gage. Together, we have broad expertise in evolutionary biology, population genetics, genomics, ecology, animal behaviour and molecular biology. We aim to provide the right balance of being supportive and inclusive, while also giving you the freedom to develop your own ideas.

2. Great Research Environment. Norwich is ranked 4th in the UK for the number of highly cited scientists, after Cambridge, Oxford and London. Within UEA, the School of Biological Sciences at UEA is a world-leading research department with a dynamic community of PhD students and researchers.

3. Great city. In a recent survey in the Guardian, Norwich was voted the 'happiest' place to work in the UK. The stunning Norfolk Broads and North Norfolk Coast are also right on your doorstep.

About you

Applicants should: - Be creative - Be passionate about research, and about using research to address big societal challenges - Have excellent analytical skills - Be willing to learn how to code (e.g. in R or python) - Be willing to actively contribute to the research group and wider research community

Apply

Interested applicants can get in touch with me (l.spurgin[at]uea.ac.uk) or Matt (m.gage[at]uea.ac.uk). You can apply online, and view funding details, via the UEA website:



[https://www.uea.ac.uk/study/-/population-demography-and-thermal-adaptation-in-a-model-pest-insect-spurgin\\_u16sci](https://www.uea.ac.uk/study/-/population-demography-and-thermal-adaptation-in-a-model-pest-insect-spurgin_u16sci) The application deadline is 15th April.

lewisspurgin@gmail.com

## UESSEX 4 GENOMICS EVOLUTION

4 PhD studentships in Genomics, Epigenetics or Evolution

A newly established Genomics section of the School of Biological Sciences (University of Essex) is offering 4 PhD studentships, starting October 2016. The section (<http://genomics.essex.ac.uk/>) is led by Prof. Leonard C. Schalkwyk (Psychiatric and Environmental Epigenomics) and includes groups of Prof. Meena Kumari (Biological and Social Epidemiology), Dr. Antonio Marco (Evolutionary Genetics), Dr. Vladimir B. Teif (Biophysics of Chromatin and Computational Epigenetics), Dr. Jordi Paps (Evolutionary Genomics), Dr. Radu N. Zabet (Computational and Theoretical Models of Gene Regulation), and Dr. Pradeepa M. Madapura (Chromatin and Gene-regulation).

The Genomics section was created as a result of a strategic initiative to strengthen the area of genomics in the University of Essex by hiring leading experts in genome biology. Related research areas of the School of Biological Sciences include Cancer Biology, Immunology, Protein Biophysics, Environmental Sciences, Plant Biology, etc, and can be found on the web site <https://www.essex.ac.uk/bs/>. The candidate will benefit from this rich and fresh intellectual environment and the novel infrastructures. On top of the state-of-the art facilities available in the School, the Genomics section also has access to a new large computer cluster, a MiSeq DNA sequencer, as well as other major molecular biology equipment.

Applicants should have, or expect to receive, a first or upper second class degree or equivalent in a relevant subject. The research topics for the four PhD studentships are the following:

- o Deciphering the function of histone modifications and noncoding transcription at distal cis-regulatory elements with Dr. Pradeepa Madapura (<http://www.essex.ac.uk/bs/staff/profile.aspx?ID=4967>; [pmadap@essex.ac.uk](mailto:pmadap@essex.ac.uk)).

- o Using comparative genomics to study different as-

pects of the evolution of the Animal Kingdom with Dr Jordi Paps (<http://www.essex.ac.uk/bs/staff/profile.aspx?ID=4561>; [jpapsm@essex.ac.uk](mailto:jpapsm@essex.ac.uk)).

- o Modelling of epigenetic regulation in chromatin using approaches of computational biology, biophysics and next generation sequencing with Dr. Vladimir Teif (<https://www.essex.ac.uk/bs/staff/profile.aspx?ID=4511>; [vteif@essex.ac.uk](mailto:vteif@essex.ac.uk)).

- o Building mechanistic models of transcription factor activity and transcription regulation in eukaryotic systems with Dr Radu Zabet (<https://www.essex.ac.uk/bs/staff/profile.aspx?ID=4580>).

Applications should be submitted electronically by Tuesday 29 March 2016, more details can be found in the following link: <http://www.essex.ac.uk/bs/pg-studentships/default.aspx>. The target start date for this 3-year, fully-funded PhD studentship is 6th October 2016. This scholarship will be to the value of £12,500 per annum plus UK tuition fees. Additional questions and queries about the studentship and projects can be addressed to the respective supervisors.

Entry requirements and application procedures Applications should be submitted electronically by Tuesday 29 March 2016, see here for details <https://www.essex.ac.uk/pgapply/enter.aspx>. After filling your personal and academic details, select "Apply for a post-graduate research study", under Section 1 select "Biological Sciences", "Full time", "PhD in Biological Sciences" min 36 months "Colchester campus", "6th October 2016" under date commencing, and the research topics (see above) in the "Proposed research topic or area of research" box. For general information about the School of Biological Sciences at the University please visit our webpages <http://www.essex.ac.uk/bs/>. "Colchester campus", "6th October 2016" under date commencing, and the research topics (see above) in the "Proposed research topic or area of research" box. For general information about the School of Biological Sciences at the University please visit our webpages <http://www.essex.ac.uk/bs/>. The University of Essex For general information about the School of Biological Sciences at the University please visit our webpages <http://www.essex.ac.uk/bs/>. In the recent Research Excellence Framework 77% of research at the University of Essex research is 'world leading' or 'internationally excellent' (REF

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## UEssex EvolutionaryGenomics

PhD scholarship: Unravelling the origins and evolution of the Animal Kingdom using genomics - October 2016

The Animal Kingdom comprises some of the major transitions in the evolution of life, embracing a spectacular diversity product of hundreds of millions of years. Intriguing questions on its beginnings and major transitions are still a mystery: which genomic events are related to the advent multicellular animals from single cell organisms? What are the causes of the major transitions such as the emergence from animals with radial symmetry (as sponges or jellyfish) of creatures with a bilateral architecture like ourselves? How the content of metazoan genomes is related to the animals' main body plans and adaptations such as parasitism, sessility, or body size reduction? The revolution introduced by Next Generation Sequencing provides a timely chance to approach those questions using comparative genomics.

The new Genomics section of the School of Biological Sciences (University of Essex) is offering 4 PhD studentships, starting October 2016. The section (<http://genomics.essex.ac.uk/>) is led by Prof. Leonard C. Schalkwyk (Psychiatric and Environmental Epigenomics) and includes the labs of Prof. Meena Kumari (Biological and Social Epidemiology), Dr. Antonio Marco (Evolutionary Genetics), Dr. Vladimir Teif (Chromatin and Epigenetics), Dr. Radu N. Zabet (Computational and Theoretical Models of Gene Regulation), Dr. Pradeepa M. Madapura (Chromatin and Gene-regulation), and Dr. Jordi Paps (Evolutionary Genomics). This section is the result of an initiative to strengthen the area of genomics in the School by hiring young and successful experts on different areas of genome biology. On top of the state-of-the art facilities available in the School, the section also has access to new labs, a cluster of servers, a MiSeq machine, as well as other major molecular biology equipment. The candidate will benefit from this rich and fresh intellectual environment and the novel infrastructures.

The PhD student will join the group of Dr Jordi Paps to investigate different aspects of the evolution of the Animal Kingdom using genomic data (<http://www.essex.ac.uk/bs/staff/profile.aspx?ID=3D3D4561>). The applicants should show keen interest in evolutionary biology, genomics, bioinformatics, and animal

diversity; previous knowledge of Unix/Linux systems and programming languages is desired, but not required. The candidate should have a good understanding of the research field and demonstrate the ability to think independently.

Entry requirements and application procedures Applications should be submitted electronically by Tuesday 29 March 2016 see here for details <https://www.essex.ac.uk/pgapply/enter.aspx> Please ensure that for this scholarship a project proposal is submitted. Additional questions and queries about the studentship can be addressed to Dr Jordi Paps ([jpapsm@essex.ac.uk](mailto:jpapsm@essex.ac.uk)). The target start date for this 3-year, fully-funded PhD studentship is 6th October 2016. This scholarship will be to the value of £12,500 per annum plus UK tuition fees.

The University of Essex For general information about the School of Biological Sciences at the University please visit our webpages <http://www.essex.ac.uk/bs/>. In the recent Research Excellence Framework 77% of research at the University of Essex research is 'world leading' or 'internationally excellent' (REF 2014). We offer world-class supervision and training opportunities and our research students work at the heart of an internationally-acknowledged and well-connected research community. In the 2013 Postgraduate Research Experience Survey, 84% of respondents said that they were satisfied with the quality of their research degree. At Essex we win awards for our pioneering student support schemes. We are the most recent winners of the prestigious Times Higher Education award for Outstanding Support for Students. Essex is a genuine global community. With more than 130 countries represented within our student body, and 40% of our students from overseas, we are one of the most internationally-diverse universities in the UK.

[jordipaps@gmail.com](mailto:jordipaps@gmail.com)

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## UGroningen *Drosophila suzukii*

3 PhD positions Biological control of *Drosophila suzukii*, a new invasive pest species.

Project description A new invasive pest species, *Drosophila suzukii* or Spotted Wing *Drosophila* (SWD), has invaded Europe and already caused millions of euros of damage in the European fruit industry. There is an urgent need to develop new strategies to control the SWD in the Netherlands, as the current practices

of control with chemical pesticides are neither effective nor sustainable. We aim to develop an integrated pest management strategy of combined biocontrol approaches. We still know relatively little about the basic biology of this new pest species in the context of the temperate climate in the Netherlands. Therefore, we will 1) investigate the factors that control population growth, reproductive success and survival of SWD in the Netherlands. With this knowledge, we will develop an integrated pest management strategy to 2) protect fruit crops from SWD and 3) to biologically control SWD populations.

Three PhD students will be appointed, each working on a subset of the aspects of this project, which are interrelated and complementing each other. These studies will be performed and supervised in a consortium of the University of Groningen, Wageningen University, WUR-PPO-Fruit and Koppert Biological Systems.

PhD project 1: Fundamentals of SWD biology in the Netherlands (RUG & WUR) We need to increase our fundamental knowledge of the factors that control population growth, reproductive success and survival of SWD in the Netherlands. This includes the population genetic structure, seasonal periods of activity, mortality factors and population dynamics. We will monitor the infestation dynamics of SWD in the Netherlands, and identify those factors that control pest outbreaks, using a combination of field observations, field and laboratory experiments and population genetic techniques.

PhD project 2: Crop protection strategies: a “push-pull” approach (WUR) To protect the fruit crops from SWD, we will develop an integrated set of tools for pest management. In this PhD project, we will develop pheromone lure traps for monitoring and controlling SWD density, and powerful repellents to avoid oviposition by SWD in fruit crops. We will assess the responses of SWD to chemicals that can be developed for lure traps or as oviposition deterrents, using a combination of behavioural and sensory assays in the laboratory, and test these chemicals in field trials.

PhD project 3: Biological control strategies: selective breeding of natural enemies (RUG) To biologically control SWD populations, we will select a potent natural enemy (e.g. predators, parasitoids and/or micro-organisms) that can curtail the population growth of SWD over the growing season. The potential of several natural enemies as biological control agents will be investigated in laboratory and field experiments, followed by a “selective breeding” approach to increase the virulence of the most promising natural enemies.

Research environment Within the project, the 3 PhD candidates will be closely collaborating with each other,

and with the academic and private partners in the consortium. Project 1 will be partially based in Groningen and partially in Wageningen (ca ~4 months/year), project 2 will be fully based in Wageningen, and project 3 will be fully based in Groningen.

The PhD projects are embedded in the research teams of Prof. Marcel Dicke (Laboratory of Entomology, Wageningen University), Dr Bart Pannebakker (Laboratory of Genetics, Wageningen University), Prof. Bregje Wertheim and Prof. Leo Beukeboom (Groningen Institute for Evolutionary Life Sciences, University of Groningen). Our teams consist of ecologists, geneticists, entomologists, molecular biologists and evolutionary biologists. The research will be done in close collaboration with the biological control company Koppert Biological Systems and with the Applied Plant Research Institute WUR-PPO-Fruit.

Qualifications The successful candidate will have an MSc degree in Biology or Plant Sciences with a specialization in Ecology, Evolution, Entomology or similar, with experience in insect ecology and behavioural studies on insects. The candidate will be open and communicative, proficient in the English language and have good statistical skills. We are looking for highly motivated candidates who can work in a multidisciplinary team in a collaborative spirit. Within the 3 projects, PhD students are encouraged to supervise MSc thesis students when such opportunities arise.

Specific requirements: Project 1: A field / insect evolutionary ecologist with experience and affinity with molecular techniques and population genetics. A driver's license and strong interpersonal skills are required for conducting the research at commercial fruit farms. During the field seasons (June - September) the candidate will be based at Wageningen University, and in the

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## UKentucky Lexington Insects

PhD Assistantship in Insect Overwintering Biology Department of Entomology University of Kentucky, Lexington, KY

Contact: Nicholas Teets Assistant Professor Email: n.teets@uky.edu Phone: (859)-257-7459 Lab website: [www.teetslab.weebly.com](http://www.teetslab.weebly.com) Description: The Insect Stress Biology Lab at University of Kentucky is seeking a highly motivated individual for a PhD in insect evolutionary physiology and functional genomics. The successful applicant will conduct research on the cell and molecular adaptations that drive the evolution of cold tolerance insects. We are particularly interested in the mechanism of rapid phenotypic plasticity at low temperature. Research is conducted on both model insects like *Drosophila melanogaster*, and non-model stress-adapted species like Antarctic arthropods. For more information on the Insect Stress Biology Lab, visit the lab website ([www.teetslab.weebly.com](http://www.teetslab.weebly.com)).

Department: The Department of Entomology at University of Kentucky offers excellent graduate training in diverse areas of entomology. The Entomology graduate program is ranked in the top 10 nationally, and it is consistently rated as one of the most productive programs at the University of Kentucky, measured by the total number of student publications and presentations. Students from our department go on to have successful careers in a variety of sectors, including academia, industry, government science, and extension, to name a few.

Qualifications: Qualified candidates should possess at least a bachelor's degree in entomology, biology, or a related field. Preference will be given to students with previous research experience, either through completion of a Master's degree or undergraduate research. Desired qualities include the ability to work well in a team, excellent written and oral communication skills, and attention to detail. Information on graduate admissions at University of Kentucky can be found at: [www.research.uky.edu/gs/prospectivestudents/admission.html](http://www.research.uky.edu/gs/prospectivestudents/admission.html) Start Date: The successful applicant will ideally start either summer or fall, 2016.

Application Procedures: Interested applicants should submit 1) a CV (including GPA and GRE scores), 2) a cover letter detailing research experience, interests, and career goals, and 3) the name and contact information for three professional references to n.teets@uky.edu. Screening will begin immediately and continue until the position is filled.

"Teets, Nicholas M" <n.teets@uky.edu>

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## ULausanne 2 FungalGenomicsBioinformatics

2 PhD student positions - Linking the Genomics of Symbiotic Fungi to the Growth of Globally Important Plants (Uni. Lausanne, Switzerland) 2 PhD student positions are available in the Sanders' group to study the relationship between the genotype of symbiotic mycorrhizal fungi and the growth of cassava. Cassava feeds almost one billion people in the world. Our research in the laboratory, and in the field, shows that genetic variation in mycorrhizal fungi is associated with large differences in cassava growth. We will study this in more detail to find out which aspects of genetic variation in these fungi causes high growth rates in cassava. The two PhD student positions will involve genomics techniques and advanced bioinformatics to understand genetic variation in the genomes of these fungi. Secondly, this information will be coupled with field experiments conducted in Colombia where genomic and transcriptomic data from both the plant and the fungus will be put together.

It is intended that the results of this project will lead to real practical applications in the future to increase production of food in areas of the world where starvation is a major problem.

Candidates must be highly motivated and have knowledge in at least one of the following fields: molecular biology; quantitative genetics; bioinformatics The two successful candidates will not do the same project but should be complimentary to each other.

More information about our work can be found at <http://people.unil.ch/iansanders/> The project is a collaboration between the University of Lausanne, Dr Marco Pagni at the Vital-IT center of the SIB Swiss Institute of Bioinformatics and Prof. Alia Rodriguez at the National University of Colombia.

The PhD positions are each for a three year period and are funded by the Swiss National Science Foundation. Salary follows the regulations of the SNSF. Our PhD program requires that applicants already have a masters degree.

To apply send a CV and motivation letter in English by email to [ian.sanders@unil.ch](mailto:ian.sanders@unil.ch) by not later than 10th March 2016.

Prof. Ian R. Sanders Dept. of Ecology & Evolution University of Lausanne Biophore Building



1015 Lausanne Switzerland Tel (direct): +41 21 692 4261 Tel (Secretary): +41 21 692 4260 Fax: +41 21 692 4265 Email: [ian.sanders@unil.ch](mailto:ian.sanders@unil.ch) [http://www.unil.ch/dee/page7238\\_en.html](http://www.unil.ch/dee/page7238_en.html) \*\*See my new website\*\* <http://people.unil.ch/iansanders/> Ian Sanders <Ian.Sanders@unil.ch>

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## ULincoln UK CanineGenetics

Fully funded PhD studentship in canine genetics: Linking phenotypes with genotypes for canine chemosensory perception

School of Life Sciences, University of Lincoln, UK

We are seeking to recruit a Science graduate with MSc or a good BSc degree (or equivalent) for a project on genetics of canine chemosensory perception, starting in October 2016. Experience in molecular genetics, bioinformatics and/or behavioural research methods will be seen as an advantage. This is a fully-funded position with a stipend of £14,124 per annum for three years for both home and international students. The project will be supervised by a team of researchers with complementary expertise in evolutionary genetics (Malgorzata Pilot, primary supervisor), veterinary behavioural medicine (Daniel Mills) and molecular neurobiology (Humberto Gutierrez).

This project will address a fundamental question in chemosensory system evolution concerning the trade-off between olfaction (sense of smell) and vomeronasal sensing (detection of emotionally salient chemosignals), and at the same time contribute to improving efficiency of selection of dogs for detection work (e.g. explosives, drugs). Olfactory receptors (OR) and vomeronasal receptors (V1R) provide systems to detect molecules of odorants and chemicals that mediate pheromone perception, respectively. There is growing evidence on functional and evolutionary interactions between these two systems, but this has not been assessed yet at an intra-specific level. The aim of this PhD project is to compare OR and V1R repertoires and chemosensory perception abilities in different groups of dogs, including breeds currently used for scent detection and breeds considered as poor sniffers, and in dogs' wild ancestors, grey wolves. The project will involve the analysis of the complete set of OR and V1R genes using NGS methods, behavioural experiments to test odour and pheromone perception performance, and the analysis of genotype-phenotype interactions.

The student will be supervised by an interdisciplinary team with complementary expertise in evolutionary genetics and genomics, molecular neurobiology, neuronal cell signalling, olfaction and pheromone detection, veterinary behavioural medicine, and behaviour of domestic and wild canids. Therefore, the student will have an opportunity to obtain a broad range of research skills, and develop a unique interdisciplinary research profile. The student will be also given opportunities to attend external courses and workshops, and international conferences. The School of Life Sciences provides a great research environment and has a large international community of postgraduate students.

To apply, send a CV and cover letter to Malgorzata Pilot ([mpilot@lincoln.ac.uk](mailto:mpilot@lincoln.ac.uk)) by 17 April 2016, 11 pm of UK time. You may also contact Malgorzata Pilot for informal enquiries. Shortlisted applicants will be invited for interview.

Malgorzata Pilot School of Life Sciences University of Lincoln Joseph Banks Laboratories Lincoln, LN6 7DL United Kingdom [mpilot@lincoln.ac.uk](mailto:mpilot@lincoln.ac.uk)

Malgorzata Pilot <[MPilot@lincoln.ac.uk](mailto:MPilot@lincoln.ac.uk)>

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## ULincoln YeastPopGenomics

YeastPopulationGenomics

Next generation analyses using next-generation DNA sequencing: testing theory for the population genomics of microbes

This is a computer based project. We are looking for a student who is strong in bioinformatics and theory, ideally with experience with whole genome data, and ideally some experience with microbes.

This is a fully-funded position with stipend and fees covering three years.

Main supervisor: Associate Professor Matthew Goddard, University of Lincoln, UK and University of Auckland, New Zealand; <http://goddardlab.auckland.ac.nz>  
Co-supervisors: Prof Stuart Humphries, University of Lincoln

Collaborator: Assistant Professor Chris Hittinger, University of Wisconsin-Madison, USA,

Please contact Mat Goddard - [mgoddard@lincoln.ac.uk](mailto:mgoddard@lincoln.ac.uk) - for all enquiries, and include a CV and covering letter.

Background



Microbes are key component of natural, agricultural and commercial ecosystems due to their metabolic actions and ecological functions[1]. For example, bacteria and fungi are key components of soil that at least provide and recycle nutrients for plant growth, and perform many other ecological roles[2]. An array of microbes transform crops to higher value commodities (cheese, coffee, cocoa, beer, wine etc)[3]. Pathogenic microbes potentially cause disease, for example *Campylobacter* is responsible for >280,000 food poisoning cases in the UK per year and c. 100 deaths, costing the UK economy >£580m per year, much of this imposed on the NHS[4]. If it were not for microbes modern day sewage treatment plants would cease to function.

If we are to understand ecosystems in their totality, let alone reliably harness and manipulate such ecosystems to render them safe or productive, we need to know how the microbial components work. Unfortunately, while a few species of microbes have been very well genetically and molecularly described, the population biology and ecology of even the most-well studied of microbes remains cryptic[5-7]. This is simply because the ecology and population biology of microbes is hard to study.

Recent step-changes in DNA sequencing technology have opened up unparalleled opportunities in this area[8,9]. This technology provides three crucial aspects that were not attainable before: 1, it can access and analyse microbes that are not easily cultured in the laboratory as DNA may be extracted directly from the environment; 2, billions of cells may be analysed rather than hundreds due to the constraints of individual analyses of colonies on agar plates; and 3, whole genome sequence data from individual isolates may now be gathered at a reasonable cost.

This project will primarily use the whole genomes of multiple individual from natural population of closely related commercially and academically important species of microbes *Saccharomyces cerevisiae* and *S. uvarum* - to analyse these populations and test the applicability of current theory, and develop new theory specific for microbial population biology and ecology. These two species are research super-models and important in wine, bread and beer production. We will analyse populations that derive from New Zealand and the important and powerful difference is that *S. cerevisiae* is a recently introduced species, but that *S. uvarum* is an ancient endemic species[13-15]. This crucially will allow us to compare and contrast patterns and processes in microbial populations that have very different recent evolutionary histories and potential ecologies. There will be the opportunity for the successful student to work with other types of data as well, specifically microbial community data.

We will:

1 analyse and develop theory for the analyses of population structure, as Goddard has done previously[16,17], but here with the power of whole genome data that will also account for gene-flow and recombination between sub-populations.

2 Following the first and only study to estimate the life-history parameters of microbes[18], use whole genome data to quantify the extent of meiosis, mitosis and modes of inbreeding.

3 use the above data to parameterise and then develop new theory to analyse populations that are part clonal, part sexual, as microbial eukaryotes are.

4 estimate signals of selection in genomes and compare and contrast the two species to evaluate if this recovers insights into their histories of invasion and endemism.

1. Hanson, C. A., Fuhrman, J. A., Horner-Devine, M. C. & Martiny, J. B. H. Beyond biogeographic patterns: processes shaping the microbial landscape. *Nat Rev Micro* (2012). doi:10.1038/nrmicro2795

2. Hughes Martiny, J. B. et al. Microbial biogeography: putting microorganisms on the map. *Nat Rev Micro* 4, 102112 (2006).

3. Chambers, P. J. & Pretorius, I. S. Fermenting knowledge: the history of winemaking, science and yeast research. *EMBO Rep* 11, 914920 (2010).

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## UMaine Orono EvolutionaryPhysiology

I am seeking a highly motivated MS graduate student to join my research group at the University of Maine (Orono, ME). My lab studies the evolutionary and ecological physiology of mammals in relation to climate. The project will involve a combined lab/field approach to characterize the energetics and physiology of a small mammal species in relation to ambient temperatures and humidity. The exact species will be decided in consultation with the candidate, potential species include chipmunks, flying squirrels, hares or small mustelids.

Location: Orono, ME

Salary: \$15,000/yr +tuition

Qualifications

Applicants must meet the requirements of the Graduate School (<http://sbe.umaine.edu/graduate/-program-requirements/degree-offerings/a-pplication-to-the-program/>) and possess a BSc in Biological Sciences or equivalent. Experience working with small mammals, and working in field conditions is preferable. Knowledge of the collection of physiological data (respirometry) is a plus

Please send an email to Dr. Danielle Levesque ([danielle.l.levesque@gmail.com](mailto:danielle.l.levesque@gmail.com))

(1) a cover letter discussing your interest in the project and applicable experience;

(2) a CV

(3) transcripts (unofficial is ok)

(4) GRE scores (unofficial is ok)

The position is funded for two years and includes a stipend, tuition waiver and partial health insurance.

Closing Date: 14 April 2016 Start Date: 1 Sept 2016  
Danielle Levesque, PhD Assistant Professor of Mammalogy and Mammalian Health School of Biology & Ecology 347 Hitchner Hall, University of Maine Orono, ME 04469 Phone: +1 (207) 581-2511 Fax: +1 (207) 581-2537

Danielle Levesque <[danielle.l.levesque@maine.edu](mailto:danielle.l.levesque@maine.edu)>

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## UPortsmouth EvolutionPollination

The University of Portsmouth, UK, is offering support for one PhD student to work with Scott Armbruster investigating: "Mechanisms of major evolutionary transitions between pollination mutualisms in \*Dalechampia\* vines" (Research Project Code: BIOL2231016)

-Support is available only to UK and EU/EEA students.

Project detail: Although evolutionary shifts between ecological relationships among organisms contribute significantly to the origin and maintenance of biodiversity, how such transitions occur remains poorly understood. As a result of rapid environmental change worldwide (e.g. changing climate, widespread deforestation), important plant-animal mutualisms are being lost or degraded. Understanding how transitions between mutualisms have

occurred in the past may help in mitigating future biodiversity loss. Application of modern methods of molecular phylogenetics, combined with phenotypic selection analysis, population genetics, natural product chemistry, SEM studies of development, and biosynthetic and developmental genetics, to species of Dalechampia vines (Euphorbiaceae) with divergent pollination mutualisms should generate insights of unprecedented resolution into the mechanisms of major shifts in pollination ecology.

Further information and application instructions are available at:

<http://www.port.ac.uk/postgraduate-research/-funding/phd-biology/>

Questions can be addressed to [scott.armbruster@port.ac.uk](mailto:scott.armbruster@port.ac.uk)

"[wsarmbruster@alaska.edu](mailto:wsarmbruster@alaska.edu)"

<[wsarmbruster@alaska.edu](mailto:wsarmbruster@alaska.edu)>

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## UppsalaU PlantEvolution

PhD POSITION IN PLANT EVOLUTIONARY ECOLOGY AT UPPSALA UNIVERSITY

We are seeking a highly motivated PhD student with interests in plant ecological genetics, conservation and evolution. The candidate will be working in a collaborative project between the labs of Drs. Nina Sletvold and Sophie Karrenberg, studying the effects of population size on genetic and ecological processes using the orchid *Gymnadenia conopsea* as the study system. More detailed information on the project and how to apply can be found at <http://www.uu.se/en/about-uu/join-us/details/?positionId=3D3D91488> For more details regarding the position please contact Assoc. Prof. Nina Sletvold ([nina.sletvold@ebc.uu.se](mailto:nina.sletvold@ebc.uu.se))

"[nina.sletvold@ebc.uu.se](mailto:nina.sletvold@ebc.uu.se)" <[nina.sletvold@ebc.uu.se](mailto:nina.sletvold@ebc.uu.se)>

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## USouthBohemia CzechRepublic AntPlantInteractions

A highly motivated postgraduate student is sought to join a project exploring the shifts that occur in a mutualistic ant-plant network when tropical rain forest is logged, fragmented, and converted to oil palm plantation in Malaysian Borneo. The student will conduct

field surveys for ant-inhabited trees, measure ant and plant fitness correlates, and perform experimental manipulations of the mutualistic communities, in particular in relation to forest regeneration. The studentship will provide the opportunity to collaborate with two cutting-edge large-scale manipulations of tropical forests: 1. The Stability of Altered Forest Ecosystems project (SAFE), the world's largest rain forest fragmentation experiment. 2. The Sabah Biodiversity Experiment (SBE), a project assessing the impacts of different diversities of tree planting on ecosystem functioning. There will also be opportunities to develop the project in a direction of the student's own choosing. Duties will include spending extensive periods of time in the field in Malaysian Borneo.

The successful applicant will join the Ant Research Group (<http://antscience.com/>) at the Institute of Entomology, Biology Centre Academy of Sciences, Ceske Budejovice, Czech Republic, under the supervision of Tom Fayle (<http://www.tomfayle.com/index.htm>). The laboratory is a dynamic, multinational group studying ant ecology, evolution and biogeography, and is embedded within the Department of Ecology and Conservation Biology, a world-class centre for interaction network research with regular publications in Science, Nature and other leading journals. The deadline for applications is February 29th 2016, with a start date of May 1st 2016. The student will receive a scholarship from the University of South Bohemia and employment on an ongoing grant for three years, sufficient to cover living expenses in Czech Republic. Applicants from all countries are eligible.

Required - A master's degree (non-negotiable requirement for PhD study in Czech Republic). - Interest in the ecology of insects or plants. - 1st or 2.1 undergraduate degree in ecology or related subject (or equivalent). - Enthusiasm for working in the field for extended periods of time in challenging conditions in tropical rain forest. - Ability to work independently. - Experience in the use of ecological statistical analyses.

Desirable - Previous experience of tropical field work. - Research experience with plant or insect ecology. - Experience of molecular laboratory work, specifically DNA barcoding for species identifications.

To apply please send a CV, contact details for three references, and cover letter stating qualifications, previous work and motivation to Tom Fayle (tmfayle@gmail.com).

Tom Fayle <tmfayle@gmail.com>

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## USouthDakota 2 Bioinformatics

Graduate Student Opportunity in a New Lab at the University of South Dakota

I will be starting a lab group in the Department of Biology at the University of South Dakota, Fall, 2016. I am looking for graduate students (MS or PhD) interested in molecular ecology. Specifically, in collaboration with Andrew Russell at the University of Exeter, we have collected 10+ years of genetic data in the cooperatively breeding species, the chestnut-crowned babbler. I am looking to recruit one or two students interested in bioinformatics to work with me and Dr. Erliang Zeng answering questions about heritability of traits (e.g. helping), population structuring, and the like (this is relatively open depending on the interests of the student(s)). Although considerable data is already available for use, some opportunity may exist to gain lab experience if desired.

Some statistical background would be useful and attention to detail is a requirement.

If interested, please contact Andrea Liebl ([a.l.liebl@exeter.ac.uk](mailto:a.l.liebl@exeter.ac.uk)).

Andrea L. Liebl, PhD Postdoctoral Research Fellow University of Exeter, Cornwall <http://www.andrealliebl.com/> Andrea Liebl <[A.L.Liebl@exeter.ac.uk](mailto:A.L.Liebl@exeter.ac.uk)>

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## UTorontoMississauga Evolutionary Genomics

The Ness lab is recruiting multiple funded graduate positions (M.Sc. or Ph.D.) to explore evolution in the genome. In our lab you'll have the chance to combine field work, experimental evolution, and molecular biology with genomics to study how the genome influences patterns of biological diversity. Students will be able to develop their own interests and/or join ongoing projects including the effects of de novo mutations, variation in recombination rates and how mutation and recombination influence adaptation and genetic drift to shape evolution. For more information about ongoing research and opportunities check out the lab page

(<http://sites.utm.utoronto.ca/ness>).

The graduate program in Ecology and Evolutionary Biology at the University of Toronto is across all three campuses and offers incredible opportunity for broad intellectual and professional training ([www.eeb.utoronto.ca/grad.htm](http://www.eeb.utoronto.ca/grad.htm)). In the Department of Biology at University of Toronto @ Mississauga there are ~30 research labs providing a stimulating research environment ([www.utm.utoronto.ca/biology/home](http://www.utm.utoronto.ca/biology/home)) and graduate students in the lab will be encouraged to travel to national and international conferences.

We encourage applicants from a wide diversity of backgrounds including Biology, Computer Science or Mathematics. Expertise in evolutionary biology, genomics, population genetics, bioinformatics and computer programming will be considered an asset.

Applications and queries should be sent to [rob.ness@utoronto.ca](mailto:rob.ness@utoronto.ca). Please include a short statement of interest (<1 page), with a CV (including 2-3 references) and a copy of your transcript. You can find more information at <http://sites.utm.utoronto.ca/ness> Dr. Rob W. Ness Assistant Professor Department of Biology, University of Toronto @ Mississauga Mississauga, ON, Canada <http://sites.utm.utoronto.ca/ness> “[rob.ness@utoronto.ca](mailto:rob.ness@utoronto.ca)” <[rob.ness@utoronto.ca](mailto:rob.ness@utoronto.ca)>

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## UVienna EcolEvolGenomics

Graduate position: UVienna.EcolEvolGenomics

A PhD position is available in the Department of Botany and Biodiversity Research, Faculty of Life Sciences, University of Vienna. The project will investigate the mechanisms of diversification in bromeliads (Bromeliaceae; the Ananas / pineapple family), a 'textbook' adaptive radiation in the tropical plant diversity hotspots of Meso- and South America. Integrated within an international research consortium, you will study the ecological & evolutionary genomics of speciation in tillandsioid bromeliads (*Tillandsia* and related genera) using 'target capture' resequencing of candidate genes and pathways for key adaptive traits and neutral reference genome regions. You will analyze these data jointly with ecological and spatial information, using the latest tools from population genomics, phylogenomics, and niche modelling. The results will provide a strong basis for identifying the drivers of speciation in this highly diverse and ecologically important group of flowering plants, and potentially in species radiations more generally.

Work place: The Department of Botany and Biodiversity Research houses several research groups active in ecological & evolutionary genomics, plant systematics, niche modelling, conservation biology, structural & functional botany, and plant-animal interactions. Molecular laboratories and extensive computing resources are available locally and at the Vienna Scientific Cluster, and second generation sequencing (NGS) facilities are available in the nearby Vienna Biocenter Core Facilities. The project is integrated within an international consortium involving three Universities in Switzerland and several research groups in Mexico and other Meso- and South American countries. The position is initially for 3 years, with the possibility of a 4th year extension. University of Vienna offers an attractive and dynamic research environment, embedded within a city with exceptionally high quality of life and with numerous outdoor activities within easy reach.

Start date: Anytime, but ideally before June 2016 for optimal match with the consortium's field work plans.

Requirements: Experience in the use of molecular genetic markers in ecology or evolutionary biology; prior experience with / exposure to the analysis of second generation sequencing data would be beneficial; good knowledge of English, written and oral; willingness to acquire basic knowledge of Spanish to facilitate participation in a (moderate) amount of field work.

To apply: Applications must include a motivation letter (<1 page), CV, list of publications if applicable, and contact details of two references. Please submit your application via the website of the Job Center at the University of Vienna (<http://jobcenter.univie.ac.at/en/home/>; email: [jobcenter@univie.ac.at](mailto:jobcenter@univie.ac.at)) no later than 20.03.2016, mentioning job reference no. 6472. For more information please contact: Christian Lexer,

[christian.lexer@univie.ac.at](mailto:christian.lexer@univie.ac.at).

[christian.lexer@univie.ac.at](mailto:christian.lexer@univie.ac.at)

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## WageningenU PelargoniumGenomics

Vacancy for a PhD position 'Pelargonium genomics for overcoming cytonuclear incompatibility and bridging species barriers.'

Wageningen University, The Netherlands. Research in this project focusses on the occurrence of cyto-nuclear incompatibilities in the horticulturally important sect. *Ciconium* clade within the popular ornamental crop lin-



eage Pelargonium (Geraniaceae). One of the obstacles to producing better and more varieties of Pelargonium cultivars is overcoming potential (and actual) species crossing barriers. The Pelargonium clade is characterised by the occurrence of widespread genome instability, and at the species-level by the occurrence of both cytonuclear incompatibility (CNI) and bi-parental cytoplasmic inheritance. You will apply genotyping-by-sequencing of plastomes and mitomes of all 18 species known from the Ciconium clade, in order to i) accurately trace cytotypes (plastome + mitome) in Pelargonium breeding, and ii) to better understand the organelle genomic basis for CNI's known to occur in this group. In addition to organelle genomics, you will characterise structure, diversity and relative abundance of transposable elements quantitatively for all species and cultivars involved, enabling accurately profiling and monitoring of nuclear genomic backgrounds in Pelargonium crossings.

Using this genomic reference library you will explore cases of CNI and also cytoplasmic male-sterility among Ciconium species by genotyping progeny from their reciprocal crosses. You will investigate whether plastomes and mitomes are altered in these cases and how these alterations affect the fertility of respective hybrid genotypes.

We seek a bright, highly motivated, and enthusiastic person able to work both as part of a team and independently. The ideal candidate has a master degree in evolutionary biology, plant sciences or genetics, with good background in bioinformatics, genomics and computational biology. Candidates from other programs such as ecology or bioinformatics, with a strong interest in evolution and genetics are also invited to apply. Experience with NGS technologies and genomic data analysis is a plus, but training will be provided. The language in the lab is English. A high standard of spoken and written English is required.

Further information can be obtained from Freek Bakker (freek.bakker@wur.nl) and applications should be sent to <http://www.wageningenur.nl/en/Jobs/Vacancies.htm> "Bakker, Freek" <freek.bakker@wur.nl>

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## WesternUCanada Sociogenomics

PhD positions in sociogenomics at Western University, Canada.

The Social Biology Group (<http://www.uwo.ca/biology/faculty/thompson/>) in the Department of Biol-

ogy at Western University (London, Canada) is recruiting two doctoral candidates in 2016 to advance any of the following four projects. We will match the precise project to the skill, aptitude and experience of successful candidates.

### 1) Molecular coordination of social traits in honeybees

Discover how genes and gene networks influence the evolution and expression of social traits. We need an evolutionary-minded student with an aptitude for molecular genetic or bioinformatics analyses, or both, to identify genes and gene networks that regulate worker sterility in response to queen pheromone. There are opportunities to work with live bees, but experience with beekeeping is not a requirement.

Some background information is available in:

Sobotka et al 2016. Structure and function of gene regulatory networks associated with worker sterility in honeybees. *Ecology and Evolution* doi: 10.1002/ece3.1997.

Mullen et al. 2014. Gene co-citation networks associated with worker sterility in honey bees. *BMC Systems Biology* 8: 38

### 2) Comparative biology of social and non-social insects

Discover the genetic and neural circuits that coordinate reproduction in social versus non-social insects. We need a student with experience in Drosophila biology and genetics to help identify genes and neurons essential for pheromone responsiveness and ovary de-activation - first in flies, then in other insects!

Some background information is available in:

Camiletti et al 2014. How flies respond to honey bee pheromone: The role of the foraging gene on reproductive response to queen mandibular pheromone. *Naturwissenschaften* 101: 25-31.

Camiletti et al 2013. Honey bee queen mandibular pheromone inhibits ovary development and fecundity in a fruit fly. *Entomologia Experimentalis et Applicata* 147: 262-268.

### 3) Molecular coordination of social traits in termites

Discover the molecular basis of termite social life! We are probing the Eastern subterranean termite genome for genes associated with caste, sociality and invasiveness. We seek a candidate with interest or expertise in next-generation sequence analysis, gene network analysis, or in the general social and evolutionary biology of insects.

Some background information is available in:

Wu et al. 2015. Subterranean termites: the evolution of a pest. *PCT Canada* 3: 34-42. <http://>



[/www.pctonline.com/Digital/pcc/pccanada201503/-index.html](http://www.pctonline.com/Digital/pcc/pccanada201503/-index.html) Gao and Thompson 2015. Social context affects immune gene expression in a subterranean termite. *Insectes Sociaux*. 62: 167-179.

Scaduto et al 2012. Genetic evidence for multiple invasions of the Eastern subterranean termite into Canada. *Environmental Entomology*. 41: 1680-1686.

#### 4) Developing and testing sociobiological ideas

Bridge the gap between selfish gene theory and real gene discovery. We have developed a conceptual roadmap for social gene discovery, and we seek a free-thinking student with an interest in population genetic modeling or comparative sequence analysis, or both. The successful candidate would help develop a conceptual and empirical framework for predicting the type, location and qualities of genes that underlay social traits - first in honey bees, but ultimately in any social genome.

Some background information is available in:

Mullen and Thompson 2015. Understanding honey bee worker self-sacrifice: a conceptual-empirical framework. *Advances in Insect Physiology* 48: 325-354.

Thompson GJ et al 2013. Genes underlying altruism. *Biology Letters* 9: 20130395.

#### How to apply

Western University is located in the City of London (pop. 400 000) and has a large and vibrant Department of Biology <http://www.uwo.ca/biology/index.html>. We have strong links to the London Regional Genomics Centre (LRGC) and SHARCNET super-computing facilities. In addition, we run an active research group, with a well-equipped molecular laboratory. We have access to live termites and maintain a small apiary. Funding is available for Canadian students. International students are welcome to apply provided they have access to scholarships from their home country <http://www.uwo.ca/biology/graduate/prospective/index.html>. If interested in applying, please send your c.v., contacts for references, and a one page cover letter to Graham J Thompson ([graham.thompson@uwo.ca](mailto:graham.thompson@uwo.ca)). The anticipated start date for all positions is from September 2016, with alternate starts in January 2017 and May 2017. Informal inquires are welcome :)

Graham J. Thompson

Associate Professor Department of Biology, Faculty of Science Western University

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## West VirginiaU Conservation Genomics

Ph.D. Graduate Research Assistantship - Conservation Genomics, School of Natural Resources, Wildlife and Fisheries Resources Program, West Virginia University  
STARTING DATE: August 2016 (option to start earlier in the summer)

CLOSING DATE: Position is open until filled. Review of applicants will begin on February 29.

DESCRIPTION: The School of Natural Resources at West Virginia University is searching for a Ph.D. student to study conservation genomics of lake sturgeon in the Great Lakes. The student will use genotyping-by-sequencing (GBS) to analyze DNA from lake sturgeon populations throughout the Great Lakes in an effort to determine evolutionary relationships and to identify management units. The position will involve laboratory work, bioinformatics, and frequent interactions with Great Lakes management agencies. The student will be working towards a Ph.D. in Forest Resources Science with an emphasis in Wildlife and Fisheries Resources with Dr. Amy Welsh at West Virginia University (<http://wildgenomics.forestry.wvu.edu/>). The project is in collaboration with Dr. Louis Bernatchez at Université Laval and Dr. Tim King at USGS-Leetown Science Center.

QUALIFICATIONS: B.S. and M.S. in genetics, evolutionary biology, fisheries, wildlife, biology, or related field. Minimum GPA of 3.25 and combined quantitative/verbal GRE scores of 300. Experience in population genetics is required. Computer and/or bioinformatics skills preferred.

STIPEND: \$19,848/year plus health insurance and tuition waiver.

CONTACT: Interested individuals should send a letter of interest, CV, unofficial copy of transcripts and GRE scores to Dr. Amy Welsh ([amy.welsh@mail.wvu.edu](mailto:amy.welsh@mail.wvu.edu)).

Amy Welsh <[Amy.Welsh@mail.wvu.edu](mailto:Amy.Welsh@mail.wvu.edu)>

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## Jobs

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### Alberta GroundSquirrelHeadTech

Head Field Technician Required - Columbian ground squirrels Kananaskis, Alberta, Canada

We are looking for a head field technician to assist with, and coordinate, fieldwork on the ecology of a wild population of Columbian ground squirrels. The head technician will supervise 3 volunteers for the period of Apr 9 to Aug 31, 2016. Duties will include monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals, data entry and data verification. Fieldwork will involve live-trapping and handling of animals, behavioural observation, radio-telemetry (to locate natal burrows) and assistance with the measurement of physiological (metabolism) traits on free-ranging animals. The successful candidate will have previous fieldwork experience, ideally in a field camp/station setting, have experience in data entry and management and show a high level of responsibility. Good organizational, multi-tasking and supervisory abilities are essential. Applicants who have experience working with terrestrial vertebrates will be given priority. Additionally, you should have an interest in a number of the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and animal

behaviour. Periods of time will be spent camping and, as such, successful applicants need to enjoy the outdoors, be up-beat, positive, responsible and work well as a member of a team.

All fieldwork is carried out in the spectacular Rocky Mountains of southwestern Alberta, Canada, home to some of the most majestic wildlife in North America. You will be staying at the University of Calgary's R.B. Miller research station in Sheep River Provincial Park, Alberta (<http://bgs.ucalgary.ca/facilities/-facilities>). You will interact with other researchers working with ground squirrels on a diversity of projects in behavioural and population ecology. Additionally, the field station is home to a number of other researchers working on a variety of projects, ranging from insects to large mammals.

Salary is \$1800/month. Food and accommodation are provided. The successful candidate will be required to provide for their own travel to Saskatoon, Saskatchewan. Travel between the field station and Saskatoon is provided. If you wish to apply for this position, please send a CV with a cover letter and contact details of three references (with e-mail address), by email to Jeff Lane (contact info below), by February 28, 2016. Please indicate in your application that you are applying for the head technician position (we are also posting for volunteers). Note that only those eligible to work in Canada (Canadian citizens or landed immigrants, Amer-

ican citizens eligible for TN status or foreign nationals with work permits or working holiday visas) will be considered.

We thank everyone for applying, but only those selected for interview will be contacted. Only applicants available for the entire period will be considered.

Contact: Dr. Jeff Lane Department of Biology University of Saskatchewan jeffrey.lane@usask.ca [www.lanelab.ca](http://www.lanelab.ca) "Lane, Jeffrey" <jeffrey.lane@usask.ca>

Qualifications: BS in Biology, Zoology or Entomology. Candidates with general knowledge of terrestrial arthropod (preferably arachnid and/or myriapod) morphology and systematics, good organizational skills and attention to details, and a good command of MS Word and Excel are preferred, with more experienced databasing ability desirable. For more information and to apply please visit: [careers.amnh.org/applicants/Central?quickFindQ947](http://careers.amnh.org/applicants/Central?quickFindQ947) All applicants must apply electronically through the AMNH Careers Website.

[egaughan@amnh.org](mailto:egaughan@amnh.org)

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## AMNH New York InvertZool

The Division of Invertebrate Zoology at the American Museum of Natural History has the following position open: Scientific Assistant - Full Time.

The American Museum of Natural History (AMNH) houses one of the world's largest collections of biodiversity, including over 32 million biological specimens and 4 million fossils. The Division of Invertebrate Zoology is searching for a Scientific Assistant to assist the continued growth and management of the collections and associated resources (archives, databases, and tissues) of Arachnida and Myriapoda. The Division contains the world's largest collection of spiders and second-largest collection of scorpions, as well as the largest collection of minor arachnid orders and one of the largest collections of myriapods in North America, with worldwide representation of taxa, emphasizing material from Africa, North America and elsewhere in the New World. The majority of specimens are preserved in ethanol, although large slide-mounted and frozen tissue collections are also represented.

Duties: The successful applicant will assist the curator in management of the collections including specimen sorting, labeling, preparation, accessioning and databasing new acquisitions; systematic arrangement, storage and organization of the collection; conservation (ethanol levels, pH, rehydration, label integrity, rehousing into better containers, etc.); routine collections tasks (assistance to visitors, response to requests for information, retrieving, packing and shipping loans to other institutions, unpacking and curating loan returns and donations to AMNH, databasing accessions, loan and visitor activity); museum and local community service (collection tours and related activities); training and supervision of students and volunteers; management of frozen tissues and associated data.

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## Australian NatIU Computational Biologist

Dear colleagues

I have funds to employ a computational biologist/bioinformatician for up to 2.5 years to work on next generation sequence analysis and phylogenetics. The successful candidate will be employed at the Australian National University. If you are interested to learn more, please email me ([allen.rodrido@anu.edu.au](mailto:allen.rodrido@anu.edu.au)).

Allen Rodrigo

Prof Allen Rodrigo PhD DSc FRSNZ Director Research School of Biology ANU College of Medicine, Biology and Environment RN Robertson Building 46 Sullivans Creek Road The Australian National University Acton ACT 2601 Australia

[allen.rodrido@anu.edu.au](mailto:allen.rodrido@anu.edu.au)

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## Baja California Mexico Bioinformatician

### BIOINFORMATICIAN POSITION

We are looking for a bioinformatician or computational biologist to join the group of Dr. Lago-Lestón in the Department of Biomedical Innovation at CICESE, Baja California, Mexico. The project aims to study the diversity and the function of the microbial communities present in Southern Gulf of Mexico. The successful applicant will work with other members of the team

and other colleagues in order to analyze large-scale genomic datasets predominantly obtained by NGS based approaches such as amplicon and shotgun metagenomes and metatranscriptomes data generated on the Illumina platforms including HiSeq 2500 and MiSeq. Activities include taxonomic and functional assessments, genome assembling, transcriptomes characterization, gene finding and annotation and establishment, maintenance and optimization of analysis pipelines and procedures for new collected data and their integration with public and commercial data sources.

The successful applicant should have Computer Science, Statistics or Bioinformatics background and experience in genomic data analysis and data mining is desirable but not essential. This experience should include any of the following:

- Expertise in high throughput sequence analysis including microbial comparative genomics, 16S diversity and metagenomics - Coding experience in Python and R would be desirable - Practical experience with creation and maintenance of biological databases - Skilled in statistical analysis of sequence data - Experience with establishing online bioinformatics tools is favored

Salary will be commensurate with experience. Position will be open until filled. CV and any question can be addressed to Dr. Lago-Lestón (alago@cicese.mx)

Dra. Asunción Lago Lestón Investigadora Titular Departamento de Innovación Biomédica CICESE Ensenada, Baja California, México Tel. +52 646 1750500 Ext. 27264

Asuncion <alago@cicese.mx>

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## BethuneCookmanU Florida PlantEvolution

Hello,

I'd like to share with you an opening in my department for a plant biology position. We would be glad to receive candidates with a specialization in evolutionary plant Genetics/Genomics, complementing existing strengths of the department, as long as the candidate is able to teach senior level plant physiology.

Contact valerok@cookman.edu

TENURE-TRACK POSITION ASSISTANT/ ASSOCIATE PROFESSOR of Biology - Plant Biology Bethune-Cookman University, a private Historically

Black University, seeks a suitable applicant dedicated to excellence in teaching and research, and also to the continued enhancement of the academic environment for students and colleagues.

**Job Description** The Department of Natural Sciences in the College of Science, Engineering and Mathematics at Bethune-Cookman University is currently seeking a candidate for a 9-month tenure-track position to begin in the Fall of 2016. Applicants should hold a Ph.D. in Plant Biology, Botany or a related field, have postdoctoral experience, and be able to teach an upper level course in Plant Physiology as well as introductory biology courses and courses in their area of expertise. The successful candidate will be expected to establish and maintain an active research program, including participation of undergraduate students in their research. Research areas that will complement current efforts may include, but are not limited to, Evolutionary Genetics, Molecular Biology, Cell Biology, Environmental Toxicology, Environmental Chemistry, Plant-Microbe interactions, and Plant Ecology. The ideal applicant will show strong potential for collaboration across disciplines within the College and University and demonstrate experience in pedagogy, curriculum development and/or assessment. **Essential Functions** The person appointed will have the following responsibilities: Development and maintenance of a distinguished and interdisciplinary research program Development of her/his own scholarly activities and professional capabilities Active and effective participation in undergraduate instruction including student advising and mentoring Active and effective participation in departmental, college, and university administrative governance

To apply for the position, please submit the following: an online application form\*, a cover letter, a current CV (with contact information), a list of three to five professional references, a statement of teaching philosophy (max. one page), a research statement (max. three pages), and copies of graduate transcripts (official transcripts required only if hired).

\*Select the appropriate position from the BCU HR Web-site: <http://www.cookman.edu/facultyStaff/hr/-index.html> Send all Information to both Human Resources and the Faculty Search Committee Chair Human Resources email address: hr@cookman.edu Faculty Search Committee Chair, Dr. Katharina Valero: valerok@cookman.edu

Katharina Valero <valerok@cookman.edu>

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## Frankfurt Curator Ichthyology

Jobposting - Ref. #01-16006

The Senckenberg Society for Nature Research (SGN), an institution of the Leibniz Association with almost 800 employees, conducts state-of-the-art natural science research at leading research institutions located in seven of Germany's federal states. The SGN is in charge of the UNESCO natural World Heritage Site "Grube Messel".

The Senckenberg Society for Nature Research, headquartered in Frankfurt am Main, Germany, intends to fill at the Department of Marine Zoology the position of a Curator of Ichthyology - (Full time)

Your tasks: Assume responsibility for the management and curatorship of Senckenberg's extensive collection of marine and freshwater fishes. Oversee the rearrangement of the fish collections and their relocation to a new building. Oversee the transfer of offices, laboratories, and an ichthyological library to the new premises, which are currently being rebuilt, meeting highest curatorial standards. Supervise technical assistants. Conduct collection-based research on the taxonomy, systematics, and phylogeny of marine fishes. Participate in joint marine research with other scientists at the Department of Marine Zoology and beyond.

Your profile: Advanced degree in biology/zoology or related field (preferably doctoral degree). At least five years of work experience in curatorship and management of zoological (preferably ichthyological) collections. Familiarity with systematics of fishes. Outstanding research record in systematic ichthyology, documented by publications in peer-reviewed scientific journals. Fluency in English, both spoken and written; good knowledge of German will be an asset. Firm commitment to your work and sense of responsibility.

We offer: An attractive and challenging position in a research institute of international standing. Employment should start as soon as possible and is initially limited to 28 February 2018. A salary that reflects the tasks and responsibilities of the position based on the collective agreement for public service in the state of Hesse (TV-H). A discounted 'job ticket' for public transportation in the Rhine-Main area.

Senckenberg is an equal opportunities employer and places an emphasis on fostering career opportunities for women. Qualified women are strongly encouraged to

apply. Senckenberg is certified by "audit berufundfamilie". We guarantee adherence to the severely disabled directives and the law on part-time employment. The duty station will be Frankfurt am Main.

Interested? Please send your complete application documents (CV, certificates and references, letter of motivation), preferably in electronic form (as a single PDF file) quoting reference #01-16006 by 22 March 2016 to:

Dr. Tobias Schneck c/o Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt am Main E-Mail: [recruiting@senckenberg.de](mailto:recruiting@senckenberg.de)

For more information, please contact Dr. Dieter Fiege, [dieter.fiege@senckenberg.de](mailto:dieter.fiege@senckenberg.de), phone: +49-69-7542-1265.

– Mit freundlichen Grüßen / Best Regards

Isabel Gajcevic, M.A. 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 Gruppe Personal & Soziales -1319 Elsen, Carina

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

Fax: 0049 (0)69 / 7542-1467

Mail: [recruiting@senckenberg.de](mailto:recruiting@senckenberg.de) Home-

page: [www.senckenberg.de](http://www.senckenberg.de) SENCKENBERG Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß §22 BGB) Senckenberganlage 25 60325 Frankfurt am Main Direktorium: Prof. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Uwe Fritz, PD Dr. Ingrid Kröncke Präsidentin: Dr. h. c. Beate Heraeus Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt) Before printing, think about the environment

[recruiting@senckenberg.de](mailto:recruiting@senckenberg.de)

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## Hungary Bioinformatics

Bioinformatics research assistant position in Szeged, Hungary

The Csaba Pál & Balázs Papp labs within the Synthetic and Systems Biology Unit of the Biological Research



Center of the Hungarian Academy of Sciences are seeking a talented and motivated BIOINFORMATICIAN to join systems and synthetic biology projects as a Research Associate.

We are looking for a highly motivated bioinformatician to develop and run data analysis pipelines for next generation sequencing experiments in the field of genome engineering, human microbiome analysis and evolutionary systems biology. Our experiments have a specific focus on prokaryotic de novo metagenomic and whole genome sequencing, whole genome re-sequencing and amplicon sequencing, such as 16S rRNA applications for the analysis of microbial composition.

Requirements:

Previous experience with NGS data analysis (e.g. Illumina) and solid knowledge of scripting languages (R, Perl) is required, as well as good communication and teamwork skills. Strong biological insight and experience in statistical analysis is a plus. We offer a competitive salary and the possibility of a flexible working schedule.

For further information please contact: kintses.balint@brc.mta.hu

Applications should be submitted via e-mail before 16 March 2016 along with the following documents:

1. A cover letter in English - brief explanation of the applicant's background and reasons for applying
2. Curriculum vitae in English
3. List of publications (if applicable)

[www.brc.hu/sysbiol](http://www.brc.hu/sysbiol) [facebook.com/sysbiol](https://www.facebook.com/sysbiol)

References:

- 1) Pál, Csaba, Balázs Papp, and György Pósfai. 2014. "The Dawn of Evolutionary Genome Engineering." *Nature Reviews Genetics*
- 2) Lázár, Viktória, István Nagy, Réka Spohn, Bálint Csörgő, Ádám Györkei, Ákos Nyerges, Balázs Horváth, et al. 2014. "Genome-Wide Analysis Captures the D  
Papp Balázs <pappb@brc.hu>

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## ImperialCollege MicrobeGenomics

The MRC Centre for Outbreak Analysis and Modelling is looking for a Research Assistant/Associate to develop novel statistical and computational methods to track the transmission of bacterial pathogens using genomic

data. The MRC Centre has built upon a world-leading research group in the Department of Infectious Disease Epidemiology at Imperial College London to undertake applied collaborative work with national and international agencies in support of policy planning for emerging and endemic infectious diseases.

Bacterial pathogens are responsible for some of the deadliest human diseases such as tuberculosis, tetanus, meningitis, pneumonia or even stomach cancer. Understanding the evolution and epidemiology of these bacterial pathogens is therefore of major biomedical importance. In particular, a good understanding of transmission routes is necessary to design control measures that can effectively limit the number of individuals becoming infected. Genomic data is increasingly being gathered in clinical microbiology, and can be used to answer fine epidemiological questions, even at the level of direct transmission between hosts.

However, there is currently a lack of analytical methods to take full advantage of this new wealth of information. Working closely with Dr Xavier Didelot, the post-holder will develop the methodology required to perform such analysis and create new software tools which will be applicable by microbial researchers around the world. To be valid, the new methods will need to account for both between-host epidemiology and within-host evolution. Thorough testing of the methods and software will be performed using simulated datasets, as well as real datasets from outbreaks of *Staphylococcus aureus*, *Clostridium difficile*, *Mycobacterium tuberculosis* and *Neisseria gonorrhoeae*.

The successful candidate will be members of both the MRC Centre and the Department, and will be based at the St Mary's Campus, Paddington.

The role requires being close to completing a PhD or equivalent (for appointment as Research Assistant) and holding a PhD or equivalent (for appointment as Research Associate) in one of the following areas: mathematics, statistics, computer science, infectious disease epidemiology or population biology. You will also need to be able to demonstrate experience of developing mathematical models, performing statistical inference and programming in at least one high level language.

The post is full time for a fixed-term of up to 36 months with a starting date between 1st April 2016 and 1st July 2016.

For informal enquiries please contact Dr Xavier Didelot ([x.didelot@imperial.ac.uk](mailto:x.didelot@imperial.ac.uk)).

Our preferred method of application is online via our website <http://www3.imperial.ac.uk/employment> (job reference: SM026-16KO). Please complete and upload

an application form as directed.

“x.didelot@imperial.ac.uk” <x.didelot@imperial.ac.uk>

## LasCrucesResearchStation CostaRica StationDirector

The position is not directly stated as such. However, the director position is open to any who qualify regardless of research interest. The past Director Zak Zahawi was focused on restoration research. As such, the station's focus was geared towards restoration projects and researchers in this area. Nevertheless, we do you have EEB researchers use our stations.

As you can see in the description a Ph. D Evolutionary Biology is one of the preferred education backgrounds.

Based on this I sent it to EvolDir.

Best,

Andres Santana, M.Sc. Graduate Program Coordinator - Costa Rican Office (506) 25240607 ext. 1511 - [www.tropicalstudies.org](http://www.tropicalstudies.org) Skype: andres.santana\_otscro / twitter: @ots.tropicaledu

The Organization for Tropical Studies is currently seeking a:

Station Director

for the Las Cruces Research Station & Wilson Botanical Garden.

The Organization for Tropical Studies (OTS) is seeking applicants for the position of Station Director for the Las Cruces Research Station and Wilson Botanical Garden. The position is based in San Vito - Coto Brus, Costa Rica.

Application deadline: March 15, 2016

1. Definition of job position:

The main responsibility of the Station Director is to supervise station operations and activities, including scientific and educational programs as well as long-term projects. The Station Director coordinates and manages the station following OTS policies and guidelines. The Station Director also oversees management of the Wilson Botanical Garden and the satellite Las Alturas Research Station.

2. Required Qualifications: Ideally, candidates for the Las Cruces Station Director position should possess the following qualifications:

a. Education

§Ph.D. in Biology, Ecology, Evolutionary Biology, Environmental Science, Conservation, Botany, Horticulture, Science Education, or related discipline.

§Research and field experience preferably in Costa Rica or Central America.

§Bilingual Spanish/English required.

b. Experience

§Five years of demonstrated management experience, preferably at field-based research facility or botanical garden.

§Experience with budget management, project management, legal compliance, risk management, and conducting or overseeing the successful completion of academic and/or research programs.

§Active field research program; field experience in a tropical environment or at a tropical botanical garden.

§Demonstrated success in grant-writing.

§Ability to promote the involvement of local and international scientists and NGOs.

§Knowledge of international environmental research programs and/or organization(s).

§Extensive knowledge of Costa Rica or Latin America, including culture, politics and governmental operations, and research community.

§Knowledge of the U.S. higher education-system and direct experience with U.S. college students.

§Demonstrated ability to coordinate and be part of an interdisciplinary teaching and research team.

§Experience in facilitating organization-wide teamwork among diverse individuals.

c. Demonstration of academic achievement and continuing involvement in professional activity, which might include

§Ongoing research program in science or science pedagogy.

§Publication of results or outreach.

§Professional society engagement.

3. The duties and responsibilities of the Stations Director include: a. Administration: Responsible for the oversight of the administrative functions of the Research Station and Botanical Garden including staff management, operations, financial and physical plant management, risk management, and other administrative duties related to the operation of the facility. Specifically:

§Provide direction and supervise growth of Las Cruces Research Station.

§Oversee management, growth, and accessions for the Wilson Botanical Garden in conjunction with on-staff horticulturist and gardeners.

§Oversee management of the Las Alturas Research Station, a rustic, satellite field station administered by Las Cruces.

§Supervise the Station Administrator and other senior and scientific staff.

§Working closely with Station Administrator, oversee facility resources and budget.

§Establish and supervise facility and asset maintenance, repair, and replacement schedules in conjunction with Station Administrator and central OTS administration.

§Prepare and oversee grants and contracts related to the facility.

§Work together with HR Department to recruit and retain qualified staff.

§Build and support a strong commitment to team work at the Station and with the two sister stations run by OTS.

§Work with colleagues in central offices in San Jose (CRO) and North America (NAO) build and maintain collaborative relationships

— / —

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>

## MichiganStateU ResTech SwitchgrassAdaptation

Laboratory/Field Research Technician position is available to work on a large collaborative project studying adaptation in the bioenergy feedstock switchgrass. The research will utilize new genetic mapping populations to identify genomic regions responsible for adaptation between northern upland and southern lowland ecotypes of switchgrass. These mapping populations have been planted at an unprecedented geographical scale, spanning ten common garden field sites distributed over 17 degrees of latitude, making them ideal for studies of

regional adaptations. The technician will be primarily responsible for maintaining and gathering data from the switchgrass common garden located at MSU's Kellogg Biological Station (KBS). The technician will also work in the laboratory of David Lowry on MSU's main campus, especially during winter months. The research will often involve all-day physical activity outdoors. The technician will be expected to organize data collection efforts and coordinate these efforts with the larger team across the central United States. For more information please contact David Lowry at [dlowry@msu.edu](mailto:dlowry@msu.edu) and visit the following website: <https://utdirect.utexas.edu/apps/hr/jobs/nlogon/160127014481>. Additional Information: \* A Resume is required in order to apply \* A Letter of Interest is required in order to apply. \* A List of 2 References is required in order to apply.

Purpose: The research assistant will work on experiments studying switchgrass ecology, physiology and genomics.

Essential Functions: Assist in the establishment, maintenance, and completion of switchgrass field experiments. Assist in the collection, processing, and analysis of plant samples harvested from field experiments. Utilize a variety of scientific instruments to collect data from field experiments. Lab processing of fields samples and greenhouse work.

Marginal/Incidental functions: Other related functions as assigned, including assisting in other experiments conducted by collaborating researchers. General lab tasks and routine equipment maintenance.

Required qualifications: High school graduation or GED. This position requires an independent, organized, and motivated individual with demonstrated research skills. Six months to a year of experience in a related field. Drivers License. Applicant selected must provide a current three-year Driving Record from their current state of residence. If not currently a resident of Michigan, must obtain a Michigan State Drivers License within 30 days after entering Michigan as a new resident. Equivalent combination of relevant education and experience may be substituted as appropriate.

Preferred Qualifications: BA or BS in ecology, biology, agronomy, or other related field and previous experience with field research. Experience in plant propagation, field plot establishment and maintenance, plant physiological measurements, such as leaf gas exchange, light interception, tissue characterization, and sample preparation for nutrient analysis are preferred skills. Familiarity with data logger programming and operation is also desirable.

Working conditions: May work in all weather conditions

May work in extreme temperatures May work around standard office conditions May work around chemicals Repetitive use of a keyboard at a workstation Use of manual dexterity Climbing of stairs Climbing of ladders Lifting and moving Must be able and willing to commute between Michigan State University and Kellogg Biological Research Station on a semi-regular basis.

David B. Lowry Assistant Professor Plant Biology Department Michigan State University Plant Biology Laboratories Room 268 517-432-4882 <http://davidbryantlowry.wordpress.com/> David Lowry <dlowry@msu.edu>

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## MonashU EvolutionaryBiol

Dear Evoldir community,

The School of Biological Sciences at Monash University (Melbourne, Australia) is advertising for a Lecturer (= Assistant Professor) in Ecology, broadly defined, and they will consider applications from researchers working on evolutionary questions.

The department houses an interactive community of academics, with research strengths in ecology and evolution, and it is a great environment for collaboration. For information about our school, see:

<http://www.monash.edu/science/schools/biological-sciences> Instructions on how to apply can be found at the link:

<http://www.jobs-monash.jxt.net.au/academic-jobs/-lecturer-biological-sciences/575340>

The closing date for applications is:

Tuesday, March 22 2016 (11:55 pm AEST)

Timothy Connallon <tim.connallon@monash.edu>

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## PrincetonU ResTech EvolutionaryGenetics

The Ayroles laboratory at the Lewis-Sigler Institute for Integrative Genomics seeks applicants for a research specialist and/or lab manager position. Our group takes a multi-disciplinary approach to investigate the genetic

basis for variation in complex traits addressing broad questions in evolutionary and medical genetics. We work with various *Drosophila* species as well as humans. We are looking for a highly motivated individual to carry out large-scale genomics projects and to support various lab activities. In addition to research, this technician will also assist in training undergraduate students and will be responsible for the day-to-day management of the lab, including maintaining equipment and the inventory of laboratory materials and supplies. The research technician may be responsible for the development and execution of research projects (which can lead to authorship on scientific publications). The ideal candidate is one who seeks professional development as a scientist and is therefore interested in reading the current scientific literature and conducting an independent research project. She/he will take ownership of her/his project. The position is open and review of applications will begin immediately. The position will start as soon as possible. Salary will be commensurate with experience and will include the full Princeton benefits package.

Responsibilities will include:

- *Drosophila* maintenance, crossing, and screening
- Molecular biology including DNA/RNA preparation, PCR, qRT-PCR, next generation sequencing.
- Lab organization, maintenance, and purchasing
- Participation in group meetings

Essential Qualifications/Skills: - Bachelors degree in biology or related field

- One to three years of experience in a research laboratory working with a (broadly-defined) "model" genetic system such as *Drosophila*, *C. elegans*, mouse, *Arabidopsis*.
- Experience with executing molecular biology protocols (ideally with a focus on next generation sequencing techniques)
- Capacity to work both independently and collaboratively
- Strong attention to detail and meticulous lab notebook keeping
- Excellent communication skills
- Enthusiasm for evolutionary biology and/or genetics To apply, submit a cover letter and resume via [jobs.princeton.edu](http://jobs.princeton.edu), requisition 1600041

Princeton University is an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin,



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

“Kara J. Dolinski” <dolinski@Princeton.EDU>

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## QueensU Tier I CRC Bioinformatics

Tier I Canada Research Chair in Bioinformatics Faculty of Health Sciences and Department of Pathology and Molecular Medicine Queen’s University, Kingston, Ontario, Canada

The Faculty of Health Sciences and the Department of Pathology and Molecular Medicine at Queen’s University are seeking an international leader and innovator in the area of bioinformatics. Applicants should have an established research program focused on precision medicine, particularly in relation to the identification of cancer diagnostic and prognostic/predictive markers and potential therapeutic targets. The successful candidate will become the designated nominee for an approved Tier I Canada Research Chair (<http://www.chairs-chaire.gc.ca/programme/index-eng.aspx>). This is a tenured appointment at the level of Professor.

### Position Overview

Candidates must hold a PhD or MD/PhD (or equivalent). The main criteria for selection are an established record of global leadership and innovation in bioinformatics, and a track record of mentorship and training of high-quality personnel in various emerging areas in the field. Queen’s University is committed to establishing an international reputation in health related informatics, building on existing assets that include: the High Performance Computing Virtual Laboratory (HPCVL), a cluster of computer systems and storage resources shared by five universities and three colleges; the biobank resources and ongoing capabilities of the Canadian Cancer Trials Group (formerly known as the NCIC Clinical Trials Group), which is a major national and international cooperative oncology clinical trials organization; and, the national database of chronic disease management developed by the Canadian Primary Care Sentinel Surveillance Network (CPCSSN), a trans-Canadian network of 11 primary care networks. In addition, robust linkages exist between HPCVL and the NCIC CTG with the informatics programs of the Ontario Brain Institute (<http://www.braininstitute.ca>) and the Ontario Institute for Cancer Research (<http://oicr.on.ca>), respectively.

The successful candidate will be expected to play a leadership role in developing additional strength in bioinformatics at the University through recruitment of new faculty, and by establishing collaborative links between existing researchers in the School of Computing and the Departments of Biomedical & Molecular Sciences and Pathology & Molecular Medicine, as well as scholars in other disciplines. Queen’s has excellent undergraduate and graduate programs and the chairholder will have abundant opportunities to participate in education through teaching, training and supervision. Salary is commensurate with qualifications and experience.

### Application Process

The University invites applications from all qualified individuals. Queen’s is committed to employment equity and diversity in the workplace and welcomes applications from women, visible minorities, Aboriginal peoples, persons with disabilities, and LGBTQ persons. All qualified candidates are encouraged to apply; however, in accordance with Canadian Immigration requirements, Canadian citizens and Permanent Residents of Canada will be given priority.

To comply with Federal laws, the University is obliged to gather statistical information about how many applicants for each job vacancy are Canadian citizens / permanent residents of Canada. Applicants need not identify their country of origin or citizenship, however, all applications must include one of the following statements: “I am a Canadian citizen / permanent resident of Canada”; OR, “I am not a Canadian citizen / permanent resident of Canada”. Applications that do not include this information will be deemed incomplete.

A complete application consists of: (i) a cover letter (including one of the two statements regarding Canadian citizenship / permanent resident status specified in the previous paragraph), (ii) a full and current curriculum vitae (including a list of publications, awards and grants received), and (iii) a summary of the proposed plan of research. Please send your application electronically to Dr. Roger Deeley, Chair of the search committee (c/o Ms. Barbara Latimer: [bal@queensu.ca](mailto:bal@queensu.ca)).

The University will provide support in its recruitment processes to applicants with disabilities, including accommodation that takes into account an applicant’s accessibility needs. If you require accommodation during the interview process, please contact Ms. Barbara Latimer: [bal@queensu.ca](mailto:bal@queensu.ca).

Academic staff at Queen’s are governed by a Collective Agreement between the Queen’s University Faculty Association (QUFA) and the University, which is posted at:





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

## **RBGKew PlantFungalTreeOfLife**

Three positions open The Plant and Fungal Trees of Life project (PAFTOL) Royal Botanic Gardens, Kew

1. Senior Researcher (PAFTOL Sampling & Project Co-ordination)
2. Senior Researcher (PAFTOL Phylogenomics)
3. Lead Developer-Bioinformatician (PAFTOL)

Kew is a global resource for plant and fungal knowledge. We are seeking talented, creative individuals with outstanding track records to help us build the Plant and Fungal Trees of Life, a major piece of global science infrastructure that is central to RBG Kew's Science Strategy 2015-2020. This is a unique opportunity to be part of a team addressing a critical challenge in the life sciences. Are you up to the task? If so, read on to find out more.

The project: There are few grander challenges in science than the tree of life - uncovering the complete evolutionary history linking all life on Earth. As part of RBG Kew's Science Strategy 2015-2020, we are initiating a five-year multimillion-pound project, the Plant and Fungal Trees of Life (or PAFTOL, for short), to complete the tree of life for all genera of plants and fungi, drawing on our outstanding collections, our broad collaborative networks and the latest high-throughput sequencing technologies. This ambitious project will create a unifying framework for comparative plant and fungal research and takes us a step closer to building the tree of life for all known species. We will generate high impact findings publishable in top science journals, but we want the results to reach beyond the science community. To achieve this we will build innovative big-data and visualization tools accessible to a scientist or a school child. PAFTOL has recently secured generous funding from the Calleva and Sackler Foundations, and we are now ready to get the work underway. This is a truly exciting time to join Kew and become an integral part of a high-profile, cutting edge global endeavour.

The team: At Kew, you'll be joining a truly multidisciplinary team comprising experts from across a range of fields including systematics, evolution, genomics, bioin-

formatics, spatial analysis, data architecture and software development. At this time, we are recruiting into three senior positions in phylogenomics, sampling/co-ordination and software development/bioinformatics. We expect to hire three further support positions later this year. You'll work alongside a highly supportive team of Kew staff who have actively developed the PAFTOL concept.

The roles: We are currently recruiting into the following three roles:

Senior Researcher (PAFTOL Sampling & Project Co-ordination) <https://careers.kew.org/-vacancy/senior-researcher-paftol-sampling-project-coordination-254748.html> Senior Researcher (PAFTOL Phylogenomics) <https://careers.kew.org/-vacancy/senior-researcher-paftol-phylogenomics-254749.html> Lead Developer-Bioinformatician (PAFTOL) <https://careers.kew.org/vacancy/lead-developerbioinformatician-paftol-254750.html> For further info: <http://science.kew.org/strategic-output-plant-and-fungal-trees-life> <http://www.kew.org/kew-science/kews-science-strategy> Closing date: 15 March 2016 Interview dates: 21-23 March 2016

W.Baker@kew.org

## **SanDiegoZoo ConservationResearch**

The Genetics Division of the San Diego Zoo Institute for Conservation Research has two open positions for Research Associates to work in our cell culture laboratory and assist with development and utilization of our Frozen Zoo. This collection includes approximately 10,000 accessions of early passage diploid fibroblast cultures that represent a crucial resource for research and recovery of endangered species.

We are seeking applicants with excellent skills in sterile technique and experience in cell culture methodologies, including establishing and maintaining primary cell cultures. One position will also involve assisting with production of induced pluripotent stem cells to support programs in genetic rescue of endangered species.

A job description and application instructions can be found at: <https://www.hrapply.com/sandiegozoo/-Setup.app> Applicants will be selected for interviews from the submissions through this site.

Applicants should also send a letter of interest and a CV to [kbade@sandiegozoo.org](mailto:kbade@sandiegozoo.org) attn: Genetics Division

## Positions

We are excited to be offering these challenging positions that will continue our record of accomplishments in banking viable cell cultures from over 1000 vertebrate taxa to date and take our conservation efforts into new directions.

Thank you for sharing this information with your colleagues and any individuals potentially interested in applying.

Oliver Ryder

“Ryder, Oliver” <oryder@ucsd.edu>

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## SUNY OswegoNY SystematicsBotany

### ASSISTANT PROFESSOR-BOTANIST

The Department of Biological Sciences at the State University of New York at Oswego invites applications for a full-time tenure track botanist at the Assistant Professor level with preference given to candidates specializing in plant structure or development and in advanced microscopy.

We hope to identify candidates who can use our microscopy resources on campus (confocal and SEM) to investigate aspects of plant structure, anatomy, and development to elucidate evolutionary relationships across plant lineages. A focus of this position would be teaching Plant Kingdom, an evolutionary survey of plant lineages. In addition, the candidate would teach one or more sections of a senior level, capstone Evolution course. This course is a required seminar that relies heavily on peer-reviewed literature to discuss historical and current investigations into evolutionary mechanisms and processes.

DATE POSTED: February 18, 2016

REVIEW DATE: Review of applications will begin March 18, 2016 and will continue until the position is filled.

The Department of Biological Sciences offers B.A. and B.S. degrees in Biology and Zoology to approximately 550 majors. Faculty and students have access to Rice Creek, a 400+ acre field station with a new building of labs and classrooms; the Molecular Biology and Biochemistry Center; the Mass Spectrometry and Proteomics Center; The Environmental Research Center;

and microscopy, greenhouse, and live animal facilities. Classes in our new building, the Richard S. Shineman Center for Science, Engineering, and Innovation, started in Fall 2013. Links to more information can be found at: [www.oswego.edu/biology](http://www.oswego.edu/biology). SALARY: Commensurate with qualifications and experience.

DATE OF APPOINTMENT: August 2016.

DESCRIPTION OF RESPONSIBILITIES: Candidates will be expected to teach Plant Kingdom, Evolution, and to offer courses in area of specialty, and contribute additionally to the core curriculum. Research suitable for undergraduate student involvement and service to the department and university are expected.

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.

REQUIRED QUALIFICATIONS: Ph.D. by the time of appointment. Commitment to excellence in teaching and providing meaningful learning experiences to students from diverse backgrounds is required.

PREFERRED QUALIFICATIONS: Post-doctoral research experience, teaching experience, and/or grantsmanship.

Preference will be given to candidates specializing in plant structure or development and in advanced microscopy (i.e., CLSM and/or SEM).

QUESTIONS: Inquiries can be directed to the Chair of the Search Committee, Dr. C. Eric Hellquist, [eric.hellquist@oswego.edu](mailto:eric.hellquist@oswego.edu)

APPLICATIONS: Submit a cover letter, curriculum vitae, a statement of teaching philosophy/interests, a statement of research interests, unofficial copies of academic transcripts (official transcripts will be required prior to appointment), and names and email addresses of three references electronically at:

<https://oswego.interviewexchange.com/-jobofferdetails.jsp?JOBID=3D68788> C. Eric Hellquist  
Associate Professor Department of Biological Sciences  
324 Shineman State University of New York Oswego  
7060 State Route 104 Oswego NY 13126 315-312-2523

Spring 2016 office hours: Monday 9:00-10:30, Tuesday 11:00-12:30, and by appointment

“eric.hellquist@oswego.edu”  
<[eric.hellquist@oswego.edu](mailto:eric.hellquist@oswego.edu)>

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**UCambridge**  
**CharlesDarwinProfessorship**  
**EvoDevo**

Dear Colleagues

The University of Cambridge has just opened a search for the Charles Darwin Professorship of Animal Embryology, a prestigious endowed chair.

The Chair is endowed by the Bles Fund, which states that it is for “the promotion and furtherance of biology as a pure science”. Previous holders of the chair have done work of fundamental significance in embryology and developmental biology. The most recent holder of the chair was Professor Ron Laskey.

The prime criterion for selection will be “an outstanding research record of international stature in some aspect of animal embryology”. Clearly this could include evolutionary developmental biology. The chair may be held in any Department or Institute of the School of Biology in Cambridge.

The advertisement has just appeared online on the Cambridge University website <http://www.jobs.cam.ac.uk/job/9519/>, and will shortly appear in Nature and Science. The link for the further particulars is <http://www.admin.cam.ac.uk/offices/academic/secretary/professorships/index.html> The deadline for applications is March 17th.

Please dont hesitate to contact me if you have any questions

Chris Jiggins

Professor of Evolutionary Biology Department of Zoology University of Cambridge Tel: (+44)(0)1223 769021 Mob: (+44)(0) 7549-524-481 <http://www.heliconius.org/> [http://heliconius.zoo.cam.ac.uk/@mel\\_rosina](http://heliconius.zoo.cam.ac.uk/@mel_rosina)

Fellow of St John's College, Cambridge, UK. CB2 1TP

Chris Jiggins <c.jiggins@zoo.cam.ac.uk>

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**UCorua Spain 9mnth Bioinformatics**

UCoruña (Spain) NGS - Bioinformatics

Bioinformatic (Next Generation Sequencing) position is available at the University of A Coruña, Spain. The job consist on the implementation and use of the appropriate software for the de novo transcriptome assembly, annotation and analysis. Candidates should have a strong NGS background, particularly with RNA-seq data of non-model organisms.

APPLICATION: Please send a detailed C.V. (including a list of publications, awards and grants received), to the following e-mail address: [sergio.roiloa@udc.es](mailto:sergio.roiloa@udc.es). Questions and requests for more information should be directed at the same address. The deadline for applications is February 29th, 2016. The position will be for 9 months (starting date approx.: 1st April 2016).

(more information: [https://sede.udc.gal/services/-electronic\\_board/EXP2016/000116](https://sede.udc.gal/services/-electronic_board/EXP2016/000116))

Dr. Sergio R. Roiloa Assistant Professor Unit of Ecology - Faculty of Science University of A Coruña 15071 A Coruña Spain <http://ciencias.udc.es/profesorado-bave/-bioloxia-animal-bioloxia-vexeta1-e-ecoloxia/rodriguez-roiloa-sergio> Scholar profile: <http://scholar.google.com/citations?user=89yOVjkAAAAJ&hl=en> SERGIO ROILoa <[sergio.roiloa@udc.es](mailto:sergio.roiloa@udc.es)>

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**UHelsinki Genomics**

Professor/Associate Professor/Assistant Professor in Genetics, with speciality in genomics

The position is shared between the Department of Biosciences and the Institute of Biotechnology and may be filled as assistant professor, associate professor or professor, depending on the candidates' merits and career stage. Duties of the professor/associate professor/assistant professor include conducting internationally competitive research on any aspect of genomics. She/he should also have appropriate competence in overlapping areas of genetics, bioinformatics and/or other relevant fields. The professor/associate professor/assistant professor will play a central role as an

educator, spearheading masters- level training in genomics, organized jointly between the Department of Biosciences and the Institute of Biotechnology and will also participate in doctoral education via appropriate graduate programmes. In addition, he/she will facilitate public understanding and applications of genomic knowledge.

The professor/associate professor/assistant professor shall carry out and supervise scientific work, provide education based on it, follow developments in research, and participate in societal interaction and international cooperation in his or her field. According to the Regulations of the University of Helsinki, an appointee to a professorship shall hold a doctoral degree and have top-level scholarly qualifications, including the supervision of scientific research. The appointee shall have the ability to provide top-level teaching based on research, as well as to supervise theses and dissertations. The appointee shall also have documentation of international cooperation in the research field that he/she represents. Furthermore, the position also calls for academic leadership skills.

An appointee to the position of assistant/associate professor in the tenure track system shall hold a doctoral degree, have the ability to conduct independent scholarly work and have the teaching skills necessary for the position. In addition, applicants for assistant professorships shall demonstrate their ability and motivation for an academic career through publications and other means.

When assessing the qualifications of the applicants, attention shall be paid to scientific publications and other research results of scientific value, teaching experience and pedagogical training, the ability to produce learning material, other teaching merits, and, if necessary, a teaching demonstration as well as participation in doctoral education. Account shall also be taken of the applicant's activity in the scientific community, success in obtaining external research funding, international research experience and international elected positions as well as leadership and interaction skills.

To successfully attend to the duties of the position, appointees must have good English skills. A knowledge of Finnish and or Swedish may also be useful for undergraduate instruction, but is not essential.

The position overview is available on the Faculty website <http://www.helsinki.fi/bio/faculty/administration/open/index.html> The salary for the position will be based on the demands level chart for teaching and research personnel in the salary system of Finnish universities. The demands level for professors is 8-10 and for assistant/associate professors 7. In addition, the appointee

will be paid a salary component based on personal performance. The salary for a professor is 5,000-8,000 euros per month and for an assistant/associate professor 4,200-5,000, depending on the appointee's qualifications and experience. The closing date for applications is April 10, 2016.

Please submit your application using the University of Helsinki Recruitment System via the Apply link. Applicants who are employees of the University of Helsinki are requested to leave their application via the SAP HR portal. The English-language application must be accompanied by: - a CV - a list of publications - a brief report of the following qualifications: research and scientific activities, research plan, description of teaching qualifications, participation in administrative duties - a report on other activities of which the applicant wishes to inform the Faculty

or, alternatively, an academic portfolio containing the above documents (see instructions at [www.helsinki.fi/bio/faculty/materials/portfolio-ohjeet.eng.pdf](http://www.helsinki.fi/bio/faculty/materials/portfolio-ohjeet.eng.pdf)) The attachments are asked to be submitted as a single PDF file.

Candidates should be prepared to submit ten publications and/or manuscripts approved for publication of their choosing to expert assessors after the closing of the application period, if so requested by the Faculty. The publications are submitted as PDF files. More information

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## UMassachusetts Lowell Bioinformatics

Tenure-Track Faculty Position in Bioinformatics at the University of Massachusetts Lowell

The University of Massachusetts Lowell Department of Biological Sciences invites applications to fill a full-time tenure-track faculty position, rank negotiable, to start September 2016. We seek an individual experienced in bioinformatics and quantitative biology, who would apply computational, mathematical and other quantitative tools to analyze complex, high-throughput data.

Examples would include the development of new computational tools to analyze whole genomes or transcriptomes, model intra- and extracellular signaling networks, and to model systems-level processes within populations and ecosystems. This area would leverage our campus strengths in computer science to develop and apply new tools to understanding living processes. In addition to the broad range of research interests within the Biological Sciences Department, UMass Lowell has a diverse group of science and engineering faculty who use multiple model systems to evaluate new technologies (e.g. nanomedicine, biomaterials, robotics and tissue engineering), therefore candidates interested in establishing collaborations with faculty in these fields are strongly encouraged to apply. The successful candidate will be expected to establish a vigorous, externally funded research program, and contribute to the departments teaching mission. Teaching responsibilities may include the development of an undergraduate Bioinformatics course, in addition to upper-level courses in areas of interest to the candidate.

The University of Massachusetts Lowell is committed to increasing diversity in its faculty, staff, and student populations, as well as curriculum and support programs, while promoting an inclusive environment. We seek candidates who can contribute to that goal and encourage you to apply and to identify your strengths in this area.

To be considered for this position, please submit all required application materials to the UMass Lowell Human Resources website: <https://jobs.uml.edu/-applicants/jsp/shared/frameset/Frameset.jsp?time=3D1456428954304> Review of applications will begin immediately and continue until the position is filled. However, the position may close once an adequate number of qualified applications are received.

“Garb, Jessica” <Jessica\_Garb@uml.edu>

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## UNAB Chile Bioinformatics

Faculty Position in Computational Biology with Emphasis on Metabolomics and Proteomics

The recently established Center for Bioinformatics and Integrative Biology (CBIB) at Universidad Andres Bello (UNAB), Santiago Chile seeks a faculty member to establish externally funded, internationally recognized, and interdisciplinary research programs in bioinformatics and/or computational biology.

The CBIB hosts a group of six young faculty members focused on basic science and its applications. Current areas of research include nanotechnology, microbial genomics, metagenomics, extremophile biology, biotechnology, protein dynamics and simulation, and protein engineering and metabolism. The CBIB has strong bonds with national and international collaborations including UC Davis Chile, US Air Force, and universities throughout Europe and the USA.

There is one open tenure-track faculty position at the assistant professor academic level, aimed at complementing our current expertise. We seek applicants concentrating in the areas of genomics and systems biology, particularly with expertise in metabolomics and proteomics (molecular biology experience is a plus). Successful applicants will join the CBIB team and are expected to perform research and teaching duties. Applicants must have a PhD in Bioinformatics, Computational Biology, Computer Science, Mathematics, Genomics, or related discipline, with postdoctoral research experience, evidence of success in obtaining extramural funding, and a solid publication track record.

Application Procedure: Applicants should submit an electronic application, upload a cover letter emphasizing specific qualifications, curriculum vitae, a description of research interests, and names and contact information of 3 references at: [eduardo.castro@unab.cl](mailto:eduardo.castro@unab.cl)

Review of applications will begin on March 25, 2016 and will continue until positions are filled. Only complete applications will be considered. For further information about the Center for Bioinformatics and Integrative Biology, please visit [www.cbib.cl](http://www.cbib.cl). For questions relating to this opportunity, please contact Eduardo Castro-Nallar, Principal Investigator, Center for Bioinformatics and Integrative Biology, Universidad Andres Bello at [eduardo.castro@unab.cl](mailto:eduardo.castro@unab.cl)



Eduardo Castro-Nallar, PhD Center for Bioinformatics and Integrative Biology Universidad Andrés Bello República 239, 8370146, Santiago [www.castrolab.org](http://www.castrolab.org) +56 2 2770 3520 +56 9 5644 2354

castronallar@gmail.com

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## UPittsburgh SummerFellowship EvolutionaryEcol DeadlineExtended

PLE Early Career Fellowship

Pymatuning Laboratory of Ecology

Summer 2016

The University of Pittsburgh's Pymatuning Laboratory of Ecology (PLE) is pleased to offer a summer research fellowship of \$10,000 plus up to three months of station fees and residency costs for the primary investigator (PI). PLE is a vibrant research and education facility located on Lake Pymatuning in Northwest Pennsylvania. PLE's research facilities are spread across 350 acres and include access to a variety of aquatic and terrestrial ecosystems. Its 10,000+ square feet of laboratory facilities include a field laboratory adjacent to an open field that can be used for large-scale replicated experiments, a modern molecular laboratory, and facilities for animal, plant and aquatic studies. While the station is open to hosting projects in a variety of disciplines, past work has largely focused on ecology and evolutionary biology.

This opportunity is open to researchers holding PhD degrees in any science discipline that can benefit from PLE's resources (<http://www.biology.pitt.edu/facilities/pymatuning>). The purpose of the fellowship is to permit researchers to explore new projects or collect preliminary data. Fellowship funds can be used at the PI's discretion to facilitate the research but not for compensation. Preference will be given to individuals and projects with the potential to develop into long-term research activities at PLE. We especially encourage applications from individuals in the postdoctoral or early faculty phases of their careers but researchers holding PhD degrees at all stages of their careers are encouraged to apply.

For more information about the fellowship program or research opportunities at PLE, please contact the Director, Dr. Cori Richards-Zawacki ( [cori.zawacki@pitt.edu](mailto:cori.zawacki@pitt.edu)).

Applicants should submit a single .pdf file including their CV, a 2-3 page proposal outlining the proposed research,

a budget detailing how the fellowship funds will be spent, and planned dates of residence to [cori.zawacki@pitt.edu](mailto:cori.zawacki@pitt.edu), placing the words "PLE Early Career Fellowship" in the subject line of the email. Review of proposals will begin \*February 15, 2015\*.

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Corinne L. Richards Zawacki, Ph.D. [cori.zawacki@pitt.edu](mailto:cori.zawacki@pitt.edu) Associate Professor, Department of Biological Sciences and Director, Pymatuning Laboratory of Ecology University of Pittsburgh

"At night I went out into the dark and saw a glimmering star and heard a frog and nature seemed to say, well do not these suffice?" - Ralph Waldo Emerson

Cori Zawacki <[cori.zawacki@pitt.edu](mailto:cori.zawacki@pitt.edu)>

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## UppsalaU BioinformaticsEvolutionaryGenetics

Position in Bioinformatics / Evolutionary Genetics, Uppsala University

A bioinformatics position is available in the research group of Jochen Wolf at the Evolutionary Biology Centre in Uppsala, Sweden. The position is initially limited to 1-year and after evaluation can be extended.

The research group environment. We take an integrative approach to the study of evolutionary processes applying a large range of methodology ranging from field work to population genetic modeling of large genome-scale data sets to functional characterization at the single cell level. One of the main questions in the group is to understand the micro-evolutionary processes and genetic mechanisms underlying species divergence. In addition, we engage in comparative approaches to study genome evolution across larger timescales. Empirical systems currently include birds (swallows and corvids), marine mammals (pinnipeds and killer whales), the European hemiclinal water frog system, and experimental evolution in fission yeast. Find below a selection of recent publications illustrating recent research activities or consult the current lab website (<http://www.ieg.uu.se/evolutionary-biology/wolf/>).

The position. The successful applicant will be responsible for management of large transcriptome and genome sequencing data sets, help with administration and compilation of source code, and for the most part, will engage actively in ongoing research projects. The applicant is

expected to be familiar with UNIX environments and has experience in standard bioinformatic approaches using high throughput DNA and RNA sequencing data from platforms such as Illumina or Pacific Biosciences. Common tasks will involve data management, genome assembly and annotation (Birds ca. 1.2 Gb, marine mammals: ca. 3Gb), multiple sequence alignments, short-read mapping and genotyping. Proficiency in relevant programming languages (e.g. awk, bash, Perl, Python, C) is naturally assumed. A background in population genomics or comparative genomics is a clear asset. Depending on the applicant's background there will be some autonomy in that he or she can develop own research questions or participate in teaching activities.

The environment. The Evolutionary Biology Centre (<http://www.abc.uu.se/>) is one of the world's leading research institutions in evolutionary biology. It is part of Uppsala University which is considered one of Europe's leading universities in the subject of biology bridging a broad variety of disciplines. The scientific environment with numerous seminars, journal clubs and social activities offer excellent possibilities for contacts and collaborations. Our lab is part of the Department of Evolutionary Biology (<http://www.ieg.uu.se/evolutionary-biology/?languageId=1/>), an active environment addressing fundamental evolutionary questions with a wide range of different approaches. As a member of the Science for Life Laboratory (<http://www.scilifelab.se/>) we make extensive use of high performance computing resources (<https://www.uppmax.uu.se/uppnex>) and extended bioinformatic infrastructure (<http://www.scilifelab.se/platforms/bioinformatics/>). We also actively interact with research groups of the nearby BioMedicalCentre (<http://www.imbim.uu.se/Research>). The lab is situated in the student town of Uppsala that offers rich opportunities in cultural and outdoor activities. Sweden's capital Stockholm is less than an hour's train ride away.

By the end of 2016 the research group will transition to the Department of Evolutionary Biology at the Ludwig-Maximilians-Universität (LMU) in Munich, Germany. Munich University is consistently ranked among the top Universities worldwide, in particular the life science branch with its newly inaugurated campus offering excellent technical facilities and many interaction possibilities including the gene center, several Max-Planck-Institutes and the Helmholtz Centre (<http://www.campusmartinsried.de/en/336-2/#>). With the highest concentration of supercomputing in Germany the Leibniz Supercomputing Centre and its local partners provide access to state-of-the art computing facilities (<https://www.lrz.de/english/>). Munich is Bavaria's capital, a vibrant, yet relaxed city with many traditions

still alive considered by many to have a high quality of living

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## URochester Evolutionary Genomics

Faculty Position in Ecology & Evolutionary Biology  
University of Rochester

The Department of Biology at the University of Rochester (<http://www.rochester.edu/College/BIO/-index>) invites applications for an open rank faculty position in ecology and evolutionary biology. We are seeking candidates working in evolutionary and ecological genomics, broadly defined, who have a strong computational component to their research.

The successful candidate will contribute to the Departments existing strengths in evolutionary genetics and genomics (<http://www.rochester.edu/-college/BIO/people/faculty/ecology-evolutionary-biology/index.html>) and benefit from state of the art infrastructure and core facilities at the University, as well as the newly established Goergen Institute for Data Science (<http://www.rochester.edu/data-science/>).

Candidates with a strong record of accomplishment should upload application materials to our online application system (<https://www.rochester.edu/faculty-recruiting/login>). Complete applications include: a CV; a statement of research interests/plans; pdfs of three publications; and a statement of teaching experiences and interests. We anticipate the individual will be active in both research and teaching in computational biology. Instructions for supplying three letters of recommendation are provided on the application website. Review of applications will begin March 9 and continue until the position is filled.

The University of Rochester is an Equal Opportunity Employer, has a strong commitment to diversity, and actively encourages applications from candidates from groups underrepresented in higher education.

EOE Minorities / Females / Protected Veterans / Disabled

jbrisso3@UR.Rochester.edu

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## UStAndrews Bioinformatics

Dear EvolDir Community:

The School of Biology at the University of St Andrews is inviting applications to fill a Lectureship or Readership position. We seek to appoint someone with interests in bioinformatics, evolutionary 'omics or quantitative biology, broadly speaking. Details and contact information are below, and informal enquiries are welcomed.

Kind regards, Nathan Bailey

Lectureship or Readership in Bioinformatics – University of St Andrews, School of Biology

**Appointment:** The School of Biology at the University of St Andrews seeks to appoint a Lecturer or Reader (scale dependent on experience) whose research and teaching interests fall within the broad area of bioinformatics, evolutionary 'omics and quantitative biology.

**Role:** We seek an individual who will cultivate a funded research programme, develop collaborations with other research groups in St Andrews and deliver excellent science. They will play a leading role in the St Andrews Bioinformatics Unit and the Institute for Data Intensive Research, both of which are cross-school units dedicated to developing modern computational resources for analysing large NGS and other 'big data' datasets. Research collaborations with groups in other schools and centres at the University of St Andrews, the James Hutten Institute and beyond present excellent opportunities for developing integrative research programmes.

The appointee will also play a principal role in developing and teaching bioinformatics, evolutionary genomics and similar coursework in quantitative biology at the undergraduate and masters level. Quantitative skills and informatics are increasingly relevant in modern biological research, and the appointee should have the capacity to enhance our teaching profile in these areas, as well as mentoring postgraduate students at the Masters and PhD levels.

**Qualifications:** Applicants must have a PhD in a relevant field and be able to demonstrate evidence of high-quality publications and appropriate teaching experience. For the Lecturer post, evidence of an independent research programme and external funding success are desirable; for the Reader post they are essential. The School of Biology at St Andrews has recently earned an Athena SWAN Bronze award and is committed to equality of

opportunity.

Informal enquiries can be made to Prof Malcolm White (mfw2@st-andrews.ac.uk), tel: +44(0) 1334 463432) or Dr Nathan Bailey (nwb3@st-andrews.ac.uk, tel: +44(0) 1334 463367). Applications are particularly welcome from women who are under-represented in Science posts at the University. You can find out more about Equality and Diversity at <https://www.st-andrews.ac.uk/hr.edi/>. The University of St Andrews is committed to promoting equality of opportunity for all, which is further demonstrated through its working on the Gender and Race Equality Charters and being awarded the Athena SWAN award for women in science, HR Excellence in Research Award and the LGBT Charter; <http://www.st-andrews.ac.uk/hr.edi/diversityawards/>. Please quote ref: AC5751MR

Closing Date: 22 March 2016

Link: <https://www.vacancies.st-andrews.ac.uk/ViewVacancy.aspx?enc=mEgrBL4XQK0+ld8aNkwYmH6Ecv/iBYfQg2TdCBgk3LJo69yXVOu1VwMTzsFLEtUsXwrY9671VH6R2L9VeBxnJlecyDjyfq0MB985kjRwj33IQk9RDSmutVLBcFifLTyNhI6WnRXtQdNQzRzvTORlyw> School of Biology Salary: Lecturer Â£38,896 - Â£47,801 Reader Â£49,230 - Â£55,389 per annum Start: As soon as possible

Nathan Bailey <nwb3@st-andrews.ac.uk>

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## UTexas Tyler InsectEvolution

### POSITION ANNOUNCEMENT

ASSISTANT PROFESSOR, INSECT EVOLUTIONARY ECOLOGY DEPARTMENT OF BIOLOGY THE UNIVERSITY OF TEXAS AT TYLER

The Position: The Department of Biology at The University of Texas in Tyler is seeking to fill a 9-month, tenure-track position in insect evolutionary ecology. Any area of evolutionary ecology will be considered but preference will be given to candidates using integrative approaches and cutting-edge technologies, and addressing broad questions in evolution. The incumbent is required to establish a strong, extramurally funded research program in his/her area of expertise. S/he is also expected to have a strong commitment to undergraduate and graduate education and mentoring. Participation in departmental, college, and university committees and outreach programs is expected. Preference will be given to candidates with a demonstrated record of collabora-

tive research.

Qualifications: Ph.D. in a relevant field (entomology, evolution, ecology, population genetics, etc.) with a minimum of two years of postdoctoral experience. (ii) Demonstrated research creativity, productivity, and grantsmanship. (iii) Ability to develop a strong, extramurally-funded research program. (iv) Demonstrated record of collaborative research (v) Evidence of effective teaching and other communication skills. (vi) Teaching experience at undergraduate or graduate levels is highly desirable.

Available resources: The Department of Biology offers a stimulating intellectual environment and has an excellent reputation in research and teaching. Twelve faculty members undertake research in diverse sub-disciplines, including genomics, bioinformatics, population genetics, evolution, ecology, neurobiology, microbiology, molecular biology, and physiology. Research seminars by invited speakers are held weekly. The multidisciplinary Center for Environment, Biodiversity, and Conservation is housed in the Department of Biology. A new expansion with state-of-the-art research and teaching labs has just been completed along with renovation of all existing teaching labs. Three large and sophisticated walk-in environmental chambers are available for research as is a confocal microscope. A computer lab connects UT Tyler to the Texas Advanced Computer Center via a 10 Gb internet connection. The School of Pharmacy opened its doors in August 2015. Shared equipment and facilities, including a brand new vivarium, are available at UT Tylers sister institution, the University of Texas Health Northeast. For additional information, please visit [www.uttyler.edu/biology](http://www.uttyler.edu/biology). Location: Tyler is located 90 miles east of Dallas in the scenic Piney Woods area of East Texas. Tyler is the cultural center of East Texas, a region with over one million people, and boasts many amenities such as museums, a planetarium, a ballet, a symphony orchestra, and a renowned performing arts center. One of the 14 campuses of the UT System, UT Tyler offers excellence in teaching, research, artistic performance and community service. More than 80 undergraduate and graduate degrees are available at UT Tyler, which has an enrollment of more than 8,000 high-ability students at its campuses in Tyler, Longview, and Palestine.

Applications: Please include (as a single PDF file) a) cover letter; b) detailed curriculum vitae; c) statement of research interests and professional goals, d) statement of teaching interests and philosophy; e) reprints of 3 relevant publications and email to. Dr. John Placyk, Chair, Evolutionary Ecology Search Committee, Department of Biology, The University of Texas at Tyler, 3900 University Blvd., Tyler, TX 75799. E-mail: jpla-

cyk@uttyler.edu. Additionally, please arrange to have 3 reference letters sent to the same address.

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

The University of Texas is an Affirmative Action/Equal Opportunity Employer. Women and minorities are strongly encouraged to apply. The successful applicant must be able to demonstrate eligibility to legally work in the United States. This position is security-sensitive and subject to Texas Education Code Section 51.215 which authorizes employer to obtain criminal history record information. The position is contingent upon availability of funding.

John S. Placyk, Jr., Ph.D., Assistant Professor Department of Biology University of Texas at Tyler 3900 University Blvd. Tyler, Texas 75799 Office: 903-566-7147 Fax: 903-566-7189

[http://www.uttyler.edu/biology/biology\\_research/-placyk/index.php](http://www.uttyler.edu/biology/biology_research/-placyk/index.php)

“A well-known scientist (some say it was Bertrand Russell) once gave a public lecture on astronomy. He described how the earth orbits around the sun and how the sun, in turn, orbits around the center of a vast collection of stars called our galaxy. At the end of the lecture a little

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

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## VirginiaTechU PollinatorBiodiversity

Virginia Tech is looking for an Assistant Professor in Pollinator Biology & Ecology <http://listings.jobs.vt.edu/-postings/63916> Virginia Techs Department of Entomology invites applications for a tenure-track position at the level of Assistant Professor in the area of Pollinator Biology & Ecology starting in the Fall 2016 semester. This is a nine-month, 70% research and 30% teaching appointment based on campus at Virginia Tech, a land-grant university in the scenic New River Valley of Virginia.

The successful candidate will be expected to develop an extramurally funded research program focused on



pollinating insects with emphasis on regional and national concerns related to pollinator declines, species biodiversity losses, ecosystem services, and/or conservation biology. Knowledge of apicultural practices is desirable but not required. Preference will be given to individuals with post-doctoral experience and a demonstrated ability to secure extramural funding and publish in high quality, peer-reviewed journals. The incumbent is expected to teach courses at the undergraduate and graduate-level, contribute to innovative curricula in entomology and related disciplines, and mentor undergraduate and graduate students. The incumbent will also support the mission of the land-grant university by participating in outreach and engaging local, state, and regional stakeholders. The successful candidate will have access to existing honey bee colonies, apiculture facilities, and land for field research, including diverse native habitats, as well as agronomic, vegetable, and orchard field plots.

Applicants are required to hold a Ph.D. in entomology, zoology, or a closely related field. Applicants with experience in pollinator biology including, but not limited to, the ecology, physiology, molecular biology, genetics, pathology, or behavior of honey bees and/or other pollinating insects are strongly encouraged to apply.

Paul Marek <pmarek@vt.edu>

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### 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 state-

ment 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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## Other

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### Alberta Internship GroundSquirrel

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

We are looking for 3 volunteers to assist with fieldwork for the period of April 9 to Aug 31, 2016 and an additional 3 volunteers for the period of May 1 to Aug 31, 2016. The project investigates the ecology of Columbian ground squirrels. As a member of the study, assistants will be involved with monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals. Fieldwork will involve live-trapping

and handling of animals, radio-telemetry, behavioural observation and assistance with the measurement of physiological (metabolism) traits on free-ranging animals. This is an excellent opportunity to gain experience working with a collaborative research team on a long-term study of a wild mammal.

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

Food and accommodation are provided. Volunteers are required to provide for their own travel to Saskatoon, Saskatchewan. Travel between the field station and Saskatoon provided. Training will be provided and no experience is necessary, but candidates should have an interest in a number of the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and animal behaviour. Periods of time will be spent camping and, as such, successful applicants need to enjoy the outdoors, be up-beat, positive, responsible and work well as a member of a team.

If you wish to apply for one of these posts then please send a CV with a cover letter and contact details for three references (with e-mail addresses), by email to Jeff Lane (contact info below), by Feb 28, 2016.

Contact: Dr. Jeff Lane Department of Biology University of Saskatchewan Email: [jeffrey.lane@usask.ca](mailto:jeffrey.lane@usask.ca) Web: [www.lanelab.ca](http://www.lanelab.ca) Lane, Jeffrey“ <[jeffrey.lane@usask.ca](mailto:jeffrey.lane@usask.ca)>

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### ConservationGeneticsCourse Scholarships

Scholarships Available for Recent Advances in Conservation Genetics Course (ConGen2016) lake Balaton, May30-June10, 2016

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 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.

Scholarship will include full (or half) tuition for the course, transportation to and from Budapest International Airport, lodging and food at the Balaton Limnological Institute. For the details see [www.congen2016.com](http://www.congen2016.com). 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.

The scholarship will not be considered if you have not already submitted your registration. If you haven't submitted your registration, please go to <http://congen2016.com/home/registration/> Dr. Taras K Oleksyk Associate Professor of Biology Director of the Caribbean Genome Center University of Puerto Rico at Mayaguez Mayaguez, PR 00680 [Dna.lab@upr.edu](mailto:Dna.lab@upr.edu)

Taras K Oleksyk <[taras.oleksyk@upr.edu](mailto:taras.oleksyk@upr.edu)>

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### 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](mailto:jessica.gurevitch@stonybrook.edu) AND Jesse Hollister [jesse.hollister@stonybrook.edu](mailto: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](mailto:jessica.gurevitch@stonybrook.edu)>

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## Evolution Phasic Tonic Receptors

Dear Colleagues:

Could someone recommend me an introductory paper on the evolution of tonic vs phasic receptors? I have been looking since yesterday early afternoon and have not found appropriate references. If "yes", please send me the paper (or link) to [blayjorge@gmail.com](mailto:blayjorge@gmail.com)

Gratefully,

Jorge

Jorge A. Santiago-Blay, PhD <http://paleobiology.si.edu/staff/individuals/santiagoblay.cfm>  
"Santiago-Blay, Jorge" <[BLAYJ@si.edu](mailto:BLAYJ@si.edu)>

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## FacultyMentoringNetwork applications

HHMI's BioInteractive (<http://www.hhmi.org/biointeractive>) and the Quantitative Undergraduate Biology Education and Synthesis (QUBES: [qubeshub.org](http://qubeshub.org)) project invite applications for a Faculty Mentoring Network (FMN) focused on adapting quantitative BioInteractive modules for undergraduate introductory biology courses. BioInteractive has a growing collection of quantitative and data based modules on statistics, graphing, and data manipulation, however these were initially designed for high school and AP biology. Participants in this FMN will work together and with the HHMI BioInteractive staff to adapt and implement these modules in their own introductory biology courses.

The Faculty Mentoring Network combines a face to face workshop experience with a mentored, long term community interaction on the QUBES site. The group will begin working at the National Academies Special Topics Summer Institute on Quantitative Biology (<http://qubeshub.org/groups/summer2016>), June 19-24 2016. After the meeting participants will continue to work online with a group of peers and mentors to adapt and implement quantitative modules in their courses during the Fall 2016 semester. This work will take advantage of the QUBESHUB infrastructure and include short online

meetings every other week. Upon completion of the Faculty Mentoring Network participants will post their materials and teaching guidelines on the BioInteractive partner page on QUBES.

Applicants must be teaching introductory biology or an equivalent course in Fall 2016, and be able to attend the Quantitative Biology Summer Institute June 19-24. For more information, visit: <https://qubeshub.org/groups/-hmbiointeractivefmm> Questions? Contact Melissa Csikari (csikarim 'at' hmi 'dot' org) or Kristin Jenkins (kristin.jenkins 'at' bioquest 'dot' org).

Kristin P. Jenkins, PhD Director

BioQUEST Curriculum Consortium bioquest.org (608) 622.9394 POBox 126 Boyds, MD 20874-0126

Kristin Jenkins <kristin.jenkins@bioquest.org>

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### Melbourne VolFieldAssist Mistnetting

We are looking for a volunteer field assistant to help with research on sexual selection and seasonal colour change in superb fairy-wrens. We need an experienced mistnetter, who is organised, respectful of animals and enjoys being outdoors. The work involves mistnetting for superb fairy-wrens (banding, blood samples, photography and spectral measurements) and behavioural observations of free-living birds. Work will be conducted from May-September, in an open woodland approximately 1 hour east of Melbourne CBD. Our field site is in a beautiful location, with many opportunities to see native wildlife, including kangaroos, wallabys and echidnas. The park has many beautiful birds, such as crested shrike-tits, sacred kingfishers, spotted pardalotes and red-browed finches. Food and local travel expenses are compensated. Accommodation may also be provided (to be discussed with the applicant). For more information please contact Alex McQueen: alex.mcqueen@monash.edu

“alexandra.mcqueen@monash.edu”  
<alexandra.mcqueen@monash.edu>

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### NHGR Institute GenomeAnalysisLectures

Dear Colleague:

We are pleased to announce that the National Human Genome Research Institute will once again be presenting its Current Topics in Genome Analysis lecture series.

Given the rapid advances in genomics and bioinformatics that have taken place in the past few years, we feel that an intensive review of the major areas of ongoing genome research would be of great value to students, fellows, and our colleagues. A mixture of NHGRI and outside speakers will present the lectures and, as you will see from the schedule below, we have designed the series to cover the major areas of genomics. The lectures are geared at the level of first-year graduate students, are practical in nature, and are intended for a diverse audience.

The 14 lectures will be held in the Lipsett Amphitheater, NIH Clinical Center (Building 10) on Wednesday mornings from 9:30 am to 11:00 am each Wednesday, beginning on February 17, 2016. For those of you at a distance, archives of all lectures will also be available through the series Web site (<http://genome.gov/-CTGA2016>) on a delayed basis.

A mailing list has been set up for this series, and we ask all participants to subscribe to this list. The series organizers will be using this mailing list to remind everyone of upcoming lectures, as well as to notify participants of any announcements or changes to the lecture schedule. To subscribe to this mailing list, please point your Web browser to:

<https://list.nih.gov/archives/nhgri-ctga2016-l.html>

Click the link marked 'Subscribe or Unsubscribe' and follow the instructions on the subsequent page to subscribe.

This activity has been approved for AMA PRA Category 1 Credits.

We look forward to your participation, and please feel free to get in touch if you have any questions.

Best regards,

Andy Baxevanis and Tyra Wolfsberg

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February 17 Biological Sequence Analysis I Andy Baxe-

vanis, NHGRI

February 24 The Genomic Landscape circa 2016 Eric Green, NHGRI

March 2 Genome-Scale Sequence Analysis Tyra Wolfsberg, NHGRI

March 9 Biological Sequence Analysis II Andy Baxevanis, NHGRI

March 16 Regulatory and Epigenetic Landscapes of Mammalian Genomes Laura Elnitski, NHGRI

March 23 Applications of Genomics to Improve Public Health Colleen McBride, Emory University

March 30 Spring Break (No Lecture)

April 6 Introduction to Population Genetics Lynn Jorde, University of Utah

April 13 Identifying the Genomic Basis of Rare Diseases David Valle, The Johns Hopkins University School of Medicine

April 20 Genomic Approaches to the Study of Complex Genetic Diseases Karen Mohlke, University of North Carolina at Chapel Hill

April 27 Expression Analysis, Functional Enrichment, and Network Inference John Quackenbush, Dana-Farber Cancer Institute

May 4 Pharmacogenomics Howard McLeod, Moffitt Cancer Center

May 11 Genomic Medicine Bruce Korf, University of Alabama at Birmingham

May 18 Genomics of Microbes and Microbiomes Julie Segre, NHGRI

May 25 Next-Generation Sequencing Technologies Elaine Mardis, Washington University in St. Louis

“Baxevanis, Andy (NIH/NHGRI) [E]”  
<andy@mail.nih.gov>

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## NSW Australia VolFieldAssist Birds

\*\*I'm actually not sure this is most appropriate for the job section as it is a volunteer job...\*\*

Seeking Volunteer Field Assistant for Avian Project in NSW, Australia Outback Opportunity Type: Volunteer Closing Date: 31 March, 2016

We are looking for volunteers to assist in an on-

going research project studying the cooperatively breeding chestnut-crowned babbler in the outback in Australia. We have been studying this system since 2004 and information on the system can be found here: [http://biosciences.exeter.ac.uk/staff/index.php?web\\_id=3Dandy\\_russell&tab=research](http://biosciences.exeter.ac.uk/staff/index.php?web_id=3Dandy_russell&tab=research) or [andrealiebl.com](http://andrealiebl.com) (check out the video on this page made by a previous field assistant!) We are hoping to find someone who can start in early July and continue through the end of the breeding season (October/November). We are not able to pay for travel expenses to Australia, but accommodation at a research station (<https://www.fowlersgap.unsw.edu.au/>) will be provided as well as a contribution towards food.

Required: Ability to work both individually and as a team Willingness to work early mornings and long days Relatively fit (there will be a lot of walking on uneven surfaces) Interest in ecology (our interests in ecology span a relatively large niche and we do work in physiology, metabolism, call variation, etc as well)

Desired: Bush experience Technologically inclined 4WD/off road driving experience Knowledge of Australian birds Ringing experience This is a great opportunity to gain fieldwork experience in an amazing location.

If you're interested (or have any questions), please contact Andrea Liebl ([a.l.liebl@exeter.ac.uk](mailto:a.l.liebl@exeter.ac.uk)).

Andrea L. Liebl, PhD Postdoctoral Research Fellow University of Exeter, Cornwall <http://www.andrealiebl.com/> Andrea Liebl <[A.L.Liebl@exeter.ac.uk](mailto:A.L.Liebl@exeter.ac.uk)>

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## Passing RichardLevins

Richard Levins died on January 19, 2016. The following announcement was sent out by his children. There is a remembrance for him on March 6

Dear friends, colleagues, comrades and broader community of Richard Levins,

As some of you know, our father, Dick Levins, died on January 19 after a slow decline related to his congestive heart failure. He spent his last days and nights not in the hospital but at home in his comfortable assisted-living apartment, surrounded by his family and friends. We buried him the next day in Mount Auburn Cemetery.

We will host a memorial event at 1:30pm, on Sunday, March 6 at Harvard's Knafel Center, Radcliffe Yard,



Harvard Square, Cambridge to mourn, celebrate and reflect on his remarkable life and our shared loss. We will gather between 1:30 and 2pm. At 2pm, a few family members and friends will speak, followed by an opportunity for anyone in attendance to share remembrances and tributes. Light refreshments will be served afterwards.

The Knafel Center (the old Radcliffe gym) is an easy walk from the Harvard Square T stop. Although its formal address is 10 Garden St., the Knafel Center is actually on Mason St., mid-way between Garden St. and James St./Phillips Place.

Please feel free to forward this message to others who knew Dick or his work - the mailing list we are using is sure to be incomplete.

Alejandro, Ricardo and Aurora Levins Morales

Steven Orzack <orzack@freshpond.org>

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### PennStateU SummerInternship InsectDiversityEvol

The research team at the Frost Entomological Museum seeks four undergraduate summer interns to assist with projects related to insect biodiversity and evolution. Interns will receive training in fieldwork, curation, biodiversity informatics, specimen collection and preparation, microscopy, diagnostics, and, depending on his/her project: taxonomy, rearing, dissection, GC-MS, transcriptomics, niche modeling, 3D reconstruction, histology, and novel approaches to visualizing insect anatomy. Announcement here: <https://wp.me/p4sOIf-FH> To apply, please see the Penn State jobs website: <https://psu.jobs/job/61792> Applicants must submit the following materials by March 31, 2016:

(1) resume, including relevant courses (2) a list of three references (3) cover letter describing research experience, interests, and career goals

The internships last 8 weeks and can be extended up to 10 weeks, depending on the project. The stipend is approximately \$550 per week, and incumbents are responsible for their own housing.

Contact info:

Andrew R. Deans, director Frost Entomological Museum  
Department of Entomology 501 ASI Building Pennsylvania State University University Park, PA 16802 USA  
adeans@psu.edu

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.

“adeans@psu.edu” <adeans@psu.edu>

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### PortlandStateU NSFREU PlantGenomics

NSF Research Experience for Undergraduates (REU) in Plant Ecology and Genomics

We are looking for two enthusiastic students interested in enhancing their research skills and experience in plant ecology, genomics, and bioinformatics in the Cruzan lab at Portland State University in Portland, Oregon.

Successful applicants will become part of a research team working on dispersal and gene flow in upland prairie plants in Oregon and Washington under pressure from climate change. Dispersal is critical for colonization, gene flow, and range expansion. It is one of the most important but least understood aspects of the ecology of plants. Our research utilizes genomic techniques to detect the effects of dispersal over different spatial scales. This is an integrative research program that includes field work, wet lab preparation of genomic DNA for next-generation sequencing, bioinformatics processing of sequence data, and analysis of patterns of gene flow using GIS and landscape genetic methods. Students will be exposed to a wide range of methods and are expected to develop an independent research project within the scope of the larger research program. More information on our research is posted on our lab website: <http://web.pdx.edu/~cruzan/index.html>

Students will be fully supported for 10 to 12 weeks during the summer of 2016. Funding is provided from an REU supplement to our National Science Foundation Macrosystems Biology grant. Housing will be provided on campus along with a daily allowance for food and a \$500 weekly stipend. The start of the REU is negotiable with optimal start dates between May 1 and June 17.

To apply please email us an updated copy of your CV (including GPA) and a short (one page) statement of your research interests and experience, as well as goals for your education and career. Students with experience in computer programming and/or bioinformatics are en-

couraged to apply. Application deadline is 29 February 2016. Feel free to email us with questions.

Pam Thompson, Postdoctoral Research Associate: thompson@pdx.edu

Mitch Cruzan, Principle Investigator: cruzan@pdx.edu

Mitch Cruzan Professor of Biology Portland State University PO Box 751 Portland, OR 97207 USA Web: <http://web.pdx.edu/~cruzan/> cruzan <cruzan@pdx.edu>

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## Pyrenees VolFieldTech PlantSpeciation

Field assistants summer 2016: Volunteer positions in evolutionary biology

Nick Barton's group at the Institute of Science and Technology (IST) Austria requires volunteers to assist with field work on plant speciation in the Pyrenees (Spain) this coming summer (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 includ-

ing 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 March 31st, please send a statement of your background, CV, why you are interested and the length of time you would be available via email to maria.clara.melo@ist.ac.at

Maria Clara MELO HURTADO  
<maria.clara.melo@ist.ac.at>

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## SMBE nominations

Dear EvoDir,

\*Nominations for President-elect and 2 Councillors due by Tuesday, March 15, 2016

I am writing to solicit nominations for SMBE President-Elect and 2 Councillors whose terms will begin on January 1, 2016. All of these positions are for a duration of three years. As the society grows and thrives, members of council play very important roles in guiding its development and in soliciting and implementing programs that support our members, enrich opportunities for young scientists from around the world, oversee our two excellent journals (MBE and GBE) as well as our annual meeting and satellite meetings.

Nominations will be reviewed by the nomination committee who will then put forward a slate of two candidates for each position for membership vote. Past council members are listed at

<https://www.smbc.org/smbc/ABOUT/Council.aspx>

Please send nominations with a brief statement in support of your suggestion (self nominations are accepted) to:

Soojin Yi (soojinyi@gatech.edu) and James McInerney (secretary.smbc@gmail.com)

NB: we ask the nominators to confirm \*explicitly\* that the person they are nominating has already confirmed their willingness to run for office. In addition, please keep in mind that the candidates have to be an active member of SMBE in the time of election.

Please send your nominations by Tuesday March 15, 2016.

We look forward to hearing from you.

Sincerely yours,

James McInerney Secretary of SMBE, on behalf of the Nomination Committee

Nomination Committee: Soojin Yi, Chair (Georgia Tech, soojinyi@gatech.edu)

Belinda Chang (University of Toronto, belinda.chang@utoronto.ca)

Arndt von Haeseler (Center for Integrative Bioinformatics Vienna, arndt.von.haeseler@univie.ac.at)

Bing Su (Chinese Academy of Sciences, Kunming Institute of Zoology, sub@mail.kiz.ac.cn)

Mike Steel (University of Canterbury, mike.steel@canterbury.ac.nz)

and

James McInerney, SMBE Secretary (University of Manchester), ex officio per by-laws (secretary.smbc@gmail.com)

Secretary SMBE <secretary.smbc@gmail.com>

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## Travel Awards to Botany Meeting

We are pleased to announce the PLANTS program, funded by the National Science Foundation and Botanical Society of America, that brings 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](http://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](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](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 (monfilak@cmich.edu), or Heather Cacanindin (hcacanindin@botany.org).

"aksakai@uci.edu" <aksakai@uci.edu>

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## 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](http://www.colorado.edu/smithlab)) under the guidance of Dr. Julienne 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. Julienne Ng ([julienne.ng@colorado.edu](mailto:julienne.ng@colorado.edu)). Applications close 4th March, 2016.

Please direct any questions to Dr. Julienne Ng ([julienne.ng@colorado.edu](mailto:julienne.ng@colorado.edu)).

[julienne.ng@gmail.com](mailto:julienne.ng@gmail.com)

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## UColorado Boulder SummerREU PlantPhylogenetics

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](http://www.colorado.edu/smithlab)) under the guidance of Dr. Julienne 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.

Students will be provided a stipend of \$500/week, dormitory housing and transportation.

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 CV, unofficial transcripts, and the contact details of two professional references (including title, how you know them, phone number and email address) to Dr. Julienne Ng ([julienne.ng@colorado.edu](mailto:julienne.ng@colorado.edu)). Applications close 4th March, 2016.

Please direct any questions to Dr. Julienne Ng ([julienne.ng@colorado.edu](mailto:julienne.ng@colorado.edu)).

[julienne.ng@gmail.com](mailto:julienne.ng@gmail.com)

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## UHawaii SummerREU Biodiversity

Summer 2016 Research Experiences for Undergraduates at the University of Hawaii

Participants in the Summer 2016 Research Experience for Undergraduates (REU) program will take advantage of high-throughput DNA sequencing and phylogenetic methods to study the identity and origins of Hawai'i's

native, endemic and invasive organisms. REU participants will be mentored by a diverse faculty from the departments of Biology, Botany, and Microbiology, the Hawai'i Natural Energy Institute at the University of Hawai'i at Mānoa, and Kapi'olani Community College in Honolulu, Hawaii.

The 10-week REU summer program provides participants with stipends of \$5,250, and covers the costs of accommodations, food and travel to Hawaii. This unique experience allows participants to gain hands-on research experience, providing an excellent stepping stone for future graduate studies.

Applications for Summer 2016 are due March 15, 2016. Please visit the program website for further information and to apply. <http://manoa.hawaii.edu/biodiversity-REU/> Questions can be addressed to program coordinators Dr. Stuart Donachie (donchie@hawaii.edu) and Dr. Stephanie Kraft-Terry (kraft2@hawaii.edu).

Robert C. Thomson Assistant Professor Department of Biology University of Hawaii at Manoa Honolulu, HI 96822 thomsonr@hawaii.edu <http://thomsonlab.org/-thomsonr@hawaii.edu> <thomsonr@hawaii.edu> "thomsonr@hawaii.edu" <thomsonr@hawaii.edu>

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## UMinnesota Undergrad Research Plant Adaptation

Summer 2016 REU. Plant Evolutionary Genetics. University of Minnesota. St. Paul, MN

Ruth Shaw (B's Research Group in the Dept. of Ecology, Evolution & Behavior at the University of Minnesota is seeking applicants for an NSF Research Experience for Undergraduates (REU) position in summer 2016 to study the process of ongoing adaptation in experimental populations of partridge pea (*Chamaecrista fasciculata*) in prairie habitat. The student will work closely with Dr. Ruth Shaw to develop an independent project in the area of plant evolutionary genetics, with possibilities including estimation of heritability and phenotypic selection on various plant traits and studies of population dynamics. The student will gain invaluable experience in performing field work and in conducting an independent research project, from hypothesis formulation through oral and written dissemination of results, as grounding for future work in inquiry-based scientific research. The student must be a U.S. citizen or permanent resident and should be enrolled as

an undergraduate in Fall 2016. The ideal candidate should enjoy working outdoors and have an interest in learning about the evolution and ecology of plants in the Midwest prairies, and candidates planning to pursue a graduate career in evolution, ecology, or conservation biology are particularly well-suited for this position. The REU intern will receive a stipend of \$5,000 and room and board in the Twin Cities (with occasional overnight travel to field sites). Costs of travel to and from the Twin Cities will also be provided. The deadline to apply for this position is March 11, 2016, and the 10-week internship is expected to begin on Monday, June 13 and end on Friday, August 19. Please contact Ruth Shaw (shawx016@umn.edu) for more information. The University of Minnesota provides equal access to and opportunity in its programs, facilities, and employment without regard to race, color, creed, religion, national origin, gender, age, marital status, disability, public assistance status, veteran status, sexual orientation, gender identity, or gender expression. Individuals of underrepresented groups are especially encouraged to apply. Please spread the word to any interested and qualified undergraduates.

To apply, please e-mail the following application materials to Ruth Shaw (shawx016@umn.edu) with the subject line REU (no later than March 11, 2016:

- 1) a statement explaining the following:
  - Why you are interested in this position?
  - What previous experience do you have that is relevant for this position?
  - What are your future plans?

Please call this opportunity to the attention of undergraduates likely to be interested:

Ruth G. Shaw Professor and Editor in Chief, \*Evolution\* Dept of Ecology, Evolution and Behavior 100 Ecology 1987 Upper Buford Circle University of Minnesota St. Paul MN 55108

shawx016@umn.edu



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## UNSW Sydney Internship EvolBiol

Job: UNSW\_Sydney.Internship.EvolBiol

Scientific Internship/Apprenticeship in Evolutionary Biology at i-deel, E&ERC, UNSW, Australia

Our lab ([www.i-deel.org](http://www.i-deel.org)) is offering one scientific internship/apprenticeship (or volunteer position) for up to 6 months to help set up our lab. We are located at the Evolution & Ecology Research Centre (E&ERC) within the School of Biological, Earth and Environmental Sciences (BEES) at the University of New South Wales (UNSW), Sydney, Australia. The intern will be engaged in variety of scientific work (mainly, setting up zebrafish behavioural and physiological experiments, helping conduct comparative or meta-analyses and database management). We expect the apprentice will learn essential skills as well as gain experience necessary for conducting their own projects. This is why an ideal candidate will be someone who plans to undertake a PhD in the future, within the fields of Evolutionary Biology, Ecology and Behavioural Sciences (i.e. someone with BSc or MSc). We will provide an allowance to cover accommodation and food (~up to AU\$2000 per month). The intern needs to hold a working holiday visa or be an Australian or New Zealand resident. Please read our webpage to see what kind of research we conduct ([www.i-deel.org](http://www.i-deel.org)). If you are passionate about our science and would like to join our team, please contact Shinichi Nakagawa ([s.nakagawa@unsw.edu.au](mailto:s.nakagawa@unsw.edu.au)) with your CV and one page letter of motivation.

Best regards

Shinichi

Dr Shinichi Nakagawa (Associate Professor) Room 568, Biological Sciences Building (D26) School of Biological, Earth and Environmental Sciences (BEES) The University of New South Wales Randwick NSW 2052, Sydney, Australia Mobile: 0422 655 854 Office : 0293 859 138 Website: <http://www.i-deel.org/> Shinichi Nakagawa <[s.nakagawa@unsw.edu.au](mailto:s.nakagawa@unsw.edu.au)>

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## USussex VolFieldAssist SpainWasps

VOLUNTEER FIELD ASSISTANT sought for 8 weeks starting early/mid-April 2016, to help with a study of paper wasp (*Polistes*) behavioural ecology in southern Spain. The work will involve helping a PhD student to census and observe colonies as part of experiments to elucidate the basis of helping behaviour in these wasps, which live in small colonies of <20 individuals. The successful applicant must be prepared to work hard and have an interest in behavioural/evolutionary biology, and have enthusiasm and fitness level suitable for fieldwork. Successful applicants will obtain excellent experience of cutting-edge insect behavioural ecology. A driving licence and any ability to speak Spanish would be an advantage, but are not essential. Because the work involves recording colour marks on individual animals, the job would not be suitable for someone who is colour-blind. See our research group website for more information about the kind of work we do (<http://www.sussex.ac.uk/lifesci/fieldlab/>).

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

Send a covering letter and CV, including contact details (including e-mail addresses/tel nos.) for the applicant and 2-3 referees who would be available to provide references during March 2016. Include a clear sentence in your cover letter stating whether you hold a clean driving licence and would be prepared to drive in Spain if need be (a driving licence is not essential, but we need to know whether you have one). Email as a single Word document to: [j.field@sussex.ac.uk](mailto:j.field@sussex.ac.uk).

Or post a hard copy to: Prof Jeremy Field, School of Life Sciences, John Maynard Smith Building, University of Sussex, Brighton BN1 9QG, UK.

Applicants must be available for an informal interview at Sussex University, and review of applications will begin on 19 March with interviews the following week.

Informal enquiries: [j.field@sussex.ac.uk](mailto:j.field@sussex.ac.uk)

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

[j.field@sussex.ac.uk](mailto:j.field@sussex.ac.uk) <<mailto:j.field@sussex.ac.uk>>  
<http://www.sussex.ac.uk/lifesci/fieldlab/> Tel 01273 877135

Jeremy Field <[J.Field@sussex.ac.uk](mailto:J.Field@sussex.ac.uk)>

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### UTexas Austin SummerUndergradRes

Switchgrass (*Panicum virgatum*) is emerging as an important biofuel candidate in the United States. Our labs (see list of collaborators below) collectively study the ecology, genetics/genomics, physiology and agronomy/plant breeding of Switchgrass. We are seeking a talented and diverse group of undergraduate students interested in conducting a variety of research in Switchgrass biology across the US.

Program description: This program is an opportunity for undergraduate students to participate in mentored independent research on the biology of Switchgrass. The program is funded through the NSF Research Experience for Undergraduates (REU) program and is associated with our ongoing interdisciplinary work on the ecology, physiology, and genomic responses of switchgrass to future climate change. Summer students will be immersed in research and learn basic and applied biology through active participation in primarily field-based work. Working as part of our research team, they will contribute to group research projects, design short research projects, and present their work in an end-of-summer student symposium.

Each position is supported for 8-10 weeks beginning the first week of June. Students are awarded a \$4500 stipend, plus a housing and food allowance, and some funds to help defray the cost of traveling to the designated University.

Who Should Apply: Undergraduates that are not in their senior year (typically 2nd or 3rd year students), who are either U.S. citizens or permanent residents studying in the U.S.

Application process: The application deadline is February 15, 2016. Applicants should submit a cover letter describing any relevant research experience, along with

their motivation for joining our research group, and include a copy of their current transcript (unofficial transcript or screenshots are acceptable). Applicants should also ensure that two letters of recommendation are submitted on their behalf. Only applications that are complete will be considered. Applications and requests for further information should be directed to:

Dr. Brandon Campitelli e-mail: [brandon.campitelli@utexas.edu](mailto:brandon.campitelli@utexas.edu) Subject: Switchgrass REU 2016

For more information regarding this opportunity, and ongoing research, please visit our website: [https://sites.cns.utexas.edu/juenger\\_lab/summer-research-opportunities](https://sites.cns.utexas.edu/juenger_lab/summer-research-opportunities) Collaborating professors and institutions:

Prof. Thomas Juenger; University of Texas at Austin; [https://sites.cns.utexas.edu/juenger\\_lab/home](https://sites.cns.utexas.edu/juenger_lab/home)

Prof. David Lowry; Michigan State University; <https://plantbiology.natsci.msu.edu/directory/david-lowry/> Prof. Felix Fritschi; University of Missouri, Columbia; <http://plantsci.missouri.edu/faculty/-fritschi.cfm>

Prof. Yanqi Wu; Oklahoma State University; [http://biopec.okstate.edu/?page\\_id=155](http://biopec.okstate.edu/?page_id=155) Prof. Rob Mitchell; USDA-ARS, University of Nebraska, Lincoln; <http://www.ars.usda.gov/-pandp/people/people.htm?personid=31809>

Prof. Arvid Boe; South Dakota State University; <https://www.sdstate.edu/resources/directory/directory-detail.cfm?view=detail&ci=234> Brandon E Campitelli, PhD Postdoctoral Researcher, Dept. of Integrative Biology College of Natural Sciences Clinical Assistant Professor, Biology of Biofuels Freshmen Research Initiative University of Texas at Austin

[brandon.campitelli@utexas.edu](mailto:brandon.campitelli@utexas.edu)

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### UTexas ElPaso REU DesertBiodiversity

REU Opportunity Summer 2016: "Research Experience for Undergraduates in Chihuahuan Desert Biodiversity"

The University of Texas at El Paso (UTEP) Department of Biological Sciences invites applicants for the NSF sponsored Research Experience for Undergraduates (REU) in Chihuahuan Desert Biodiversity. This is a 10 week summer program. The goal of this program is to provide undergraduate students with experience in hypothesis-driven collaborative research utilizing

field based and/or laboratory methods and fully engage students in projects associated with the ecology and evolution influencing Chihuahuan Desert biodiversity.

The program provides:

- \* High quality research experience in ecology and evolutionary biology in the field and/or lab
- \* Research opportunities at the Indio Mountains Research Station (IMRS), a 40,000 acre facility controlled by UTEP
- \* One-on-one and group mentoring from active research faculty in multidisciplinary fields
- \* Training in bioethics and other relevant professional skills

The program includes

- \* \$5250 stipend for 10 weeks
- \* Housing in shared apartments and field station
- \* Travel reimbursement of up to \$600

For more information on the program, research projects or to apply please visit: <http://science.utep.edu/cdb-reu/> Enquiries: CDB-REU@utep.edu<mailto:CDB-REU@utep.edu>

"mlmoody@utep.edu" <mlmoody@utep.edu>

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## ViewsOfScienceReligion

Dear Sir or Madam,

I am writing to ask for your participation in an ongoing research project that investigates the views of life scientists and medical professionals regarding the relationship between personal belief and evolutionary science.

My name is Tom Kaden, and I am a postdoctoral researcher at York University, Toronto. Currently I am working in the interdisciplinary research project *Science and Religion: Exploring the Spectrum*. In the project, I and my colleagues attempt to build a better understanding of how scientists and members of the public view the relationship between evolutionary science and religion, and by extension science and religion. As part of the study we will be looking at a range of topics, including what people believe and how those beliefs are formed, perceptions of science, experiences of prejudice or discrimination, and views on public debate about science and religion.

We are especially interested in interviewing early career life scientists for this project.

We believe that the best way for us to find out about the

range of views that exist on these issues is by conducting interviews and by engaging groups of life scientists in a conversation with each other. We are looking to recruit between five and eight people for participation in a focus group discussion that would take about two hours and cover the topics mentioned above. The date and venue of the group discussion will be scheduled once enough people have expressed their interest.

All participants are invited for lunch or dinner after the discussion. Travel expenses will be reimbursed. Please be assured that all information gathered as part of this research project will be treated in the strictest confidence. Only members of the project research team based at Newman University, UK, and York University, Toronto, will have access to the raw data and all information we gather will be anonymized before it is made public.

In addition to the interviews and group discussions we invite people regardless of their location or profession to complete a brief survey on science and religion that can be found on our website: <http://sciencelreligionspectrum.org/engage-participate/> Thank you very much for considering participating in the research project. If you are interested in participating in this project, please contact me via e-mail at tomkaden@yorku.ca. I look forward to hearing from you. Please let me know if you have any further questions.

Dr. Tom Kaden 4700 Keele St 317 Bethune College Toronto ON M3N 1P3 tomkaden@yorku.ca

Tom Kaden <tomkaden@yorku.ca>

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## Washington DC BioBlitz May 20-21

Greetings, evolutionary biologists!

BioBlitzes are great opportunities to share your deep knowledge of natural history with an enthusiastic audience, have fun with other biologists, and inspire more citizen scientists.

\*We are currently recruiting field biologists and naturalists\* to participate in the National Parks BioBlitz - Washington, D.C. <<http://www.nationalgeographic.com/explorers/projects/bioblitz/washington-dc-2016/>>, and we invite you to register now <[https://nationalgeographic.formstack.com/forms/national\\_parks\\_bioblitz\\_2016\\_washington\\_dc\\_scientist\\_registration](https://nationalgeographic.formstack.com/forms/national_parks_bioblitz_2016_washington_dc_scientist_registration)> ! If you are interested in events in Maryland and Virginia

further from D.C., there is a separate registration form <[https://nationalgeographic.formstack.com/forms/national\\_parks\\_bioblitz\\_2016\\_national\\_capital\\_region\\_non\\_cornerstone\\_scientist\\_registration\\_form](https://nationalgeographic.formstack.com/forms/national_parks_bioblitz_2016_national_capital_region_non_cornerstone_scientist_registration_form)>. This is a great opportunity to help document the parks' biodiversity and to share your knowledge and enthusiasm in the field. If you're unsure where you fit in, watch this short video <<https://www.youtube.com/watch?v=KKgYcIAsQaI&feature=youtu.be>> to help you find your niche in BioBlitz. \*The deadline to register <[https://nationalgeographic.formstack.com/forms/national\\_parks\\_bioblitz\\_2016\\_washington\\_dc\\_scientist\\_registration](https://nationalgeographic.formstack.com/forms/national_parks_bioblitz_2016_washington_dc_scientist_registration)> is Friday, February 26.\* \*We are also looking for enthusiastic nature novices and college students\* to serve as iNaturalist <<http://www.inaturalist.org/>> Pro-Observers (link to registration form <[https://nationalgeographic.formstack.com/forms/national\\_parks\\_bioblitz\\_2016\\_washington\\_dc\\_pro\\_observer\\_registration](https://nationalgeographic.formstack.com/forms/national_parks_bioblitz_2016_washington_dc_pro_observer_registration)>) so please share this with appropriate groups and clubs (registration will be open at least through March, unlike above).

Background: The National Geographic Society and the National Park Service are teaming up for the 10th year to conduct a \*BioBlitz <<http://natgeo.org/bioblitz>> \*in parks in and around our nation's capital on \*May 20-21, 2016. \*BioBlitz is an \*all-taxa inventory\* in

which teams of volunteers, each led by a subject matter expert, find and identify as many species as possible within a 24-hour period. The National Parks BioBlitz - Washington, D.C. and concurrent Biodiversity Festival on the National Mall is a cornerstone event of the larger National Parks BioBlitz commemorating the centennial of the National Park Service. More BioBlitzes will be held in at least 100 national parks across the United States. BioBlitzes happening in other National Parks will have separate registration. You can see the growing list of parks here <<http://www.nature.nps.gov/biology/biodiversity/bioblitz2016.cfm>>.

\*Please share this with others who may be interested to help make this event a success.\* You can email [bioblitz@ngs.org](mailto:bioblitz@ngs.org) with general questions or [cseltzer@ngs.org](mailto:cseltzer@ngs.org) for questions about registering as an expert or amateur. We hope to see you at the National Parks BioBlitz May 20-21!

\*Carrie E. Seltzer, Ph.D.\*

Program Manager, Experiences

t. 202.862.8239

1145 17th St., NW, Washington, DC 20036

[cseltzer@ngs.org](mailto:cseltzer@ngs.org)

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## PostDocs

|  |  |    |
|--|--|----|
| AcademySciences CzechRepublic AntPlantInteractions | IndianaU EvolutionSexReproduction            | 87 |
| 81   | INRA Sophia-Antipolis EvolutionaryGenomics   | 87 |
| Bethesda Maryland HIV Evolution                    | IowaStateU Phylogenomics                     | 88 |
| CambridgeU HumanAdaptationBioinformatics           | IowaStateU PopGenomicsFig-FigWasp            | 88 |
| CambridgeU HumanAdaptationClimate                  | IST Austria MathEvolutionaryBiol             | 89 |
| CEES UOslo EvolutionDefense                        | KansasStateU QuantitativeGenomicsPhenomics   | 90 |
| CharlesU Prague NightingaleSpeciation              | Kew PlantFungalDiversity                     | 90 |
| DukeU Ecological Epigenetics                       | Kiel Germany 1PDF 3PhD CelegansEvolution     | 90 |
| GeorgeWashingtonU ComputationalBiology             | LinkopingU Sweden GenomicsSexualDimorphims   | 91 |
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## AcademySciences CzechRepublic AntPlantInteractions

A highly motivated Postdoctoral Researcher is sought to join a project exploring the shifts that occur in a mutualistic ant-plant network when tropical rain forest is logged, fragmented, and converted to oil palm plantation in Malaysian Borneo. The successful candidate will lead a team conducting field surveys for ant-inhabited trees, measuring ant and plant fitness correlates, and performing experimental manipulations of the mutualistic communities, in particular in relation to forest regeneration. They will also conduct analyses and write papers on the main project findings. The project will provide the opportunity to collaborate with two cutting-edge large-scale manipulations of tropical forests: 1. The Stability of Altered Forest Ecosystems project (SAFE), the world's largest rain forest fragmentation experiment. 2. The Sabah Biodiversity Experiment (SBE), a project assessing the impacts of different diversities of tree planting on ecosystem functioning. There will also be opportunities to develop the project in a direction of the postdoc's own choosing. Duties will include spending extensive periods of time in the field in Malaysian Borneo.

The successful applicant will join the Ant Research Group (<http://antscience.com/>) at the Institute of Entomology, Biology Centre Academy of Sciences, Ceske Budejovice, Czech Republic, employed on a grant held

by Tom Fayle (<http://www.tomfayle.com/index.htm>). The group is a dynamic, multinational group studying ant ecology, evolution and biogeography, and is embedded within the Department of Ecology and Conservation Biology, a world-class centre for interaction network research with regular publications in Science, Nature and other leading journals. The position allows the successful candidate to apply for standard research grants from the main Czech grant agency (GACR) to expand the project. The deadline for applications is February 29th 2016, with a start date of May 1st 2016, and the appointment lasting until Dec 2018. Applicants from all countries are eligible. Salary for this full time position is CZK 40,000 per month (approx. EUR 1500). Note that living costs in Czech Republic are substantially lower than in many other European countries (e.g. <http://-bit.ly/1NckQKJ>) and living costs in Malaysia are fully covered.

Required - A PhD degree in either entomology or plant ecology. - Experience and enthusiasm for working in the field for extended periods of time in challenging conditions in tropical rain forest, including ability to lead field teams. - Good publication record for career stage. - Experience in the use of ecological statistical analyses.

Desirable - Previous work on insect plant interactions. - Experience of molecular laboratory work, specifically DNA barcoding for species identifications. - Experience in use of methods for statistical analysis of interaction networks.

To apply please send a CV, contact details for three references, and cover letter stating qualifica-



tions, previous work and motivation to Tom Fayle (tmfayle@gmail.com).

Tom Fayle <tmfayle@gmail.com>

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## Bethesda Maryland HIV Evolution

The Henry M. Jackson Foundation for the Advancement of Military Medicine Inc. (HJF) is seeking a post-doctoral fellow for the HIV Research Program (MHRP) located in Bethesda, Maryland. HJF provides scientific, technical and programmatic support services to MHRP. The U.S. Military HIV Research Program (MHRP) ([www.hivresearch.org](http://www.hivresearch.org)) is at the forefront of the battle against HIV to protect U.S. troops from infection and to reduce the global impact of the disease. MHRP is one of the leading clinical research programs developing a vaccine to prevent HIV, improving treatments for HIV and co-infections and also working towards a cure.

### Job Summary

The post-doctoral fellow will be part of a team of biologists, clinicians and statisticians doing highly collaborative, multi-institutional and inter-disciplinary work on a range of questions with a strong emphasis on vaccine research. The candidate will study evolutionary processes both within and between hosts and comparative genomics to investigate commonalities and differences between HIV and other pathogens including Ebola, Dengue, MERS-CoV, Zika.

The incumbent may perform some or all of the following responsibilities:

1. Use Bayesian phylogenetic, phylogeographic and comparative genomics approaches.
2. Perform comprehensive molecular epidemiological analysis and bioinformatic analysis of large datasets.
3. Develop mathematical and computational models of evolution to explore various aspects of pathogen evolution, host adaptation and transmission.
4. Maintain current knowledge by participating in scientific conferences and reading specialty journals. Contribute to the science through independent and collaborative research including by authoring manuscripts.

### Qualifications

The successful candidate will have a Ph.D. in population genetics, evolutionary genetics, microbial genomics, comparative genomics, computational biology, mathematics,

statistics or a related area. Background knowledge in immunology, virology or structural biology is a plus.

The candidate should be a dedicated, social, detail-oriented person, who is able to work independently within a team of researchers. Excellent written and verbal communication skills are required.

To apply

Please contact Morgane Rolland

[mrolland@hivresearch.org](mailto:mrolland@hivresearch.org)

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## CambridgeU HumanAdaptationBioinformatics

Dear Evoldir members, below is a bioinformatics position within an exciting ERC project I'll be conducting with Dr Andrea Manica and Dr Andrew Friend at Cambridge, UK. Please spread the word to anyone you think might be relevant.

Best regards Anders Eriksson

– Dr. Anders Eriksson Integrative Systems Biology Lab, KAUST Evolutionary Ecology Group, Dept. Zoology, Cambridge University

Research Associate: Evolutionary Ecology Group

URL: <http://www.jobs.cam.ac.uk/job/9367/> We are looking for a bioinformatician/population geneticist to work with Dr Andrea Manica on a project investigating localised selection in humans. This ERC funded post is available for up to 50 months, with a start date of 1 April 2015.

Details of Dr Manica's research may be found here: <http://www2.zoo.cam.ac.uk/manica/index.htm> This project focuses on investigating the effect of natural selection in humans, using spatially explicit models that are informed by climate and vegetation reconstructions through time. The successful candidate will be involved both in the development of new approaches to test for selection and in their application to humans (and potentially other species).

Duties will include: collating and curating genomic data, both from the literature and ongoing collaborations; Analysing genomic data for selection, both using standard population genetics approaches and CISGeM; interacting with archaeologists and climate modellers to help result interpretation; and the preparation of manuscripts for publication.

Required experience / knowledge for the position

Essential:

A PhD in bioinformatics, population genetics or closely related subjects.

Proficient programming for the analysis of genomic data, using python and/or R.

Willingness to interact with specialist from other fields, such as archaeology and climatology

Ability to organise time, plan ahead and to work effectively independently.

Good data handling and data analysis skills.

Good communication skills (written and oral).

Ability to work in a team and strong inter-personal skills.

Desirable:

Experience with selection scans on whole genomes.

Background knowledge (e.g. from degree courses) of archaeology or anthropology.

Advanced programming skills in C.

Experience in working with High Performance Computing facilities.

Fixed-term: The funds for this post are available for up to 50 months.

We will interview during week beginning 7 March 2016

To apply online for this vacancy, please click on the 'Apply' button below. This will route you to the University's Web Recruitment System, where you will need to register an account (if you have not already) and log in before completing the online application form.

Please quote reference PF08215 on your application and in any correspondence about this vacancy.

The University values diversity and is committed to equality of opportunity.

The University has a responsibility to ensure that all employees are eligible to live and work in the UK.

aeriksson75@gmail.com

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## CambridgeU HumanAdaptationClimate

Dear Evoldir members, below is a climate scientist position within an exciting ERC project I'll be conducting with Dr Andrea Manica and Dr Andrew Friend at Cambridge, UK. Please spread the word to anyone you think might be relevant.

Best regards Anders Eriksson

– Dr. Anders Eriksson Integrative Systems Biology Lab, KAUST Evolutionary Ecology Group, Dept. Zoology, Cambridge University

Research Associate - Climate Modelling (Fixed Term)

URL: <http://www.jobs.cam.ac.uk/job/9371> We are looking for a climate modeller to work with Dr Andrea Manica and Dr Andrew Friend (Dept. of Geography) on a project investigating the role of past climate on human adaptation. This ERC funded post is available for up to 50 months, with a start date of 1 April 2015.

Details of Dr Manica's research may be found here: <http://www2.zoo.cam.ac.uk/manica/index.htm> Details of Dr Friend's research may be found here: <http://www.geog.cam.ac.uk/people/friend/> This project focuses on investigating the effect of natural selection in humans, using spatially explicit models that are informed by climate and vegetation reconstructions through time. The successful candidate will be involved in generating paleoclimate and paleovegetation reconstructions and work with population geneticists to use this information to quantitatively inform models of human evolution.

Duties will include setting up and running global paleoclimatic models using CESM; running paleovegetation reconstructions; potentially modifying CESM/vegetation models to allow for human/environment interactions; interacting with archaeologists and geneticists to help result interpretation; and the preparation of manuscripts for publication.

Required experience / knowledge for the position

Essential:

A PhD in climate modelling, or closely related subjects.

Advanced programming skills in Fortran 90/95/2003.

Experience running GCM

Willingness to interact with specialist from other fields,

such as archaeology and genetics

Ability to organise time, plan ahead and to work effectively independently.

Good data handling and data analysis skills.

Good communication skills (written and oral).

Ability to work in a team and strong inter-personal skills.

Desirable:

Experience running CESM

Experience with setting up and modifying CESM (or an equivalent climate model).

Background knowledge (e.g. from degree courses) of archaeology or anthropology.

Experience with vegetation models.

We will interview during week beginning 7 March 2016

Fixed-term: The funds for this post are available for up to 50 months.

To apply online for this vacancy, please click on the 'Apply' button below. This will route you to the University's Web Recruitment System, where you will need to register an account (if you have not already) and log in before completing the online application form.

Please quote reference PF08219 on your application and in any correspondence about this vacancy.

The University values diversity and is committed to equality of opportunity.

The University has a responsibility to ensure that all employees are eligible to live and work in the UK.

aeriksson75@gmail.com

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## CEES UOslo EvolutionDefense

Research in aquatic evolutionary ecology

“A researcher position is available at the Centre for Ecological and Evolutionary Synthesis, (CEES), <http://www.mn.uio.no/cees/english/index.html>, Department of Biosciences, <http://www.mn.uio.no/ibv/english/>. The position is for 38 months, and the estimated start date is May 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 research 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 care-

ful 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, transcript of records,

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

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## CharlesU Prague NightingaleSpeciation

Post doc position at Charles University in Prague

Genomics of speciation in nightingales

We are looking for a post-doc trained in bioinformatics and/or population genetics. The main goal of the project is to elucidate the genetic basis of reproductive isolation between two song bird species, the Common Nightingale (*Luscinia megarhynchos*) and the Thrush Nightingale (*L. luscinia*). The species hybridize in a secondary contact zone comprising F1 as well as backcross

hybrids. According to Haldane's rule F1 hybrid females are sterile, while F1 hybrid males are fertile. Using ddRAD sequencing of natural hybrid population and transcriptome sequencing of gonads and somatic tissues of both species and hybrids we aim to identify candidate reproductive isolation loci responsible for hybrid female sterility. The results should provide the first insight into genetic basis of Haldane's rule in heterogametic female organisms.

The candidate will be mainly responsible for the bioinformatic part of the project. Samples as well as most sequence data are already available. The position is available from May 2016 to December 2017 with the possibility of extension. The starting date is flexible but preferable before September 2016. The candidate will work at the Department of Zoology at Charles University in Prague under the supervision of Radka Reifova (<http://web.natur.cuni.cz/~radkas/>). The salary will be 35,000 CZK (ca 1,300 EUR) (Note that living expenses in the Czech Republic are generally lower than in Western European countries.)

If interested, please, send (1) a CV including a list of publications, (2) motivation letter and (3) a letter of reference of your PhD supervisor or research advisor to Radka Reifova ([radka.reifova@natur.cuni.cz](mailto:radka.reifova@natur.cuni.cz)) by 29th February 2016.

– RNDr. Radka Reifová, Ph.D. Phone: +420 221 95 1872 E-mail: [radka.reifova@natur.cuni.cz](mailto:radka.reifova@natur.cuni.cz), [radkas@natur.cuni.cz](mailto:radkas@natur.cuni.cz) Web page: [www.natur.cuni.cz/~radkas/](http://www.natur.cuni.cz/~radkas/) Department of Zoology Charles University in Prague Faculty of Science Viničná 7, 128 43 Praha 2

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Pokud je tento e-mail součástí obchodního jednání, PÁírodovÁá fakulta Univerzity Karlovy v Praze: a) si vyhrazuje právo jednání kdykoliv ukončit a to i bez uvedení dÁ<sup>1</sup>vodu, b) stanovuje, Áe smlouva musí mít písemnou formu, c) vylučuje pÁíjetí nabídky s dodatkem èi odchylkou, d) stanovuje, Áe smlouva je uzavÁena teprve vÁ<sup>1</sup>/2slovnÁ<sup>1</sup>/2m dosaÁením shody na vÁech náleÁitostech smlouvy.

“RNDr. Radka Reifová, Ph.D.”  
<[radka.reifova@natur.cuni.cz](mailto:radka.reifova@natur.cuni.cz)>

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## DukeU Ecological 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: 1 MARCH, 2016

"k.donohue@duke.edu" <k.donohue@duke.edu>

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## George Washington U Computational Biology

George Washington U. Postdoctoral Scientist The Computational Biology Institute (CBI) brings together GW experts and scholars from partner institutions to conduct cutting edge research, enable broad educational activities in computational biology and provides computational biology services to university researchers and public and private partners. CBI is an interdisciplinary effort, building on GW's strengths in life sciences and computational science, in addition to the wealth of research centers in the Washington, DC area. Additional information on the work of CBI can be found at: <http://cbi.gwu.edu/> The CBI is searching for a Postdoctoral Scientist in the Goecks Research Laboratory. This scientist will conduct computational biology research in the following areas:

\*innovative software development for the Galaxy platform (<http://galaxyproject.org>) using Python and JavaScript, including new methods for visualization, visual analytics, and parallelization; \*development of new computational methods and pipelines for analyzing large biomedical  $\tilde{A}\hat{-}\tilde{A}$  – *omics*  $\hat{-}\tilde{A}$  –  $\tilde{A}$  datasets; \*using novel and existing analysis tools to process and

extract patterns/information/knowledge from  $\tilde{A}\hat{-}\tilde{A}$  – *omics*  $\hat{-}\tilde{A}$  –  $\tilde{A}$  datasets, with a potential focus on cancer genomic datasets. \*leading and/or contributing to scientific manuscripts and grant applications.

Please send questions to Dr. Jeremy Goecks at jgoecks@gwu.edu

Minimum Qualifications: Requires a PhD in the field or in a related area.

Preferred Qualifications: Demonstrated programming experience, in the form of a Github profile or code samples, is ideal. Campus Location: Ashburn, VA The university is an Equal Employment Opportunity/Affirmative Action employer that does not unlawfully discriminate in any of its programs or activities on the basis of race, color, religion, sex, national origin, age, disability, veteran status, sexual orientation, gender identity or expression, or on any other basis prohibited by applicable law. Apply here: <https://www.gwu.jobs/postings/33114> "Haight, Veronica" <vhaight@email.gwu.edu>

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## Hawkesbury Inst Aust Plant Genetics

Position Title: Postdoctoral Research Fellow in Plant Ecological Genetics Academic Level: Level A fixed term (3 years) School/Office: Hawkesbury Institute for the Environment (HIE) College/Division: Research and Development Division

The Institute is seeking to appoint an energetic academic to a Level A position within the Plant, Animal, and Interactions theme. This 3-year, full-time, postdoctoral fellowship will focus on research related to understanding the capacity of trees to respond to climate change, and determining the importance of genetic adaptation and phenotypic plasticity.

The successful applicant will lead the molecular analyses from experimental design to bioinformatic and population genomic analyses. Molecular analyses will be linked to plant trait, growth and physiological responses of genotypes grown under contrasting rainfall environments in provenance trials in Western Australia, and climatic manipulations in HIE growth facilities. Expected research outcomes include a detailed understanding of genetic adaptation and physiological tolerance to climate change, along with the development of a scientific basis for the adoption of assisted gene migration to ensure drought-resilience in future forests.

The incumbent will have the opportunity to work with



a broad scientific team: Dr Paul Rymer (HIE) in population genomics and evolutionary ecology, Prof. David Tissue (HIE) in plant ecophysiology, Prof. Giles Hardy (Murdoch University) in plant ecology and stressors, and Dr Margaret Byrne (Western Australian Department of Parks and Wildlife) in conservation genetics.

Web: [www.westernsydney.edu.au/hie](http://www.westernsydney.edu.au/hie) Remuneration Package: Level A \$71,865 to \$86,824 p.a. plus 17% Superannuation and Leave Loading Position Enquiries: Dr Paul Rymer, (02) 4570 1094 or [p.rymer@westernsydney.edu.au](mailto:p.rymer@westernsydney.edu.au) Closing Date: 27 March 2016

<https://uws.nga.net.au/?jati=3DBB14A23E-B9F1-EBC4-7AEB-91B915E53D52>

"P.Rymer@westernsydney.edu.au"

<P.Rymer@westernsydney.edu.au>

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## IndianaU EvolutionSexReproduction

Common Themes in Reproductive Diversity (CTRD)

This T32 has 2 open positions for 2-year NIH traineeships to support broadly integrative training in the areas of sexual reproduction and development. Training will focus on behavior in both humans and other animals and will address key questions in three related themes: (1) genetic, epigenetic, environmental, and parental contributions to reproductive and social behavior; (2) the origins and expression of differences among the sexes; and (3) sex and immunity in health and disease. Indiana University's excellent support for research and its globally recognized strengths in animal behavior, endocrinology, human sexual health, and evolution of development will ensure high quality training. PhD in anthropology, biology, gender studies, neuroscience, psychology or a related field is required. Funding is from NIH T32 training grant, "Common Themes in Reproductive Diversity." For more information, make initial contact with one or more of the training faculty < <http://www.indiana.edu/~reprodiv/faculty.php> > who might serve as primary mentors. Positions begin as early as June 2016. Evaluations will begin as early as March 15, 2016, but positions will remain open until filled. Please check back for updates on timing.

[lisummer@indiana.edu](mailto:lisummer@indiana.edu)

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## INRA Sophia-Antipolis EvolutionaryGenomics

A 24-month postdoc position is available in our lab to study genome evolution in parthenogenetic animals.

Root-knot nematodes (*Meloidogyne* spp.) cause billions of euros economic loss to the world agriculture every year. These nematodes show an intriguing diversity of reproductive modes ranging from "classical" sexual reproduction to fully asexual reproduction. Curiously, the most devastating species are those that reproduce without sex and without meiosis. Furthermore, despite absence of sexual reproduction, these species are able to adapt and brake plant resistance.

Our lab aims at understanding how an asexual animal can be a more efficient parasite than its sexual relatives.

We have sequenced the genomes of three asexually-reproducing root-knot nematodes at high coverage and completeness. Genomes of two sexual relatives are publicly available for comparative genomics analysis.

The main goals of this postdoc project will be to: - assess the level of heterozygosity within and between isolates of parthenogenetic root-knot nematodes using PoolSeq approaches. - identify differences at the whole genome level between virulent isolates and their avirulent progenitors using GWAS. - assess the rates of accumulation of mutations per generation and use molecular clock to date the age of asexuality in these species.

We seek a highly motivated young or independent researcher with a good background in comparative and population genomics and skilled in computational biology / bioinformatics. A PhD in the relevant topics will be requested. The candidate is expected to bring GWAS, variant-calling and molecular dating skills and expertise to our research team. The candidate will be the principal investigator in this project and is expected to show good autonomy and skills for oral and written communication. Geographical mobility will be important too as the postdoc will have the opportunity to present the obtained results in international conferences.

More details, including information on how to apply, and on the salary are available at this URL: <http://edanchin.free.fr/index.php/component/content/article/52-postdoc> Etienne G.J. Danchin

Institut National de la Recherche Agronomique U.M.R.

- Institut Sophia Agrobiotech (ISA 1355) INRA-UNS-CNRS – 400 route des Chappes, BP 167 06903 Sophia-Antipolis Cedex – Tel. +33 492 386 402 Fax. +33 492 386 587

<http://edanchin.free.fr> “etienne.danchin@sophia.inra.fr”  
<etienne.danchin@sophia.inra.fr>

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## IowaStateU Phylogenomics

Postdoctoral Research Associate in Phylogenomics/Population Genomics

The Roe lab at Iowa State University seeks to recruit a Postdoctoral Research Associate with expertise in Next-Gen Sequencing/population genomics/bioinformatics. The successful applicant will collaborate with the PI to investigate the phylogenomics/population genomics of freshwater organisms (bivalves, shrimps, and fishes) For more information about the lab: <http://www.nrem.iastate.edu/research/roe/>. Candidates for the position should be able to demonstrate experience generating and analyzing genomic datasets (sequence capture, GBS, or RAD-seq); as well as experience working in a Linux/Unix shell environment; competency with at least one scripting language (e.g., Perl, Python, R). The candidate should have well-developed communication (verbal and written) and organizational skills, and leadership ability to assist the PI with the direction and training of graduate students. Qualified candidates must hold a A PhD degree in biological sciences or bioinformatics.

Terms of Appointment: Starting salary is \$45,000 plus benefits. This position is for a minimum of one year and is renewable, pending satisfactory progress. The anticipated start date is June and August 2016.

Application Instructions: For consideration, applicants must apply by April 1, 2016. Informal inquiries are encouraged prior to formal application. For formal application, please send 1) a cover letter, 2) a curriculum vitae, 3) a brief statement of research experiences/interests, and 4) names and contact information for three references to Dr. Kevin J. Roe (kjroe@iastate.edu).

Iowa State University is an Equal Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, age, religion, sex, sexual orientation, gender identity, genetic information, national origin, marital status, disability, or protected

veteran status, and will not be discriminated against. Inquiries can be directed to the Director of Equal Opportunity, 3350 Beardshear Hall, (515) 294-7612.

Kevin J. Roe, Ph.D Department of Natural Resource Ecology and Management Iowa State University 339 Science II Ames, Iowa, USA 50011 <http://www.public.iastate.edu/~kjroe/> “kjroe@iastate.edu”  
<kjroe@iastate.edu>

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## IowaStateU PopGenomicsFig-FigWasp

Postdoc: Phylo- and Population-Genomic Analyses of Fig-Fig Wasp Co-Diversification and Introgression

Postdoctoral Research Associate Department of Ecology, Evolution, and Organismal Biology Iowa State University

The Nason and Heath labs are looking to recruit a Postdoctoral Research Associate with expertise in phylo/population genomics. The successful applicant will collaborate with us on a new, NSF supported project using sequence capture and GBS data to investigate the coevolutionary history of species interactions in Central American figs and their pollinating (mutualistic) and non-pollinating (antagonistic) fig wasps. Collaborators on the project include Drs. John Nason and Tracy Heath (Iowa State University), Dr. E. Allen Herre (Smithsonian Tropical Research Institute, Panama), Dr. Charlotte Jandr (Harvard University), Dr. Carlos Machado (University of Maryland), and Dr. Robert Raguso (Cornell University). Required qualifications, terms of employment, application instructions, and a project summary follow below.

Required Qualifications

Education: A PhD degree in biological sciences or bioinformatics, or acceptable equivalent combination of education and experience.

Experience/Skills: Experience working with genomic/transcriptomic/GBS datasets; demonstrated experience working in a Linux/Unix shell environment; competency with at least one scripting language (e.g., Perl, Python, R). Demonstrated experience in the phylogenetic and/or population genetic analysis of NGS data, ideally obtained via sequence capture or GBS/RAD-seq methods. Well-developed organizational and time management skills, and leadership ability to direct (with the PIs) a large and productive project.

### Terms of Appointment

Starting salary is \$45,000 plus benefits. Funds are available for one year and are renewable for up to four years, pending satisfactory progress. The optimal start date is June 1, 2016.

### Application Instructions

For consideration, applicants must apply by April 1, 2016. Informal inquiries are encouraged prior to formal application. For formal application, please send 1) a cover letter, 2) a curriculum vitae, 3) a brief statement of research experiences/interests, and 4) names and contact information for three references to Dr. John Nason (jnason@iastate.edu).

Iowa State University is an Equal Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, age, religion, sex, sexual orientation, gender identity, genetic information, national origin, marital status, disability, or protected veteran status, and will not be discriminated against. Inquiries can be directed to the Director of Equal Opportunity, 3350 Beardshear Hall, (515) 294-7612.

### Project Summary

Figs and their fig wasp pollinators and parasites have co-evolved for ~90 million years to become both highly diverse (>750 species of figs) and ecologically important keystone± components of tropical forest ecosystems. Figs and wasps have long been assumed to represent a case of strict co-speciation, with highly specific pollinator and parasitic (non-pollinator) wasps identifying appropriate hosts via distinctive volatile chemical signals. More recent studies suggest a more complex scenario, however, involving an evolutionary history punctuated by host-shifts by individual wasp species. Although the wasp associations with fig hosts have been widely studied, the genetic consequences for the host figs of host-shifting pollinators and the mechanisms underlying host recognition remain poorly understood.

This project will fill these gaps by producing robust, detailed, many-gene phylogenies for 14 strangling fig (*Ficus*) species and their associated pollinating (*Pegoscapus*) and non-pollinating (*Idarnes*) fig wasps (~60 species) from the vicinity of Barro Colorado Island, Panama. Using transcriptome sequences, we will target ~300 genes from each of three species per lineage for capture and subsequent Illumina sequencing. Phylogenies will be inferred using Bayesian methods and will enable robust testing of phylogenetic congruence between figs and fig wasps. Further, they will guide population-level genotype by sequencing to test a priori predictions of potential cases of hybridization in the figs

and host shifting and race formation in both pollinator and non-pollinator wasps. Combined with quantification of wasp-attracting fig volatiles and fruit-surface chemicals, this work will detect and resolve the genomic consequences of host introgression due to host-shifting pollinator wasps, and link them to the chemical basis of host-recognition.

This research will significantly clarify both the patterns and processes underlying the evolutionary ecology of fig and fig wasp interactions. Our standardized, genomic approach is essential for: 1) obtaining robust fig and fig wasp species trees, 2) delimiting fig species and discriminating

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## IST Austria MathEvolutionaryBiol

IST Austria (Institute of Science and Technology Austria) invites applications for postdoctoral fellows in all fields of the natural and mathematical sciences, including evolutionary biology. Current evolution faculty are Nick Barton, Jon Bollback, Sylvia Cremer, Calin Guet, and Beatriz Vicoso.

The Institute, which is on the outskirts of Vienna, was established by the Austrian government with a focus on basic research. IST Austria has English as its working language, and its Graduate School awards PhD degrees. It has an international mix of scientists chosen solely for their individual excellence and potential contribution to research.

The Institute has set up a program for exceptional postdoctoral researchers. Appointments will be for 2-4 years. Applications will be accepted at any time, but fellows are selected twice a year in October and April. The deadline for the next round is March 15th. Applicants must have the support of one or more members of the IST Austria faculty who will host them in their research group.

The Institute offers an internationally competitive salary, full social security coverage, and additional benefits.

For further information about the program and the online application process, please refer to <http://ist.ac.at/>

istfellow IST Austria values diversity and is committed to equality. Female researchers are encouraged to apply.

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

“gpmorris@ksu.edu” <gpmorris@ksu.edu>

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## KansasStateU QuantitativeGenomicsPhenomics

Postdoc in Quantitative Genomics & Phenomics

A postdoc position is available in the Morris Lab on quantitative genomics & phenomics of biomass accumulation and environmental adaptation in sorghum.

The Morris lab studies genomics of crop adaptation to support crop improvement (Morris et al. 2013 PNAS < <http://www.pnas.org/content/110/2/453> >, Lasky et al. 2015 Science Advances < <http://advances.sciencemag.org/content/1/6/e1400218> >, Hu et al. 2015 BMC Genomics < <http://www.biomedcentral.com/1471-2164/16/1048/abstract> >). The successful candidate will lead quantitative genetics activities for a 4-year, \$8M project funded by Department of Energy ARPA-E that will dissect the genomic basis of yield and adaptation traits in bioenergy sorghum (TERRA-REF, <http://terraref.ncsa.illinois.edu/about/>).

The postdoc will be primarily responsible for: (1) conducting genome-wide association and linkage mapping using multi-environment high-throughput phenotyping data and whole genome resequencing data and (2) publishing findings in high-quality peer-reviewed manuscripts.

Other activities include improving methods for unmanned aerial vehicle (UAV) phenotyping and population genomic analyses of diverse global germplasm to dissect adaptive traits.

Salary commensurate with experience and training, up to \$50,000 + benefits.

For more details and instructions how to apply, go to the full job posting: <http://careers.pageuppeople.com/742/cw/en-us/job/492700/research-associate-agronomy>  
Review of applications starts Mar 26, 2016.

Geoff Morris, Assistant Professor Department of Agronomy | Kansas State University 3004 Throckmorton Plant Science Center | Manhattan KS, 66506 E-mail: [gpmorris@k-state.edu](mailto:gpmorris@k-state.edu) | Web: <http://www.morrislab.org> Office: 785-532-3397 | Cell: 312-909-1330 | Skype/Google ID: morris.geoff.p

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## Kew PlantFungalDiversity

Postdoctoral Fellowship in Plant or Fungal Diversity

Royal Botanic Garden Kew, London, UK is seeking an outstanding early career scientist with a PhD and specialist knowledge in plant or fungal diversity, evolution, genomics, or ecology relevant to plant health.

You will join Kew’s science staff as a postdoctoral research fellow, for three years, extendable to five on review. You will conduct and publish outstanding research within the Plant Health theme, and develop funding streams to support your science alongside a cohort of other research fellows. You will be a future leader in the science disciplines pursued at Kew.

Closing Date 18 Feb 2016

For more information, please contact Dr Richard Buggs, Senior Research Leader (Plant Health) at Kew (starting April 2016) <[r.buggs@qmul.ac.uk](mailto:r.buggs@qmul.ac.uk)>

<https://careers.kew.org/vacancy/early-career-research-fellowship-in-plant-health-251220.html>

Dr Richard Buggs | Senior Lecturer | School of Biological and Chemical Sciences, Queen Mary University of London, E1 4NS, United Kingdom | email: [r.buggs@qmul.ac.uk](mailto:r.buggs@qmul.ac.uk) | website: <http://www.sbcs.qmul.ac.uk/staff/richardbuggs.html> | office: +44(0)207 882 8441 | mobile: +44(0)772 992 0401 | twitter: @RJABuggs

Richard Buggs <[r.buggs@qmul.ac.uk](mailto:r.buggs@qmul.ac.uk)>

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## Kiel Germany 1PDF 3PhD CelegansEvolution

Kiel University, Germany

1 Postdoc + 3 PhD positions on the evolution and genetics of *C. elegans*-microbiota interactions

The positions are funded within a larger research initiative on host-microbiota interactions at Kiel University (Collaborative Research Center CRC1182 *Origin and function of metaorganisms*).



The postdoc and one PhD position are supervised by Hinrich Schulenburg (projects A1.1 and A4.3) and address the evolutionary dynamics and genomics of *C. elegans* microbiota interactions, based on evolution experiments and genome sequencing (Schulenburg group).

The second PhD project (project A1.2) is supervised by Katja Dierking (Schulenburg lab) and looks at the transcriptomic and also genetic basis of the interaction, using RNASeq and functional genetic analysis.

The third PhD project (project A1.3) is supervised by Matthias Leippe and assesses the involvement of antimicrobial peptides and proteins in shaping *C. elegans*-bacteria interactions using biochemical and functional genetic approaches (Leippe group).

For further information, please check the webpage of the Collaborative Research Center (<http://www.metaorganism-research.com/>) or the Schulenburg group (which includes Katja Dierking; <http://www.uni-kiel.de/zoologie/evoecogen/>) or the Leippe group (<http://www.uni-kiel.de/zoologie/zoophysiologie/>).

Application procedures are described on the webpage of the Collaborative Research Center (see above link; then under Jobs). Deadline for applications is 29 February 2016. If you have questions, then please contact either Hinrich Schulenburg ([hschulenburg@zoologie.uni-kiel.de](mailto:hschulenburg@zoologie.uni-kiel.de)), Katja Dierking ([kdierking@zoologie.uni-kiel.de](mailto:kdierking@zoologie.uni-kiel.de)), or Matthias Leippe ([mleippe@zoologie.uni-kiel.de](mailto:mleippe@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](mailto:hschulenburg@zoologie.uni-kiel.de) Web: [www.uni-kiel.de/zoologie/evoecogen/](http://www.uni-kiel.de/zoologie/evoecogen/) Hinrich Schulenburg <[hschulenburg@zoologie.uni-kiel.de](mailto:hschulenburg@zoologie.uni-kiel.de)>

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## LinkopingU Sweden GenomicsSexualDimorphims

Postdoc opportunity for 18 months with possible extension in the research group of Dr Urban Friberg at IFM Biology, Linkoping University Sweden. Our research group has a broad general interest in the area of evolutionary biology/genetics/genomics and ongoing projects focus on the evolution of ageing and the genetics/genomics of sexual dimorphism (see <https://www.liu.se/forskning/foass/urban-friberg?l=en> for more

information).

Most sexual species exhibit distinct differences between the sexes, despite males and females sharing the same genome. How this is accomplished is not yet fully understood. We use the model organism *Drosophila melanogaster* to learn more about this phenomenon. The successful applicant is expected to primarily work on two main projects. One aims to molecularly characterize the genetics of a recent reversal in male and female body size, while the second aims to enhance our understanding of genetic mechanisms that generate sex differences above and beyond those shaped by the sex determining pathway. There will also be opportunity to develop one's own ideas related to these questions. The successful candidate is expected to work closely with other members of the lab (see also PhD position advertised at EvolDir).

We seek a bright, highly motivated and enthusiastic person able to work both as part of a team and independently, having a PhD in evolutionary biology/genetics/genomics. Documented experience in one or several of the following topics is highly beneficial: statistics, quantitative genetics, *Drosophila* genetics/lab work, and, in particular, analyses of DNA and RNA sequence data. The working language at the department and lab is English. A high standard of spoken and written English is required.

Applications should be written in English and include i) a cover letter with information on your background, research interests and experiences, and your motivation to work on this project (max 3 pages), ii) complete CV, and iii) the names and email addresses of 2-3 referees. Applications should be sent as one PDF to [urban.friberg@liu.se](mailto:urban.friberg@liu.se). The position is open until filled, and applications will be reviewed continuously, but for full consideration please apply by March 1. The preliminary starting date is June 1 2016, but is flexible.

"urban.friberg@liu.se" <[urban.friberg@liu.se](mailto:urban.friberg@liu.se)>

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## LiverpoolSchMed MosquitoEvolutionaryGenetics

Post-Doctoral Research Assistant

The Department of Vector Biology seeks to appoint a post-doctoral research assistant (PDRA) to work with Professor Martin Donnelly <<http://www.lstmed.ac.uk/-about/people/professor-martin-james-donnelly>> on the



evolutionary genetics/ genomics of *Anopheles gambiae* with a particular focus on the evolution of insecticide resistance. Ref 006

The post holder will contribute to a project which assesses how heterogeneities in insecticide resistance influence malaria transmission. You will assist the analysis of data from a five country study on the impacts of insecticide resistance on epidemiological indicators of malaria. During your employment you will also have the opportunity to develop other research projects to support fellowship and research grant applications.

The ideal candidate will have an enthusiastic approach to work and have experience in one or more of the following areas:

\* Strong molecular biology laboratory skills \* Strong molecular genetic analytical skills \* Strong epidemiological or bioinformatics skills

It is essential that the candidate has a PhD in a relevant subject area and the ability to work as an integral, productive and co-operative member of a multi-disciplinary, diverse team including vector biology, biostatistics, epidemiology and parasitology

If you are interested in applying, please return your completed Application Form, Personal Details Form and Equal Opportunities Monitoring Form, stating vacancy reference number 006 to [jobs@lstmed.ac.uk](mailto:jobs@lstmed.ac.uk) (link sends e-mail), or by post to HR, Liverpool School of Tropical Medicine, Pembroke Place, Liverpool L3 5QA.

More details at <http://www.lstmed.ac.uk/post-doctoral-research-assistant-3> Please get in touch by email if you would like to discuss the position before applying.

Closing Date: Monday 29 February 2016, 12pm GMT.

Martin James Donnelly

Professor of Evolutionary Genetics Department of Vector Biology Malaria Programme Liverpool School of Tropical Medicine & Wellcome Trust Sanger Institute Pembroke Place Hinxton Liverpool Cambridge L3 5QA CB10 1SJ Tel +44(0) 151 705 3296 Fax +44(0) 151 705 3369 Email [martin.donnelly@lstmed.ac.uk](mailto:martin.donnelly@lstmed.ac.uk) Web <http://donnelly.openwetware.org/Home.html> Skype martin-donnelly

Martin Donnelly <[Martin.Donnelly@lstmed.ac.uk](mailto:Martin.Donnelly@lstmed.ac.uk)>

## Melbourne Avian Influenza Virus

Expression of Interest: Postdoctoral Research Scientist - Ecology and Evolution of Avian Influenza Virus

A postdoctoral research scientist is required for a new project on the ecology and evolution of avian influenza virus in wild birds funded by the Australian Research Council (ARC).

Avian influenza virus (AIV) has the potential to devastate the poultry industry and cause human pandemics. Although central to emergence, the factors that shape the genetic diversity of AIV in its wild water bird reservoir, including modes of transmission, are poorly understood. The aim of this project is to combine genomic, ecological and phylogenetic approaches to reveal key aspects of AIV evolution, as well as the risk for future viral emergence. Using sampling sites in Australia and Antarctica the project will aim to reveal the factors that shape AIV diversity on both local and global scales, the contrasting evolutionary dynamics of wild birds and poultry, and the role played by environmental transmission in AIV ecology, including its ability to ignite new epidemics.

Experience in molecular analysis of influenza viruses including, RNA extraction, RT-PCR, primer design, Sanger sequencing, Next-Generation Sequencing and bioinformatics is essential. Knowledge and experience in classical virology techniques such as influenza virus culture are desirable. The successful candidate will also be expected to assist in the organization of fieldwork and on sampling trips to collect samples from wild birds in Australia. The two-year position will commence in July 2016 and be based at the WHO Collaborating Centre for Research and Reference on Influenza, Melbourne, Australia, under the supervision of Dr. Aeron Hurt. A formal advertisement with detailed requirements, job specification, and salary will be posted at a later date.

If you are interested in the position, have appropriate qualifications, and would like more information please contact: Aeron Hurt ([Aeron.Hurt@influenzacentre.org](mailto:Aeron.Hurt@influenzacentre.org)), Eddie Holmes ([edward.holmes@sydney.edu.au](mailto:edward.holmes@sydney.edu.au)) or Marcel Klaassen ([marcel.klaassen@deakin.edu.au](mailto:marcel.klaassen@deakin.edu.au)).

PROFESSOR EDWARD C. HOLMES FAA NHMRC Australia Fellow

THE UNIVERSITY OF SYDNEY Marie Bashir Institute for Infectious Diseases & Biosecurity, Charles

Perkins Centre, School of Life & Environmental Sciences and Sydney Medical School, The University of Sydney | Sydney | NSW | 2006 | Australia T+61 2 9351 5591 F+61 2 9351 3890 Eedward.holmes@sydney.edu.au

edward.holmes@sydney.edu.au

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## Michigan State U BEACON Evolutionary Biology

\*BEACON Center for the Study of Evolution in Action\*

\*BEACON Distinguished Postdoctoral Fellows Program\*

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BEACON is an NSF Science and Technology Center headquartered at Michigan State University with partners at North Carolina A&T State University, University of Idaho, University of Texas at Austin, and University of Washington. BEACON brings together biologists, computer scientists, and engineers to study evolutionary dynamics using biological and computational techniques and to apply evolutionary principles to engineering problems. We seek outstanding post-doctoral scholars to pursue interdisciplinary research on evolution in action with BEACON faculty members, in the fields of biology, computer science, and/or engineering.

Applicants will propose a research project within the scope of BEACON's mission and must have two BEACON faculty sponsors who will serve as research mentors should the fellowship be awarded. One sponsor must be MSU faculty; the other sponsor may be from any of the five BEACON institutions. Preference is given for interdisciplinary research. The post-doc fellow will be based at Michigan State University in East Lansing. Please see our website (<http://www.beacon-center.org>) for information about BEACON mission, participants and ongoing research projects.

Applicants must submit the following, in a single PDF, to BEACON Managing Director Danielle Whittaker via email ([djwhitta@msu.edu](mailto:djwhitta@msu.edu)):

1. CV
2. A two-page description of their research plan
3. A one-page summary of their doctoral research
4. Letters of support from two BEACON sponsors (one must be from MSU)

5. Two additional letters of recommendation

Fellowships last two years and include a salary of \$50,000/year and modest funds to support research and travel. The successful applicant will help foster collaborations among faculty and disciplines and serve as a professional model for pre-doctoral trainees.

A Ph.D. in biology, computer science, engineering or related fields is required. Current MSU graduate students or postdocs are not eligible for this fellowship. US citizens or permanent residents only. Minority applicants are especially encouraged to apply. MSU is an Equal Opportunity/Affirmative Action Employer.

The deadline for applications is March 15, 2016.

– Danielle J. Whittaker, Ph.D. Managing Director BEACON Center for the Study of Evolution in Action 567 Wilson Road, Room 1441E Michigan State University East Lansing, MI 48824 (517) 884-2561 [djwhitta@msu.edu](mailto:djwhitta@msu.edu) <http://beacon-center.org> “Danielle J. Whittaker” <[djwhitta@msu.edu](mailto:djwhitta@msu.edu)>

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## NMBU Norway Systems Biology Farmed Salmon

Dear list,

We have an available researcher position in our DigiSal project ( <http://tinyurl.com/digisal> ) on the systems biology of farmed salmon, described below.

Best regards, Dr. Jon Olav Vik Department of Animal and Aquacultural Sciences Norwegian University of Life Sciences [jon.vik@nmbu.no](mailto:jon.vik@nmbu.no)

Position available: Researcher, systems biology of farmed salmon (NMBU, Ås, Norway)

The Department of Animal and Aquacultural Sciences seeks a SYSTEMS BIOLOGIST or MATHEMATICAL or COMPUTATIONAL BIOLOGIST to work on the SYSTEMS BIOLOGY OF FARMED SALMON (3-year researcher position with possibility of extension). Salmon farming is a big industry in Norway and ripe for systems biology applications thanks to the recent sequencing of the salmon genome.

The project “Towards the Digital Salmon: From a reactive to a pre-emptive research strategy in aquaculture (DigiSal)” is part of Digital Life Norway, the first call dedicated to systems biology by the Research Council of Norway. DigiSal will promote sustainable growth

of salmon farming by building model-based knowledge about how salmon responds to novel sustainable feed ingredients. This project combines nutritional expertise, cutting-edge salmon genomics, high-throughput omics technologies and model-based analysis of omics data.

The successful candidate will work within the Centre for Integrative Genetics (CIGENE), which includes comprehensive molecular lab facilities and a strong environment dedicated to bioinformatics and mathematical modeling.

Main tasks: Analyze how salmon metabolism depends on variation in diet and genotype, based on omics and microscopy data and using a variety of modelling frameworks, both top-down multivariate analysis and bottom-up metabolic network modelling.

The successful applicant will be part of a highly interdisciplinary group, with possibilities for visits to collaborators in the Systems and Synthetic Biology unit in Wageningen, the Netherlands. The researcher will work closely with a dedicated systems biology informatics manager to ensure findable, accessible, interoperable and reusable data and models.

Full advertisement: <https://www.jobbnorge.no/en/-available-jobs/job/122082/researcher-position-systems-biology-of-farmed-salmon-refno-16-00881> Application deadline: Monday 2016-03-07. Email enquiries welcome: Jon Olav Vik, [jon.vik@nmbu.no](mailto:jon.vik@nmbu.no).

Please forward this announcement to anyone you think might be interested!

[jonovik@gmail.com](mailto:jonovik@gmail.com)

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## NotreDame BroadInst MosquitoSpeciationGenomics

POSTDOC: Species boundaries and evolutionary history of a cryptic radiation of malaria vectors

A Postdoctoral position funded by a 2-year NIH grant is available April 2016 to work between two population genomics groups: that of Nora Besansky at the University of Notre Dame (<http://www3.nd.edu/~nbesansk/>), and that of Daniel Neafsey at the Broad Institute of MIT and Harvard (<http://www.broadinstitute.org/-bios/daniel-neafsey>).

We are seeking highly qualified and enthusiastic applicants with a background in population genetics and evolution, to analyze whole genome sequence data and infer speciation history in the *Anopheles funestus*\*

complex.

**BACKGROUND:** Major malaria vectors are a rarity in the mosquito genus *Anopheles*, and they are not phylogenetically clustered. On the contrary, malaria vectors are almost invariably members of sibling species complexes containing minor or non-vector species, indicating that the traits endowing major vector status have evolved recently, rapidly and repeatedly in different species complexes. Powerful insights about the genetic basis of vector traits can be gained by comparative genomics of vectors and non-vectors across these replicate systems of vector evolution. A crucial first step toward that end was taken with the assembly of 16 *Anopheles*\* genomes led by Besansky at Notre Dame and Neafsey at the Broad Institute, with the *Anopheles gambiae*\* complex as one case study (Neafsey et al 2015 Science; Fontaine et al 2015 Science). A next step is to consider other lesser known but equally important sibling species complexes. *Anopheles funestus*\* is one of the three most important and widespread vectors of human malaria in tropical Africa, but unlike *An. gambiae*\*, it is understudied. This major vector conceals a group of close relatives that are morphologically similar or identical as adults. The taxonomic complexity of this group is at least as high as the *An. gambiae*\* complex; within each named (and unnamed) species are genetically heterogeneous clusters whose interrelationships have never been resolved, and additional cryptic diversity is being reported by vector control programs. Moreover, echoing the situation in the *An. gambiae*\* complex, there is evidence for historical or ongoing introgression between *An. funestus* and at least one other taxon.

**PROJECT:** As part of this NIH project, complete de novo reference genome assemblies will be generated at the Broad for available species in the *An. funestus*\* complex, based on the DISCOVAR de novo algorithm. Additional low coverage HiSeq data will be generated from natural population samples. The successful post-doctoral candidate will use the new reference assemblies and additional light whole genome sequencing (~12 samples/taxon) to construct an initial portrait of population genomic patterns and species relationships for the *An. funestus*\* complex. Although the position is based at Notre Dame, the postdoc will have the opportunity to split time between Notre Dame and Broad, benefitting from interactions with active research groups in both stimulating locations.

**REQUIREMENTS:** (1) A PhD in genetics/genomics, evolutionary biology, or a related discipline; (2) a strong background in statistics and population genetics; (3) good communication skills and proficiency in English, both speaking and writing.

**PREFERENCES:** The ideal candidate will be a highly motivated individual with (i) proficiency in the Linux/Unix computing environment, familiarity with R, and at least one other programming language (e.g. Python or Perl); (ii) experience with the analysis of high throughput biological data sets; and (iii) an excellent record of scientific publication.

**HOW TO APPLY:** Applicants should submit a single PDF file ( tofunestus.postdoc@gmail.com) containing (1) a cover letter briefly summarizing past research accomplishments and future goals; (2) a CV; (3) the names and contact information for three references. Screening of applicants will begin immediately and continue until the position is filled.

**ADDITIONAL INFORMATION:** The University of Notre Dame is located on the northern limits of South Bend, Indiana [90 miles (150 km) east of Chicago]. Postdoctoral scholars in the Department of Biological Sciences (biology.nd.edu) have access to outstanding faculty, cutting-edge research infrastructure, and various avenues for career development. Research in the department spans the wide spectrum of the life sciencesXfrom cells and organs to whole organisms and ecosystems. This uncommon level of wide-ranging yet integrative biological inquiry provides an extraordinary environment for learning, innovation and collaboration. Centers and Institutes enhance our intellectual mission, and include the Eck Institute for Global Health, Center for Rare and Neglected Diseases,

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## Paris BlindSnakeEvolution

Postdoctoral researcher in functional morphology

Project title: Anatomy, phylogeny and origins: understanding the evolution of scolecophidian snakes.

Supervisors: Nicolas Vidal (UMR7205; nicolas.vidal@mnhn.fr) and Anthony Herrel (UMR7179; anthony.herrel@mnhn.fr).

Location: Muséum National d'Histoire Naturelle, Paris, France

Salary:  $\hat{A}\pm 2500$ Euro/month ( $\hat{A}\pm 2000$  Euro net) funded

by the LabEx BCDiv. Salary will vary with experience based on national salary scales defined by the CNRS.

We are looking for a postdoctoral researcher who is interested to work on a collaborative project devoted to a better understanding of blindsnakes (Scolecophidia). The postdoctoral researcher will collaborate closely with the supervisors to 1) sequence twenty slow evolving markers to obtain a better resolved phylogeny, 2) scan and segment  $\hat{A}\mu$ CT scans of specimens from the collection of the Museum in Paris, to be completed with specimens from other collections, 3) conduct field work to collect in vivo data on burrowing performances in live animals, 4) integrate these data in a time-calibrated phylogenetic framework established during the course of this research to evaluate the evolution of cranial anatomy and burrowing performance in blindsnakes.

Expertise in phylogenetic methods and with the analysis of  $\hat{A}\mu$ CT scans are a requirement. Experience with live animals, field work and expertise in functional morphology are considered as additional positive elements for the candidate.

Candidates should send (1) a letter of motivation, (2) a full CV, and (3) two letters of recommendation to the following e-mail addresses: nicolas.vidal@mnhn.fr; anthony.herrel@mnhn.fr

The deadline for submission of applications is May 1st, 2015.

Please contact Nicolas Vidal or Anthony Herrel for additional information.

– Anthony Herrel Associate Editor Herpetological Journal, The European Journal of Anatomy & Functional Ecology Branch Editor Functional anatomy of amphibians and reptiles Zookeys Editorial board member J. Zoology & Zoology

UMR 7179 C.N.R.S/M.N.H.N. Département d'Ecologie et de Gestion de la Biodiversité, 55 rue Buffon, Bat Anatomie Comparee, CP 55, 75005, Paris Cedex 5, France e-mail: anthony.herrel@mnhn.fr - phone: ++33-140798120 - fax: ++33-140793773 URL: [www.anthonyherrel.fr](http://www.anthonyherrel.fr) Anthony Herrel <anthony.herrel@mnhn.fr>



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## Paris CNRS Theoretical Evolutionary Ecol

Postdoc position in theoretical evolutionary ecology in Paris (France)

A postdoc position, funded by the French National Research Agency (ANR), is available to work with Florence Débarre in the SMILE group (Stochastic Models for the Inference of Life Evolution), at Collège de France in Paris (France). We are an interdisciplinary research group gathering biologists, probabilists, and bioinformaticians; our lab is located in the Latin Quarter in Paris.

We are looking for a highly motivated postdoc interested in developing mathematical and computational models of evolution, to explore various aspects of the effects of environmental heterogeneity and population subdivision on local adaptation and diversification. Background (or a strong interest) in evolutionary biology / ecology and strong quantitative skills are required for the position.

The position can start April 15th 2016 or later. It is initially for 1 year, but can be renewed twice. Salary is commensurate with experience.

Feel free to contact me if you have any questions about the position.

\*To apply:\* If you are interested in this position, please send a CV, a 1-page description of your research interests and motivation, and the contact details of potential references (all in one single pdf) to Florence Débarre (florence.debarre@college-de-france.fr). Review of applications will start on February 15th, but will continue until the position is filled.

– Florence Débarre website: <http://www.normalesup.org/~fdebarre/> SMILE Team: <http://www.lpma-paris.fr/smile/> CIRB: <http://www.college-de-france.fr/site/en-cirb/index.htm>  
 Collège de France: <http://www.college-de-france.fr/site/en-college/index.htm> [https://en.wikipedia.org/wiki/Coll%C3%A8ge\\_de\\_France](https://en.wikipedia.org/wiki/Coll%C3%A8ge_de_France) Centre Interdisciplinaire de Recherche en Biologie (CIRB) Collège de France CNRS/ UMR 7241 - Inserm U1050 11, Place Marcelin Berthelot 75231 Paris Cedex 05 France

flo.debarre@gmail.com

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## Paris Evolutionary Genetics

\*POSTDOCTORAL POSITION in Paris, France: \*

\*Adaptation of the gut microbiota to changes in lifestyle\*

A 2-year postdoctoral position in evolutionary genetics is available in Paris to study the biodiversity of the gut microbiota in human populations with contrasted lifestyles. The position is funded by the ANR (French National Research Agency) and will be supervised by Laure Ségurel (UMR 7206 Ecoanthropology and ethnobiology, head: Evelyne Heyer). Starting date is around January 2017.

Humans are not only able to adapt to the environment through changes in their own genes, but also through changes in the diversity and composition of the microorganisms living in and on them. Notably, the gut microbiota represents an important target for natural selection to act on, as well as a significant factor to consider for human health. The aim of this project is to describe the biodiversity of the gut microbiota in populations with contrasted subsistence modes (hunter-gatherers, farmers, herders), investigate the factors responsible for the loss of microbial diversity in industrialized populations and explore co-evolutionary processes between the microbiome and the host genetic variation.

The candidate will be in charge of the analysis of metagenomic data collected in the lab in Central Africa, and its interpretation in light of dietary, medical and environmental data. He/She will also analyze jointly human and microbial genomic data. Applicants for the position must have a background in evolutionary or computational biology. Ideally, the candidate will have prior experience with handling large-scale data and with the use of bioinformatics and statistical tools.

\*Contact: \*To apply, please send your CV, including the contact details of two references, and a letter describing your research interests and skills to Laure Ségurel (lsegurel@mnhn.fr)\*.\*

– Laure Ségurel CNRS Researcher UMR 7206 - Ecoanthropology and ethnobiology Musée de l'Homme, 17 place du Trocadéro, 75016, Paris, France +33 1 44 05 73 13

Laure Ségurel <lsegurel@mnhn.fr>



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## Roscoff MarineBiodiversity

A 1-year postdoctoral fellowship is available at the Roscoff Biological Station ([www.sb-roscoff.fr](http://www.sb-roscoff.fr)) of the University Pierre & Marie Curie (Paris6), France. The candidate will work in close collaboration with Dr Christophe Lejeusne ([clejeusne@sb-roscoff.fr](mailto:clejeusne@sb-roscoff.fr)) to investigate the effects of environmental gradients (e.g. pollution) on species diversity in marinas, with a special focus on non-indigenous species. Observational and experimental approaches would be run.

The postdoc will be in charge of characterizing and analyzing the diversity and structure of some harbor communities (including through integrative taxonomy approaches, and photo surveys) and its exposure to contaminants (through biomarkers and water quality assessment). Aquaria and in situ experiments would also be conducted on manipulated communities (e.g. increased diversity of introduced species).

The ideal candidate will have expertise in the analysis of community data, especially from hard substrates and/or artificial substrates. Candidates with expertise in taxonomy are very welcome (especially of sponges, tunicates, mollusks, but not only). An ability to run both aquarium and field experiments is highly desirable. Scientific diving is a plus.

The candidate will be based at the Roscoff Biological Station and will benefit from the support of its platforms for observational and experimental works (diving, in situ and aquaria experiments), and also for taxonomic expertise.

The candidate will be part of the Diversity and Connectivity group (<http://www.sb-roscoff.fr/en/divco>).

Duration: 1 year (possibly one additional year depending on funding)

Salary: about 2000 euros per month (after taxes)

Administrative requirements:

# Either non-French citizens, or French citizens having spent at least 12 months out of France over the last 36 months (3yrs)

# PhD should have been defended less than 2 years ago

Preferred start date: as soon as possible but no later than early June 2016

An ability to communicate in English is essential, and a

willingness to learn French is desirable (but not mandatory).

Interested candidates should send a detailed CV and a letter expressing their interest in this position by email to the address given ([clejeusne@sb-roscoff.fr](mailto:clejeusne@sb-roscoff.fr)). They should also provide details of two potential referees.

Review of applications will begin immediately and continue until the position is filled. Further information on the project can also be requested from the same address.

Christophe Lejeusne Associate Professor University Pierre & Marie Curie (Paris 6)

AD2M < <http://www.sb-roscoff.fr/UMR7144/> > - Adaptation & Diversité en Milieu Marin

UMR 7144 UMPC - CNRS Group Diversity & Connectivity - Div&Co < <http://www.sb-roscoff.fr/divco.html> >

Station Biologique de Roscoff Place Georges Teissier - CS90074 29688 Roscoff - France

[clejeusne@sb-roscoff.fr](mailto:clejeusne@sb-roscoff.fr) Ph.: +33-298 292 372

Christophe Lejeusne <[christophe.lejeusne@sb-roscoff.fr](mailto:christophe.lejeusne@sb-roscoff.fr)>

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## SpelmanC Atlanta MicrobialEvolution

Postdoc Position in: Microbial Evolution, Behavior and Genomics

Location: Atlanta, Georgia, USA

Funding Source: CURE Postdoctoral Fellowships [Spelman College is piloting a postdoctoral fellowship program that combines a traditional principal-investigator directed postdoctoral research experiences with mentored teaching experiences.]

A postdoc position (2.5 years) is available to conduct experimental and computational research on small eukaryotic amoeboid microbes relating to their evolution and sexual life cycle behavior. Candidates should have an inter-disciplinary training or familiarity with molecular (e.g. next generation sequencing) and computational (bioinformatics, phylogenetics) skills.

Potential research topics include (i) genomics and evolution of phenotypic traits in cryptic species, (ii) evolution of sexual-like behavior and development in amoeboids, (iii). origin, evolution and biodiversity of amoeboids

using large-scale analysis. (iv). evolution of amoeboid movement and cytoskeleton architecture. Additional projects under similar topics can be also considered based on individual experience and interest. For additional information contact: ytekle@spelman.edu

This position offers competitive salary and benefit. Candidates should complete Ph.D. training before starting this position. This position is open to US citizens and lawful permanent residents only. Screening of applicants will begin immediately and continue until the position is filled.

Spelman College is a private four-year liberal arts college located in Atlanta, GA, and ranked one of the top 100 liberal arts colleges by the US News.

Please email a copy of curriculum vitae, a short statement of research interest, names and contact information of at least three individuals familiar with your research to Dr. Yonas Tekle through ytekle@spelman.edu

350 Spelman Ln SW, Box 1183, Department of Biology, Spelman College, Atlanta, GA 30314-4399 LOCATIONS Office: AFM Science Center 271; Lab: AFM Science Center 247 Phone: 404-270-5779 (office); Fax: 404-270-5725

Yonas Isaak Tekle <yonastekle@gmail.com>

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## StockholmU BalticBiodiversity PlantEvol

\*5 Postdoctoral Fellows in Baltic Sea Research and in Plant Sciences\*

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\*Closing date: April 30, 2016\*\*\*

\*The\*\*Department of Ecology, Environment and Plant Sciences (DEEP) at Stockholm University\* conducts research and education in an international environment. Its subject areas are marine ecology, marine ecotoxicology, plant ecology, plant physiology and plant systematics. The research is both basic and applied, often with a broad and interdisciplinary approach. About 150 people work at the department, including some 30 teachers or senior researchers, 10 postdocs and 60 PhD students.

We are now recruiting:

\*3 Postdoctoral Fellows in Baltic Sea Research\*, for example including any of the following topics:

- Benthic ÅV pelagic coupling

- Mitigation of marine anthropogenic effects
- Climate change effects on the Baltic Sea ecosystem
- Baltic Sea biodiversity
- Coastal-offshore interactions

\*2 Postdoctoral Fellows in Plant Sciences\*, for example including any of the following topics:

- Plant evolution
- Interactions between plants and other organisms
- Climate change effects on plant phenology and distribution
- Plant growth and development

Each position will be linked to the research group of one of the professors, associate professors or assistant professors at the department ([www.su.se/deep](http://www.su.se/deep)). You should therefore first contact the group leader whose group you wish to join (a) to enquire whether this person would be interested to include you in his/her research group and (b) to discuss and formulate your project proposal.

Your project proposal could be a new idea of your own or it could be part of ongoing work in the group. The important aspect is that the group leader supports your application, which ensures that the infrastructure and knowledge to support your project is available.

For further information see: <http://www.su.se/english/about/vacancies/vacancies-new-list?rmpage=-job&rmjob=1128>

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## ToulouseCNRS EvolutionOfPlasticityNonGeneticInheritance

Postdoc: EvolutionOfPlasticityNonGeneticInheritance

A postdoctoral research associate position is available at CNRS (France) at the Evolution & Biological Diversity laboratory in Toulouse. The postdoc will work in the ERC team of Benoit Pujol (<http://bit.ly/1svZZ6N>) and be part of a team of scientists studying the evolutionary ecology and the adaptive potential of plant populations.

Stem elongation in response to shade is a school book example of phenotypic plasticity in plants. Our aim is to study the inheritance and the evolution of this developmental reaction norm by using experimental approaches. The aim is to assess the response to selection of stem elongation in experimental populations of *Antirrhinum majus*,/ the snapdragon. One implication of this work

will be to investigate the role of non genetic inheritance as a driver of plant adaptive evolution.

Potential projects are flexible within the scope of the project and there is scope for collaboration on other projects underway in the team.

We are looking for a candidate with a strong background in plant or animal breeding and/or evolution of phenotypic plasticity and/or plant selection experiments. Expertise in quantitative genetics and proficiency in R are welcome. Experience in managing large plant population experiments and working with experimental research assistants are welcome too. French is not mandatory. A Ph.D. in evolutionary ecology, quantitative genetics, plant breeding or closely related field is required. We seek to recruit enthusiastic and motivated young researchers with no previous experience, 3-5 years of postdoctoral research experience, or more. The initial appointment is for two years, with the potential for additional years of support conditional on performance. Start dates between early April and late May 2016, with preference for earlier dates.

To apply, please send (1) a cover letter explaining your interest in the position, (2) a CV, and (3) contact information (phone number and email) for three references to Benoit Pujol: benoit.pujol@univ-tlse3.fr

Closing date for application: March 1, 2016

Exemple of salary (depending on experience): 34,626 euros a year (monthly salary after tax ~2328 euros) for researcher with 3-5 years experience

45,600 euros a year (monthly salary after tax ~2809 euros) for researcher with 5-10 years experience

– \*Benoit PUJOL\* Researcher in evolutionary ecology at CNRS, France Quantitative genetics in the wild and non genetic inheritance

Lab. Evolution & Diversité Biologique (EDB) Office 104, Bat. 4R1, Université de Toulouse Paul Sabatier, 118 Route de Narbonne 31062 Toulouse Cedex 09 Mail: benoit.pujol@univ-tlse3.fr

“benoit.pujol@univ-tlse3.fr” <benoit.pujol@univ-tlse3.fr>

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## ToulouseCNRS ExperimentalSelectionOfPlasticity

Postdoc: ToulouseCNRS.ExperimentalSelectionOfPlasticity

A postdoctoral research associate position is available in the laboratory of Benoit Pujol (<http://bit.ly/1svZZ6N>) at CNRS in Toulouse (France) to study transgenerational phenotypic plasticity and its change in response to selection in *Antirrhinum majus*, the snapdragon.

The postdoctoral associate will work as a member of the ERC-funded ANGI project and use selection experiments to understand how selection shapes non-genetically inherited phenotypic variation at ecologically relevant traits. This central question in evolutionary biology is being tackled using up-to-date methods and a variety of approaches, including selection experiments, quantitative genetics and epigenetics. The postdoctoral associate will participate to experimental work. Potential projects are flexible within the scope of the project. The successful candidate will be part of a team of scientists studying the evolutionary ecology and the adaptive potential of plant populations. There will be scope for collaboration on other projects underway in the team.

We are looking for a candidate with a strong background in selection and/or phenotypic plasticity experimental work in plants (and/or quantitative genetics), proficiency in R and experience in handling large plant population experiments. French is not mandatory. A Ph.D. in evolutionary ecology, quantitative genetics, plant breeding or closely related field is required. We seek applicants with 3-5 years of postdoctoral research experience. The initial appointment is for two years, with the potential for additional years of support conditional on performance. Start dates between early April and late May 2016, with preference for earlier dates.

To apply, please send (1) a cover letter explaining your interest in the position, (2) a CV, and (3) contact information (phone number and email) for three references to benoit.pujol@univ-tlse3.fr <mailto:benoit.pujol@univ-tlse3.fr>

Closing date for application: March 1, 2016

SALARY (depending on experience):

Wage 34,626 euros a year (monthly salary after tax ~2328 euros) if 3-5 years experience

Wage 45,600 euros a year (monthly salary after tax

~2809 euros) if 5-10 years experience

\*Benoit PUJOL\* Researcher in evolutionary ecology at CNRS, France Quantitative genetics in the wild and non genetic inheritance

Lab. Evolution & Diversité Biologique (EDB) Office 104, Bat. 4R1, Université de Toulouse Paul Sabatier, 118 Route de Narbonne 31062 Toulouse Cedex 09 Mail: benoit.pujol@univ-tlse3.fr

“benoit.pujol@univ-tlse3.fr” <benoit.pujol@univ-tlse3.fr>

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### ToulouseCNRS France HeritabilityAndSelectionInTheWild

Postdoc: ToulouseCNRS.HeritabilityAndSelectionInTheWild

A postdoctoral research associate position is available at CNRS in the laboratory Evolution & Biological Diversity in Toulouse, France. The postdoctoral associate will participate to the ERC-funded ANGI project (PI: Benoit Pujol <http://bit.ly/1svZZ6N>). The aim is to study the heritability of traits (additive genetic variation, ecological niche transmission) and the heterogeneity of selection in wild populations of /Antirrhinum majus,/ the snapdragon.

To date, we have cumulated 6 years of data (4000 plants, 6 generations) from the /in situ/ exhaustive survey of flowering snapdragon plants in fragmented populations growing on the Mediterranean coast in southern France. The postdoctoral associate will work with other team members on the creation and analysis of this large dataset combining phenotypes (multiple vegetative and reproductive traits), locations, pedigrees, and microsatellite marker data. The postdoctoral associate will participate to field work. A large part of the data is already available. Analyses and publication preparation will therefore not be limited by the field trip seasonality.

French is not mandatory. A Ph.D. in evolutionary ecology, quantitative genetics, or closely related field is required. We seek enthusiastic and motivated applicants with no experience, 3-5 years of postdoctoral research experience, or more. Proficiency in R and expertise in quantitative genetics are welcome. Expertise in quantitative genetic and/or selection analyses conducted on wild population data is particularly welcome, even if such work was not carried out on plants. The initial appointment is for two years, with the potential for additional years of support conditional on performance.

Start dates between early April and late May 2016, with preference for earlier dates.

To apply, please send (1) a cover letter explaining your interest in the position, (2) a CV, and (3) contact information (phone number and email) for three references to [benoit.pujol@univ-tlse3.fr](mailto:benoit.pujol@univ-tlse3.fr) Closing date for application: March 1, 2016

Exemple of salary (depending on experience):

34,626 euros a year (monthly salary after tax ~2328 euros) for a researcher with 3-5 years experience  
45,600 euros a year (monthly salary after tax ~2809 euros) for a researcher with 5-10 years experience

– \*Benoit PUJOL\* Researcher in evolutionary ecology at CNRS, France Quantitative genetics in the wild and non genetic inheritance

Lab. Evolution & Diversité Biologique (EDB) Office 104, Bat. 4R1, Université de Toulouse Paul Sabatier, 118 Route de Narbonne 31062 Toulouse Cedex 09 Mail: benoit.pujol@univ-tlse3.fr

Benoit PUJOL <benoit.pujol@univ-tlse3.fr>

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### ToulouseCNRS WildPlantQuantitativeGenetics

Postdoc: ToulouseCNRS.WildPlantQuantitativeGenetics

A postdoctoral research associate position is available in the laboratory of Benoit Pujol (<http://bit.ly/1svZZ6N>) at CNRS in Toulouse (France) to study natural selection and the quantitative genetics of /Antirrhinum majus,/ the snapdragon.

The postdoctoral associate will work as a member of the ERC-funded ANGI project and use pedigree based analyses to understand heterogeneous selection, adaptive transgenerational plasticity and the quantitative genetic architecture of adaptive traits in wild plant populations in southern France. Potential projects are flexible within the scope of the project.

To date, we have cumulated 6 years of data (6 generations) from the /in situ/ exhaustive survey of plants. The postdoctoral associate will work with other team members on the creation and analysis of this large dataset combining phenotypes (multiple vegetative and reproductive traits), locations, pedigrees, and microsatellite marker data for 4000 plants. The postdoctoral associate will participate to field work every year (gen-

erally the whole month of June). Some data is currently available and ready for analysis, thus the postdoctoral associate can expect to begin working on analyses for publication during the first year of their appointment. There will be scope for collaboration on other projects underway in the team.

French is not mandatory. A Ph.D. in evolutionary ecology, quantitative genetics, or closely related field is required. We seek applicants with 3-5 years of postdoctoral research experience, proficiency in R and a strong background in quantitative genetics. Experience in wild population quantitative genetics, even if not plant related, is particularly welcome. The initial appointment is for two years, with the potential for additional years of support conditional on performance. Start dates between early April and late May 2016, with preference for earlier dates.

To apply, please send (1) a cover letter explaining your interest in the position, (2) a CV, and (3) contact information (phone number and email) for three references to benoit.pujol@univ-tlse3.fr <mailto:benoit.pujol@univ-tlse3.fr>

Closing date for application: March 1, 2016

SALARY (depending on experience):

Wage 34,626 euros a year (monthly salary after tax ~2328 euros) if 3-5 years experience

Wage 45,600 euros a year (monthly salary after tax ~2809 euros) if 5-10 years experience

\*Benoit PUJOL\* Researcher in evolutionary ecology at CNRS, France Quantitative genetics in the wild and non genetic inheritance

Lab. Evolution & Diversité Biologique (EDB) Office 104, Bat. 4R1, Université de Toulouse Paul Sabatier, 118 Route de Narbonne 31062 Toulouse Cedex 09 Mail: benoit.pujol@univ-tlse3.fr

“benoit.pujol@univ-tlse3.fr” <benoit.pujol@univ-tlse3.fr>

## TuftsU MicrobialGenomics

Post-doc position in genomics/ecology/evolution of food microbiomes in the Wolfe Lab @ Tufts University (Boston Area, USA). <https://sites.tufts.edu/wolfelab/join-the-wolfe-lab/> The Wolfe lab in the Department of Biology at Tufts University (<https://sites.tufts.edu/wolfelab/>) is seeking a post-doc to join the lab in June

2016 (start date flexible). Our lab studies the ecology and evolution of microbial communities, using tractable microbial communities isolated from food (cheese, kimchi, fermented tea) as model systems. Our work spans taxonomic boundaries (we study both prokaryotes and eukaryotes) and integrates a wide variety of techniques including experimental evolution, metagenomics, comparative genomics/transcriptomics, genome engineering, and in situ community reconstructions. Our research questions are strongly anchored in basic biology, but our work will help address emerging issues in human health and food quality/safety.

The ideal candidate will be a creative, independent, and integrative scholar with interests in discovering the ecological and evolutionary processes that generate microbiome diversity. Ideal candidates will have the following:

- a PhD in molecular biology, microbiology, systems biology, or genetics
- extensive experience in the molecular genetics of bacteria or fungi
- experience with generating and analyzing next-generation sequencing datasets
- the ability to develop and implement bioinformatics tools
- excellent time management, oral communication, and writing skills
- a track record of supporting an engaging, thoughtful, and collaborative lab environment

This position also provides ample opportunities for the post-doc to develop teaching/outreach skills. Our accessible and engaging model systems provide powerful tools to promote microbial literacy in the college classroom as well as in our local communities (<https://sites.tufts.edu/wolfelab/open-lab/>). Members of the lab communicate their science through social media, writing for online publications, and by developing novel public outreach experiences.

Current research in the lab is aimed at linking ecological and evolutionary patterns of microbial diversity with the molecular mechanisms that generate these patterns. What are the mechanisms that govern species distributions or community-level traits? How do these mechanisms evolve within a community and what are the consequences of trait evolution within microbial communities? How can we manipulate these mechanisms to control microbiome composition and function? We are also working on applied projects as part of the Tufts University Science and Sensory Center (<https://sites.tufts.edu/wolfelab/tufts-sensory-and-science-center/>) that aim to link microbiome composition with the chemical and sensory properties of microbial foods

The Wolfe lab is based in a newly renovated lab space associated with the Tufts University Medford Campus. In addition to diverse research being conducted in the Department of Biology that spans the entire breadth



of biology (<http://ase.tufts.edu/biology/>), the Sackler School of Graduate Biomedical Sciences at the Tufts Medical School has an outstanding group of microbiologists (<http://bit.ly/WDvgqA>). There are also numerous potential collaborators and resources at the Tufts Friedman School of Nutrition and the Cummings School of Vet Medicine. The academic community in the Greater Boston Area has an unprecedented collective wealth of resources in microbiology, ecology, and evolution.

To apply, email Dr. Benjamin Wolfe ([benjamin.wolfe@tufts.edu](mailto:benjamin.wolfe@tufts.edu)) with: 1) a short description of why you are interested in and qualified for the position, 2) a CV listing peer-reviewed publications, skills, and research experiences, and 3) the names and contact information for three references. Applications will be considered as they are received. For full consideration, apply on or before April 15th, 2016.

\*Benjamin E. Wolfe\* Assistant Professor Tufts University Department of Biology 200 Boston Ave., Suite 4700 Medford, MA 02155 \*Email:\* [benjamin.wolfe@tufts.edu](mailto:benjamin.wolfe@tufts.edu) \*Office phone:\* 617-627-0694 \*Lab website:\* [sites.tufts.edu/wolfelab/](http://sites.tufts.edu/wolfelab/)

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 <[benjamin.wolfe@tufts.edu](mailto:benjamin.wolfe@tufts.edu)> “benjamin.wolfe@tufts.edu” <[benjamin.wolfe@tufts.edu](mailto:benjamin.wolfe@tufts.edu)>

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## UBordeaux QuantitativeEcology

Postdoctoral position in quantitative ecology

The University of Bordeaux is recruiting a postdoctoral researcher with a modelling background in community or ecosystem ecology, to work on species interactions and ecosystem dynamics.

The postdoc will join the Integrative and Theoretical Ecology chair of the Labex COTE (<http://cote.labex.u-bordeaux.fr/ChairITE>), and will interact with Frédéric Barraquand and other members of the ITE chair. We work on collaborative research projects with partners from French research institutes (CNRS, INRA, IRSTEA, IFREMER), as well as internationally, on both ecological interactions and cross-ecosystem flows. Some of our studies focus on areas of special interest to the Labex COTE, the Gironde estuary and the Arcachon bay area.

Research in the chair ranges from general theory to applied modelling. Current projects include fitting stochas-

tic models to community-level time series to infer interaction strengths, predicting the responses of estuarine food webs to anthropogenic disturbances, ecological theory on the effects of material or biological subsidies and forest-stream linkages (e.g., decomposition processes). The candidate could develop his/her own research question in a related direction. If relevant, there will be opportunities to connect with social sciences through collaborations with ecological economists.

We are looking for a researcher with a strong modelling skillset, able to work in a team. A good knowledge of population dynamics and food web models is essential, as well as proficiency with Matlab or R. A solid background in either statistics or ecosystem ecology is a plus. Familiarity with Linux and compiled programming languages (e.g., C, Fortran) would be desirable.

The position is funded for two years by the Labex COTE. Applicants should send a cover letter describing their interest in the position, a curriculum vitae, and name and contact information of three references to [manager-labexcote@u-bordeaux.fr](mailto:manager-labexcote@u-bordeaux.fr) by April 1, 2016.

For additional information on the research project, contact [frederic.barraquand@u-bordeaux.fr](mailto:frederic.barraquand@u-bordeaux.fr)

For additional information regarding the application procedure and employment conditions, contact [manager-labexcote@u-bordeaux.fr](mailto:manager-labexcote@u-bordeaux.fr)

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Frédéric Barraquand Researcher <https://sites.google.com/site/fredbarraquand/home> University of Bordeaux Integrative and Theoretical Ecology Chair - Labex COTE <http://cote.labex.u-bordeaux.fr/ChairITE> [cote.labex.u-bordeaux.fr](http://cote.labex.u-bordeaux.fr)

“[frederic.barraquand@u-bordeaux.fr](mailto:frederic.barraquand@u-bordeaux.fr)”

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## UCalgary PlantComparativeGenomics

POSTDOCTORAL RESEARCH POSITIONS at the UNIVERSITY of CALGARY

Seeking two postdocs to work on plant comparative genomics in the Yeaman lab in the Department of Biological Sciences at the University of Calgary. Lots of de novo data to analyze. Two positions are available (2 years each), one beginning as soon as possible and the other in fall 2016 or winter 2017. Experience with searching large datasets for signatures of selection,

genome annotation, orthology identification and analysis, and/or comparative transcriptomics is absolutely necessary for the position beginning soon; the second position is oriented more towards landscape genomics and local adaptation, so experience in that area is highly desirable. Good salary, negotiable, commensurate with experience.

University of Calgary is located in a beautiful corner of the world, just one hour from the Rocky Mountains.

Please contact Sam Yeaman at samuel.yeaman@ucalgary.ca for details.

“yeaman@zoology.ubc.ca” <yeaman@zoology.ubc.ca>

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## UCalifornia Berkeley 2 Genomics

University of California, Berkeley Postdoctoral Scholar - Genomics - Department of Environmental Science, Policy & Management

**POSTDOCTORAL SCHOLAR POSITION AVAILABLE IN THE DEPARTMENT OF ENVIRONMENTAL SCIENCE, POLICY & MANAGEMENT** The Department of Environmental Science, Policy, and Management at UC Berkeley is currently seeking two Postdoctoral Scholars in Genomics and Functional Genetics in the laboratory of Dr. Neil Tsutsui. We are seeking two Postdoctoral Scholars to study the genetic basis of ant social behaviors. Previous work has focused on the genetics, behavior, and chemical ecology of the invasive Argentine ant (*Linepithema humile*). The central focus of the Postdoctoral Scholars' research will be the genetic basis of chemical communication, including the production and perception of pheromones that Argentine ants use to regulate fundamental behaviors, including foraging, queen production, and colony mate recognition.

**BASIC QUALIFICATIONS** Candidates must have completed all degree requirements except the dissertation or be enrolled in an accredited PhD or equivalent degree program in biology, genetics, or related field at the time of application.

**ADDITIONAL QUALIFICATIONS** Candidates must have a PhD, MD, or equivalent degree in biology, genetics, or related field by appointment start date.

**PREFERRED QUALIFICATIONS** Demonstrated expertise in one or more of the following areas: production and analysis of whole-genome datasets, RNAseq, RNAi-mediated gene silencing, and bioinformatic analysis of

large genomic datasets. Candidates fluent in chemical ecology, insect biology, population genetics, and/or behavioral ecology are desirable. Preferred candidates will demonstrate excellent communication skills and the ability to work both independently and as a member of a small team. Applicants must have fewer than five years of prior post-doctoral experience.

**APPOINTMENT** The targeted start date for this position is March 1, 2016. The initial appointment is for one year, with renewal based on performance and funding. This is a full-time appointment.

**SALARY AND BENEFITS** The salary range is between \$42,840 - \$50,112 commensurate with qualifications and experience and based on UC Berkeley salary scales. Generous benefits are included (<http://vspa.berkeley.edu/postdocs>)

**TO APPLY** Visit: <http://apptrkr.com/745096> Interested individuals should include a 1-2 page cover letter describing their research experience, 1-3 relevant publications, a current CV, and the names and contact information of three references.

Letters of reference may be requested for finalists. It is optional to include a statement addressing past and/or potential contributions to diversity through research, teaching, and/or service.

This position will remain open until filled.

Questions regarding this recruitment can be directed to Professor Neil Tsutsui <mailto:ntsutsui@berkeley.edu>.

All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are provided via a third party (i.e. dossier service or career center) to the UC Berkeley Statement of Confidentiality (<http://apo.berkeley.edu/evalltr.html>) prior to submitting their letters.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: <http://policy.ucop.edu/doc/4000376/NondiscrimAffirmAct> The Department is interested in candidates who will contribute to diversity and equal opportunity in higher education through their research or teaching.

The University of California, Berkeley has an excellent benefits package as well as a number of policies and programs in place to support employees as they balance

work and family.

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Mitch Gillick Jobelephant.com 5443 Fremontia Lane San Diego, CA 92115 Tel: 619.795.0837 Fax: 619.243.1484 Toll-Free Direct: 800.311.0563 Email: mitch@jobelephant.com Website: [www.jobelephant.com](http://www.jobelephant.com) Mitch Gillick <mitch@jobelephant.com>

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## UCalifornia Davis PlantPathogenEvolution

2/19/16 Postdoctoral Position in Quantitative Disease Resistance Available: May 2016 till... Location: Plant Sciences: University of California, Davis

We seek a postdoctoral researcher to work on a project investigating the evolution and networks controlling genomic disease resistance and pathogen virulence variation in the interaction between a single pathogen (*Botrytis cinerea*) and eight different eudicot plant species.

Our laboratory has been conducting extensive work to understand the molecular basis of quantitative phenotypes at a genomic level utilizing network biology in *Arabidopsis thaliana* and the necrotrophic plant pathogen (*Botrytis cinerea*) (for a list of publications please go to the Web site). We have finished the genomic sequence of 100+ *B. cinerea* isolates as well as infection assays on a broad array of *Arabidopsis* genotypes and other dicot species (Soybean, Lettuce, Chicory, Sunflower, Tomato and two Brassicas). For each plant species there were multiple genotypes representing wild and domesticated lineages. This analysis also includes whole transcriptome analysis of both the plant and pathogen. This provides a unique dataset from which to examine the effects of domestication and lineage evolution in the eudicots on a single fungal pathogen and vice versa.

Among the questions we can ask are to identify how genomic variation in the pathogen influences host specificity across the eudicots with a focus on lineage specific evolution and the potential role of domestication. We can also utilize this data to conduct GWA (Genome wide association) mapping within the pathogen and the plants to identify the loci that control quantitative resistance variation across the dicots. This will enable us to begin parsing the genetic networks that control a pathogen's specificity across plant species, plant geno-

types and how the pathogen evolves in response to the plant. These questions are directly translatable to fundamental population biology theory, ecological theory and have direct application to improving crop productivity in the face of endemic diseases as represented by *Botrytis cinerea*. Thus, there is an extensive collection of phenotypic and genomic data that are ready to be analyzed and utilized to develop and test new hypothesis surrounding quantitative disease interactions.

The project is currently funded until May of 2019. Applicants with a Ph.D. in quantitative or computational genetics will be given high priority. Knowledge of modern molecular biological techniques (e.g. PCR, Sequence analysis, in vitro protein expression etc.) and laboratory-based research is required. The position is available immediately but the start date is flexible. Salary will be commensurate with experience; the position also includes health insurance and other benefits.

The laboratory is an interactive group at the forefront of applying genomics techniques to understanding the molecular basis of quantitative phenotypes in both an ecological and applied context. We have numerous international collaborations and opportunities with an excellent track record of placing individuals in advanced positions.

To apply, please e-mail a cover letter, curriculum vitae, and the names of three references to Daniel Kliebenstein. Applications will be reviewed until the position is filled. For more information contact Dr. Kliebenstein via e-mail at [Kliebenstein@ucdavis.edu](mailto:Kliebenstein@ucdavis.edu).

Daniel Kliebenstein Professor of Plant Genomics Univ of California, Davis Dept of Plant Sci- MS3 1 Shields Ave Davis, CA 95616

Kliebenstein Lab

Member of Dynamo Center University of Copenhagen  
Dynamo Center

Daniel Kliebenstein <[kliebenstein@ucdavis.edu](mailto:kliebenstein@ucdavis.edu)>

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## UCalifornia SantaCruz FishEvolution

We are seeking a postdoctoral scientist to work on population and molecular genetic analyses of river herring (*Alosa* spp.) as part of a team conducting basic and applied research on the ecology, evolution, conservation and management of marine and anadromous fishes. The successful candidate will formulate and carry out work using molecular population genetic data and methods to study distribution and abundance, fishery bycatch, restoration, evolutionary dynamics, secondary contact, and hybridization of alewife and blueback herring (collectively known as river herring) as part of a large, bi-coastal collaboration.

Duties will involve overseeing data generation, developing and applying data analytical techniques, and disseminating results through publications, reports and presentations. In addition to standard population genetic techniques, experience with high-throughput sequencing data and its manipulation with R, Python or similar languages is desirable.

The successful candidate will work jointly with the research teams of Dr. Eric Palkovacs, in the Department of Ecology and Evolutionary Biology at the University of California, Santa Cruz (UCSC) and Dr. John Carlos Garza, at the Southwest Fisheries Science Center, both located on the UCSC Marine Sciences Campus.

The position is available right away and will be open until filled. Multiple years of funding have been secured for this work, but the initial appointment will be for one year, with possibility of extension.

Inquiries by email to Eric Palkovacs (epalkova@ucsc.edu) and/or John Carlos Garza (carlosjg@ucsc.edu).

UCSC is an Affirmative Action/EEO Employer.

John Carlos Garza, PhD Southwest Fisheries Science Center 110 Shaffer Road Santa Cruz CA 95060 USA  
Tel. 831 420-3903

“carlosjg@ucsc.edu” <carlosjg@ucsc.edu>

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## UExeter EvolutionCooperation

Dear Colleague,

I am currently advertising a one-year postdoctoral position in theoretical ecology at the University of Exeter (deadline 6th March). The postdoc will work on projects in my NERC fellowship <http://gtr.rcuk.ac.uk/projects?ref=3DNE/L011921/1>. The advert is at: [https://jobs.exeter.ac.uk/hrpr.webrecruitment/wrd/run/ETREC107GF.open?VACANCY\\_IDy5024E8VK&WVID817591jNg&LANG=USA](https://jobs.exeter.ac.uk/hrpr.webrecruitment/wrd/run/ETREC107GF.open?VACANCY_IDy5024E8VK&WVID817591jNg&LANG=USA) I'd be grateful if you would pass this on to any interested and qualified students/postdocs.

All the best Andy

Dr Andrew Higginson Senior Lecturer Psychology College of Life and Environmental Sciences University of Exeter <https://sites.google.com/site/adhigginson/> Andy Higginson <adhigginson@gmail.com>

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## UGeorgia StressEvolGenomics

A postdoctoral position studying the evolutionary genomics of abiotic stress resistance in sunflower and related, stress-adapted species is available in the Burke lab at the University of Georgia.

This position is part of a collaborative project that seeks to understand the genomic and physiological basis of adaptation to drought, salt, and low nutrient stress in a fascinating study system. The ideal candidate will have a strong background in population and/or quantitative genetics with experience handling and analyzing large, genome-scale datasets.

Funds are currently available to support this position over multiple years. The position is available immediately, but the start date is somewhat flexible. Applications will be reviewed as they are received, continuing until the position is filled.

To apply, please send your CV, a brief statement of research interests, and the names and contact information for three references to: [jmburke@uga.edu](mailto:jmburke@uga.edu)

Informal inquiries are also encouraged. Additional

project details are available upon request.

Information about the UGA Dept of Plant Biology can be found at: <http://www.plantbio.uga.edu/>

Information about the Burke lab can be found at: <http://www.theburkelab.org/> John M. Burke, Ph.D. Tel: 706.583.5511 Fax: 706.542.1805 <http://www.theburkelab.org/> University of Georgia Department of Plant Biology Miller Plant Sciences Athens, GA 30602

"jmburke@uga.edu" <jmburke@uga.edu>

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## UGlasgow GenomeEvolutionaryTransitions

We have a research opportunity open at the University of Glasgow's Institute of Biodiversity, Animal Health & Comparative Medicine (IBAHCM) working in the Evolutionary Analysis Group and the research team of Kathryn Elmer (<http://www.gla.ac.uk/researchinstitutes/bahcm/staff/kathrynelmer/>).

We are seeking a motivated, creative and enthusiastic postdoctoral researcher with expertise in genomics for a project on 'major evolutionary transitions'. The primary research effort will be on a NERC-funded project studying the molecular and genomic mechanisms underlying different reproductive modes in lizards. Complementary projects on genome evolution in 'ichs and herps' are also possible. Bioinformatic experience with NGS data and expertise in whole genome analysis is imperative, ideally with relevant experience in complex de novo genome assembly. Skills in quantitative trait mapping, comparative genomics, ecological and/or population genomics, and phylogenetics are also sought. Team working and positive attitude are a must. A strong track record of genetic and evolutionary research is necessary, and on fishes or reptiles is a benefit. Candidates must have completed their PhD by the start of contract.

The position is for 1.5 years (with possibility for extension) starting as soon as possible, and is funded through the NERC grant 'Unravelling the genetics of a major evolutionary transition' to Kathryn Elmer, Maureen Bain and Rod Page.

IBAHCM is a stimulating and interactive research environment with a wealth of opportunities for discussion, collaboration and cutting edge research in evolution, ecology, and disease. The University of Glasgow ranks in the world's top 100 universities. The University

and IBAHCM have both been recognised with Athena SWAN Bronze awards. The city of Glasgow is lively and cultural, and sits on the doorstep of the great outdoors of the Scottish Highlands, islands, and coast.

The official job description and application requirements are available on the University of Glasgow homepage (under current vacancies; <http://www.gla.ac.uk/about/jobs/vacancies/>) at job reference M00658. \*\*The advertisement closes 7 March 2016.\*\* Informal inquiries to K. Elmer welcome in advance. [kathryn.elmer@glasgow.ac.uk](mailto:kathryn.elmer@glasgow.ac.uk)

"Kathryn.Elmer@glasgow.ac.uk"  
<Kathryn.Elmer@glasgow.ac.uk>

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## UHawaii Manoa FruitFlyGenetics

Aloha! The USDA-ARS Pacific Basin Agricultural Research Center (Geib Lab) and University of Hawaii Manoa (Rubinoff Lab) have funding for a Junior Researcher (Postdoc) to work on genetics of pest fruit flies. The research project is focused on utilizing genomic approaches for improving detection and identification of tephritid pests. Most of the work involves analyzing populations of tephritid species using genome-wide analysis techniques. These techniques facilitate discovery and the development of assays for determination of source populations. In addition, position would include assisting in ongoing experiments on quantitative genetics of fruit flies to identify causative loci for traits of interest. The applicant will be expected to work independently and supervise technical staff and students, as well as work well as part of a larger research team. Experience in wet-lab molecular biology, genetics, strong interpersonal skills, as well as computational analysis of high-throughput sequence data is required. Specific background in population genetics/genomics and knowledge of linux/unix, scripting, etc. as well as performing NGS approaches (RAD-Seq, GBS (genotyping by sequencing), RNA-seq, WGS) are desired. We have advanced computing resources in-house, automated laboratory instrumentation, and a very active research program.

Salary is ~\$61,000/yr, hired through University of Hawaii Manoa, and the job will be stationed at the USDA-ARS Pacific Basin Agricultural Research Center in Hilo, HI (on the Big Island of Hawaii). Minimum PhD in genetics, biology, entomology, or similar is required. If interested, please contact Dr. Scott Geib at



scott.geib@ars.usda.gov and submit CV and contact for at least 3 references.

smg283@gmail.com

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## UHelsinki Evolutionary Genetics

A 2 YEAR POST DOCTORAL RESEARCHER POSITION in Evolutionary Genetics is available in the research group of Academy research fellow Marjo Saastamoinen. The successful applicant will be part of the Centre of Excellence in Metapopulation Research at the Department of Biosciences, University of Helsinki.

The main goal of the post doc project is to examine spatiotemporal genetic variation of the ecological model species, the Glanville fritillary butterfly (*Melitaea cinxia*) inhabiting the Åland Islands in Finland. In addition to exceptional demographic and ecological resources, substantial genomic data are now available for this species, including a high quality annotated whole genome sequence (Ahola et al. 2014 Nature Comm) and linkage map (Rastas et al. 2013 Bioinformatics). The current project will use available SNP genotype data from 20,000 individuals typed for both known candidate genes (Fountain et al. 2016 PNAS, Orsini et al. 2008 JEB; Hanski 2011 PNAS; Saastamoinen et al. 2009 Proc R Soc B; de Jong et al. 2014 Mol Ecol) and neutral loci across hundreds of populations. The successful candidate will use these data to test for associations of candidate sites with individual life-history traits, population dynamics, and landscape characteristics. Given that data are available for nearly 10 years for hundreds of populations, there is an excellent opportunity to examine both spatial and temporal patterns of genetic variation. One specific aim is to examine associations with environmental variables (using software such as Bayenv). The post doc will be part of a large team working on population genetics and genomic work on the Glanville fritillary and will work in close collaboration with Ass. Prof. Arild Husby (blogs.helsinki.fi/husby).

The successful candidate should have PhD / postdoctoral experience within the fields of evolutionary genetics or population genetics and a good core knowledge of ecology. Experience with population genetic software and R programming are required. Excellent written and verbal communication skills in English are needed and you must also demonstrate ability to work as part of a team.

The starting date is flexible but preferable before 1st

May 2016, with a probationary period of four months.

The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal work performance.

To apply, please send, in a single pdf file, your CV with publications included and a letter (max 2 pages) with a description of your research interests and, in particular, why you would be a suitable candidate for the project. The application letter should also contain possible starting dates and contact details of three references. The applications are to be addressed to Dr Marjo Saastamoinen and submitted to [biotiede-mrg@helsinki.fi](mailto:biotiede-mrg@helsinki.fi) by 21st February 2016 at 15.45 local Helsinki time.

The University of Helsinki, founded in 1640, is one of the world's leading universities for multidisciplinary research. The university has an international academic community of 40,000 students and staff members. The University of Helsinki offers comprehensive services to its employees, including occupational health care and health insurance, sports facilities, and opportunities for professional development. The International Staff Services < <http://www.helsinki.fi/intstaff/> > office assists employees from abroad with their transition to work and life in Finland.

The Department of Biosciences situated at the Viikki Science Park belongs to the Faculty of Biological and Environmental Sciences of University of Helsinki and is the largest research and teaching unit in biosciences in Finland. The Department of Biosciences is one of the largest departments of Helsinki University with its c. 25 million euro budget and over 400 staff members. Cutting edge infrastructure is available at all levels, including high-performance computer clusters, a next-gen sequencing facility, as well as molecular labs.

For more information about this position, please contact Dr Marjo Saastamoinen ([marjo.saastamoinen@helsinki.fi](mailto:marjo.saastamoinen@helsinki.fi), <http://www.mv.helsinki.fi/home/msaastam/>).

Dr Marjo Saastamoinen Academy Research Fellow Centre of Excellence in Metapopulation Research Department of Biosciences PO Box 65 (Viikinkaari 1) FI-00014 University of Helsinki FINLAND

tel. + 358 (0)50 448 4471

<http://www.mv.helsinki.fi/home/msaastam/> "Saastamoinen, Marjo A K" <[marjo.saastamoinen@helsinki.fi](mailto:marjo.saastamoinen@helsinki.fi)>

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**UKansas**  
**DrosophilaParasiteCoevolution**

The Department of Molecular Biosciences, University of Kansas, seeks a postdoctoral researcher with interests and experience in *Drosophila* host-parasite coevolution. The successful candidate will work with a research group that addresses the broad theme host-virus interaction and coevolution using *Drosophila* and its associated Nudivirus infection. This position consists of an initial 2-yr appointment and is expected to begin as early as August 18, 2016.

Required qualifications for the position includes a Ph.D. in Biology or closely related field, experience with population genetics and next-generation sequencing as evidenced by application materials, experience *Drosophila* husbandry as evidenced by application materials and some experience with coding in R, Perl, Python, etc. as evidenced by application materials.

For a complete announcement and to apply online, go to <https://employment.ku.edu/staff/5392BR>. A complete application includes a detailed resume, a cover letter, and the names and contact information for two references. Initial review of applications begins March 15, 2016. For first consideration, please apply before March 15, 2016

EO statement: The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, and genetic information in the universitys programs and activities. Retaliation is also prohibited by university policy. The following persons have been designated to handle inquiries regarding the nondiscrimination policies and are the Title IX coordinators for their respective campuses: Executive Director of the Office of Institutional Opportunity & Access, IOA@ku.edu, 1246 West Campus Road, Room 153A, Lawrence, KS 66045, 785-864-6414, 711 TTY (for the Lawrence, Edwards, Parsons, Yoder, and Topeka campuses); Director, Equal Opportunity Office, Mail Stop 7004, 4330 Shawnee Mission Parkway, Fairway, KS 66205, 913-588-8011, 711 TTY (for the Wichita, Salina, and Kansas City, Kansas medical center campuses).

“Unckless, Robert Lewis” <unckless@ku.edu>

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**ULausanne**  
**GenomicsSocialBehaviour**

POSTDOCTORAL POSITION, GENOMICS OF SOCIAL BEHAVIOUR / SUPERGENE EVOLUTION, LAUSANNE

Applications are invited for a Postdoctoral position in the research group of Michel Chapuisat (Department of Ecology and Evolution, University of Lausanne). Our group studies social evolution, with a focus on the structure and evolution of ant societies. Please look at <http://www.unil.ch/dee/page7000.html> for information and references.

In the Alpine silver ant *Formica selysi*, colony queen number is controlled by a supergene (Purcell et al. Cur. Biol. 2014). We aim to understand the origin and maintenance of this polymorphic supergene. We combine genomic, behavioural and ecological approaches. The focus will depend on the interest and background of the postdoc, and there will be scope to accommodate personal ideas or projects. The ideal candidate should have a solid background in evolutionary biology. Some experience in one or more of the following areas would be an asset: bioinformatics, genomics, transcriptomics, population genetics, evolutionary ecology, behavioural ecology.

Starting date is negotiable. The Department of Ecology and Evolution is large and thriving, and provides excellent facilities for research and training (see <http://www.unil.ch/dee/>).

Informal enquiries and applications should be sent to Michel.Chapuisat@unil.ch. Applications should include a cover letter with a statement of research interests and qualifications for the position, complete CV with publication list, and contact details of three referees, embedded in a single pdf file.

I will start reviewing the applications on February 16th, 2016, but will continue to consider incoming applications until the position is filled.

Michel Chapuisat <Michel.Chapuisat@unil.ch>

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## UMassachusetts ComparativeEndocrinology

### POSTDOCTORAL Research Associate

A postdoctoral fellowship in comparative endocrinology is available at the University of Massachusetts, Amherst beginning April 1, 2016. The fellowship is supported by an NSF grant with funding for 4 years and will examine the hormonal control of osmoregulation in lamprey.

This is a benefited, full-time Postdoctoral Research Associate position. Initial appointment is for one year, reappointment beyond the first year is contingent upon availability of funding and job performance. Primary responsibilities will include, but are not limited to: real time PCR measurement of ion transporter, hormone and receptor mRNA levels; in situ hybridization of cells expressing ion transporters, hormones and receptors; immunohistochemical and microscopic analysis of pituitary and gill; maintenance and experimental manipulation of juvenile lamprey; manipulation of hormone levels in vivo and in vitro. Qualified candidates are required to have a Ph.D. in Biology or related field. Two to three years experience studying physiology, endocrinology and/or using molecular approaches in fish biology research is preferred. Experience with radioimmunoassays, in situ hybridization, and molecular genetic approaches is highly desirable.

It is expected that the appointee will work extended hours as necessary to complete individual experiments.

Postdoctoral Research Associates at the University of Massachusetts are unionized and receive standard salary and benefits, depending on experience. Salary is subject to bargaining unit contract. Candidates must apply online by submitting a cover letter, CV, summary of research interests, and the contact details of three references willing to provide letters of recommendation to:

<http://umass.interviewexchange.com/-jobofferdetails.jsp?JOBID=3D68722>

Questions can be addressed to Dr. Stephen McCormick at [mccormick@umext.umass.edu](mailto:mccormick@umext.umass.edu).

Review of applications will begin March 7, 2016 and continue until the position is filled. Applications received by March 7th will be given priority consideration.

The University of Massachusetts Amherst is an Affirmative Action/Equal Opportunity Employer of women,

minorities, protected veterans, and individuals with disabilities and encourages applications from these and other protected group members.

Lisa Barry Biology Department Morrill Science Center South, Room 348 611 North Pleasant Street University of Massachusetts Amherst, MA 01003

Phone: 413-545-2602 Fax: 413-545-3243

Lisa Barry <[lisak@bio.umass.edu](mailto:lisak@bio.umass.edu)>

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## UMinnesota EvolutionComplexTraits

Postdoctoral positions available in the genetics, genomics and evolution of complex traits

We are looking for enthusiastic and talented postdoctoral scientists to join our new lab at the University of Minnesota in Minneapolis. The Albert lab investigates how genetic differences among individuals influence gene expression, cell biology and complex traits in species ranging from yeast to humans. We also study how these genetic architectures evolve. Typical projects in the lab combine cutting edge experimental genomic technologies with sophisticated statistical & computational analyses. We provide a great environment for experts in either one of these areas to expand into the other. Our wet lab is located directly next to the new Genome Systems Lab, a large collaborative space for computational research that we share with the groups of Chad Myers, Ran Blekhnman and Dan Knights. There are also ample opportunities to interact with an outstanding group of evolutionary geneticists and genome scientists in the UMN EEB department.

You will have considerable freedom to build your career by following your own research goals, assuming they broadly fit with the interests of our group. Opportunities also exist to join ongoing projects.

Qualifications: A Ph.D. in genetics, genomics, biology, statistics, computer science, physics, or any relevant combination thereof. Ideal candidates will have expertise in experimental and / or computational biology. Successful applicants will be deeply passionate about their research, have a track record of published achievements (publicly posted preprints are explicitly encouraged), and thrive in a collaborative, rigorous and diverse environment. The University of Minnesota is an equal opportunity educator and employer.

The positions are available immediately, and will remain open until filled. Please send a cover letter explaining your interests and how they fit in the lab, along with your CV and contact information for three references to [falbert@umn.edu](mailto:falbert@umn.edu).

For more information on the lab, please visit:

[albertlab.wordpress.com](http://albertlab.wordpress.com)

– Frank W. Albert Assistant Professor Department of Genetics, Cell Biology, & Development University of Minnesota 6-160 Jackson Hall 321 Church St SE Minneapolis, MN 55455 USA

“[falbert@umn.edu](mailto:falbert@umn.edu)” <[falbert@umn.edu](mailto:falbert@umn.edu)>

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## UMinnesota GenomeEvolution

Genome evolution, genome variation, and evolution of gene expression: Multiple post-doctoral positions.

Multiple post-doc positions are available in the laboratory of Nathan Springer ([www.cbs.umn.edu/labs/-springer/](http://www.cbs.umn.edu/labs/-springer/)) at the Univ of Minnesota. We use genome, transcriptome and epigenome information to understand the sources of heritable variation. Details for several current projects are provided below. Many research projects will involve local collaborations (Peter Tiffin - evolutionary genetics; Chad Myers - computational systems biology; Candice Hirsch - translational genomics) as well as collaborations with other institutions. Post-doctoral researchers will also be given freedom and support to develop their own research ideas that are complementary to ongoing projects.

Epigenome dynamics - The Springer group maintains an active research program to study the sources and evolution of epigenetic variation in maize. Whole-genome profiling of DNA methylation and histone modifications is used to understand how epigenetic information is used to organize the genome.

Evolution of gene expression - Changes in gene expression are part of the mechanism used by plants to tolerate abiotic stress, such as low temperature. We are studying transcriptome and epigenome changes in diverse maize genotypes subjected to cold stress in order to study the molecular sources of variation for responsiveness to abiotic stress. This project involves collaboration with Edgar Spalding (Univ of Wisconsin) to apply machine-vision approaches to document the diversity of phenotypic responses to cold stress in maize seedlings.

Transposable element contributions to gene regulation - Plant genomes are composed of interspersed genes and transposons. We are studying the contribution of transposons to gene regulation and phenotypic diversity. This collaborative project with Cory Hirsch (Univ of MN) utilizes genomic and molecular biology approaches to document the influence of transposons on nearby genes.

A Ph.D. degree in genetics, genomics, plant biology, bioinformatics or a related field is necessary. Experience in genomics and bioinformatics is preferred but not required. To apply, send a letter of application, a full curriculum vita, and contact information for three references to Nathan Springer ([springer@umn.edu](mailto:springer@umn.edu)). The University of Minnesota is an equal opportunity educator and employer.

Peter Tiffin <[ptiffin@umn.edu](mailto:ptiffin@umn.edu)>

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## UppsalaU PhylogenomicsAndMolecularClock

Postdoc/Researcher in Systematic Biology

Uppsala University is an international research university focused on the development of science and education. Our most important assets are all the individuals who with their curiosity and their dedication make Uppsala University one of Sweden's most exciting work places. Uppsala University has 40,000 students, 7,000 employees and a turnover of SEK 6,5 billion.

Description: Resolving the global tree of life has long been a main goal of Biology. In recent years, breakthroughs in high-throughput sequencing and faster phylogenetic algorithms have allowed to refine the structure of the tree in unprecedented ways. For eukaryotes, all major groups as well as many once enigmatic lineages now have genomic data available. This wealth of data has opened the door to study the deep relationships among eukaryotes with more confidence, and map onto the tree some of the main evolutionary events. Here, we propose to go further by combining phylogenetics, genomics (i.e. phylogenomics), and molecular dating to address long-standing questions in eukaryote evolution, such as the origin and spread of plastids. For this purpose, we will infer a genomic timescale calibrated with the microfossil record of protists, which presents the key benefit of being continuous and thus more comprehensive than macrofossils. This is a timely project at the forefront of microbial genomics and evolution, within a

motivating scientific environment that will lead to some exciting developments in understanding the diversity of eukaryotes.

**Qualifications:** Depending on seniority, this position will be filled either as postdoctoral fellow or researcher. Eligible for employment as postdoctoral fellow are those who have a doctoral degree or a foreign degree found to be equivalent with a doctoral degree, obtained within three years before the deadline for applications. If there are special reasons, the degree may be older than three years. Special reasons refer to absence due to illness, parental leave, commissions of trust within trade unions or other similar circumstances. Eligible for employment as researcher are those with a doctoral degree older than three years. Candidates must be fluent in English with strong writing skills. This position is for 2 years.

**Assessment:** I am looking for a highly motivated individual with strong academic proficiency within the field of (microbial) eukaryote evolution. Proven experience in bioinformatics to handle genomic-scale datasets, phylogenetics, and molecular dating will be highly valued. Documented skills in phylogenomics would be an asset.

**Application:** The application should include a letter in which the applicant describes oneself and the research interests (one A4 page) and contact information for three references. The application should also include CV and a copy of the doctoral degree. Personal circumstances (such as parental leave) that the assessment of qualifications may be credited to the applicant, should be indicated in the list of qualifications and experience.

Uppsala University is striving to promote gender equality through gender balance. The majority of employees in this category are women, which is why we would like to see men as candidates for the position.

Information about the position will be given by Fabien Burki: [fabien.burki@ebc.uu.se](mailto:fabien.burki@ebc.uu.se) (from March 1st) or [burkif@mail.ubc.ca](mailto:burkif@mail.ubc.ca)

More information can also be found here: <https://-uu.mynetworkglobal.com/en/what:job/jobID:9186> [fabien.burki@botany.ubc.ca](mailto:fabien.burki@botany.ubc.ca)

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## USaoPaulo MolecularSystematics

POSTDOCTORAL POSITION - FACULDADE DE SAUDE PÁBLICA, UNIVERSIDADE DE SÃO PAULO

The Laboratory of Public Health Entomology - Molecular Systematics at the University of São Paulo, Brazil, seeks a highly motivated and productive postdoctoral researcher to work on a FAPESP Tematico-funded research (grant no. 2014/26229-7) on malaria vector mosquitoes in rural settlements in the Brazilian Amazon.

Those interested must have a doctorate and experience in phylogenetic systematics and related fields, as well as excellent knowledge of molecular techniques used in taxonomy and population genetics of insect vectors. Computational skills and statistics will be of great importance. The candidate should collaborate in both disciplines and field work in Brazil and training of undergraduate and graduate students.

The position requires an individual with a PhD and experience in phylogenetic systematics and related fields. Outstanding molecular, computational and statistics skills are particularly advantageous. It is expected the candidate collaborates in discipline, field work in Brazil, and training undergraduate and graduate students in molecular techniques employed in systematics.

Funding is available for a minimum of 1 year, and may be extended upon both mutual and FAPESP agreement. Preference will be given to candidates with a high probability of applying for and obtaining independent funding; for example through the TDR/WHO, or other funding agencies.

The starting date is flexible, and the position will remain open until filled. For primary consideration, applicants should apply by March 17th, 2016. Informal inquiries are welcomed, prior to formal application. To apply, please send the following:

1. A Curriculum Vitae
2. Names of 3 referees willing to provide a letter of recommendation upon request
3. A brief statement of how your research goals fit with research of Culicidae lab
4. A brief statement of interest, ideas, and qualifications for independent grant applications

E-mail applications are preferred: [masallum@usp.br](mailto:masallum@usp.br)



Mailed applications are also acceptable to: Maria Anice Mureb Sallum Faculdade de Sa de P blica Universidade de S o Paulo Avenida Doutor Arnaldo 715 sala 210 01246-904 S o Paulo S o Paulo, Brasil

“masallum@usp.br” <masallum@usp.br>

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## UTulsa BiodiversityClimateVariability

A Post-Doctoral position is available in the Department of Biological Science at the University of Tulsa. This position is part of the highly integrative NSF EPSCoR project on the ecological and socio-economic impacts of climate variability in Oklahoma. This project includes Biologists, Ecologists, Climatologists, Hydrologists, Sociologists, and Economists from the University of Tulsa, University of Oklahoma, Oklahoma State University, and the Nobel Foundation. The Department of Biological Science at the University of Tulsa is serving as the biodiversity contingent of the project.

The Post-Doc will primarily be responsible for working on Oklahoma biodiversity/climate related research projects with faculty and students at the University of Tulsa and collaborators. The Post-Doc will also teach a one-semester (per year) graduate/undergraduate GIS based course on ecological modeling at The University of Tulsa. This position will have access to further GIS training and interactions with researchers at the world class South Central Climate Science Center in Norman, OK.

Dr. Bonett’s research lab at the University of Tulsa primarily uses integrative approaches to study the biodiversity, evolution, and development of amphibians (Bonett Lab: <http://ronbonett.weebly.com/index.html>). Depending on their research interests and goals, the postdoc may conduct projects and receive training in phylogenetics, genomics, transcriptomics, and comparative endocrinology/physiology. The position has potential for high research productivity, specialized training, and teaching experience.

The University of Tulsa is a private institution with ~4,500 students (3/4 undergraduate and 1/4 graduate students): <http://www.utulsa.edu>. Faculty and graduate students in our department study biodiversity of algae, bacteria, fungi, amphibians, fishes, mammals, reptiles, insects, and viruses. Tulsa is a vibrant city located in the Green Country of northeastern Oklahoma.

Tulsa has all the amenities of major US cities, but with relatively low cost of living.

### APPLICATION INFORMATION:

Applicants must have a Ph.D. in Biology or a related discipline prior to the start of the appointment (as early as June 1, 2016). The position requires significant experience with Geographic Information Systems (GIS), particularly with relevance to problems of biodiversity, conservation, ecology, and evolution.

To apply, please send a letter of Intent, CV, and complete contact information for three references to: Ron Bonett (ron-bonett@utulsa.edu)

by March 11th, 2016.

The position can start on or after June 1, 2016, and can potentially be renewed for up to two years.

Ronald M. Bonett, Ph.D. Associate Professor Department of Biological Science 800 S. Tucker Drive University of Tulsa Tulsa, OK 74104 Email: ron-bonett@utulsa.edu Office: (918) 631-3328 Lab: (918) 631-3327 <http://ronbonett.weebly.com/index.html> Ronald Bonett <ron-bonett@utulsa.edu>

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## UTurku PopulationEcology

### A POSTDOCTORAL POSITION IN POPULATION ECOLOGY (UNIV. TURKU, FINLAND)

A two-year postdoctoral position is available at the Department of Biology, University of Turku, Finland to work on the project “Populations in temporally varying environments: a demographic approach” led by Dr. Satu Ramula and funded by the Academy of Finland. Ongoing climate change, habitat fragmentation and invasive species result in increasing temporal environmental variation, which poses a challenge for many organisms that have limited dispersal capacity. This project investigates the demographic strategies of populations to temporally varying environments utilising long-term climate and population data from different organisms. More specifically, the aim is to identify organismal groups that might suffer or benefit from increased environmental variation.

Duties: The postdoctoral researcher will work on time series and climate data, conduct data analyses, write papers, and collaborate nationally and internationally with the possibility of developing additional study questions related to the project.

The successful candidate should have: 1) A PhD in

ecology, evolutionary biology or a comparable field. 2) Demonstrated ability to independently initiate, conduct, and complete research projects. 3) Demonstrated ability to generate and publish the findings in international peer-reviewed journals. A strong background in quantitative ecology is of advantage.

The starting date is preferably 1st September 2016 and the position is available until 31st August 2018. The position is subject to a four-month trial period. The salary is in accordance with the university salary system (for teaching and research personnel) level 5, where the work specific salary component is 2865.30 euro/month. In addition, there is a share increase based on the personal performance, which is, at most, 46.3% of the base salary depending on the previous relevant research and teaching experience of the candidate.

Formal applications should include 1) a motivation letter or an academic portfolio describing research interests, qualifications, and reasons for applying (max 2 pages), 2) a full CV including a list of publications and the contact details of a minimum of two referees. Please submit your application via the electronic application form of the University of Turku at <http://www.utu.fi/en/university/come-work-with-us/open-vacancies/Pages/home.aspx>, (position ID 2016). The deadline for applications is March 31st 2016.

Turku is the 6th largest city in Finland (185 000 people) with rich cultural history. It is located on the southwestern coast of the country and has excellent transport connections and recreational facilities.

For more information, contact [satu.ramula@utu.fi](mailto:satu.ramula@utu.fi).

Dr. Satu Ramula Section of Ecology, Department of Biology University of Turku FI-20014 Turku Finland email: [satu.ramula@utu.fi](mailto:satu.ramula@utu.fi) <https://www.utu.fi/en/-/units/sci/units/biology/research/projects/PopDyn/-Pages/Satu-Ramula.aspx> "satu.ramula@utu.fi" <[satu.ramula@utu.fi](mailto:satu.ramula@utu.fi)>

## UWashington GeneticsOfAging

The University of Washington has a post-doctoral position open in their "Genetic Approaches to Aging" Training Grant (see below). The position is available starting May 1, 2016. Applicants must be US citizens or Green Card holders. The successful applicant will have the choice of numerous labs (information on link below) with diverse training options, including training in the Evolutionary Genetics of Aging (e.g., <http://www.promislowlab.org>).

The Genetic Approaches to Aging Training Grant at the University of Washington (Seattle, WA) will have at least one post-doc opening for a position starting May 1, 2016, with an application deadline of April 1, 2016.

For more details, please have a look at: <http://www.uwaging.org/training-grant/post-doc-openings> The goal of our program is to train new independent investigators who will utilize contemporary molecular and genetic techniques to investigate the underlying mechanisms of aging.

Applications are scored by consideration of the qualifications of the applicant and the mentoring environment, as well as how the research specifically relates to the biology of aging. Funding is at NIH stipend levels.

For questions regarding the application process, please contact Ellen Cravens at [cravense@uw.edu](mailto:cravense@uw.edu)

Daniel Promislow Department of Pathology and Department of Biology University of Washington 1959 NE Pacific Street Box 357705, Room K-078 Seattle, WA 98195 ph: 206 616-6994 e: [promislo@uw.edu](mailto:promislo@uw.edu) w: <http://www.promislowlab.org> Daniel Promislow <[promislo@u.washington.edu](mailto:promislo@u.washington.edu)>

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## WorkshopsCourses

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Kenneth Halanych <ken@auburn.edu>

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### AuburnU Bioinformatics Jun6-10

Bioinformatics Bootcamp at Auburn University

>From June 6V10, 2016 the College of Science and Mathematics will host the third annual Bioinformatics Bootcamp X a training workshop in genomics and computational biology for researchers interested in working with modern genomic data resources. The Bootcamp is a week-long immersion experience in the command line, scripting, data handling and software skills required to process and analyze data from high-throughput sequencing experiments. Previous experience in bioinformatics is not required; interactive lectures and group data analysis activities will introduce participants to best practices in sequencing experiment design and analysis including widely used methods in genome and transcriptome assembly, annotation, differential expression and variant analysis.

The 2016 Bootcamp will feature a keynote lecture by Dr. Monica Munoz-Torres, Lead Biocurator and Bioinformatics Analyst of the Berkeley Bioinformatics Open-source Projects (BBOP), Lawrence Berkeley National Laboratory.

The Bootcamp registration fee is \$500. To apply, send a brief statement of interest and two-page CV (as a single pdf) to [bioinformatics@auburn.edu](mailto:bioinformatics@auburn.edu) <<mailto:bioinformatics@auburn.edu>> by April 1, 2016. Additional information can be found at [auburn.edu/bioinformatics](http://auburn.edu/bioinformatics)

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### Barcelona BiolNetworkAnalysis Oct24-28

Dear colleagues,

Registration is open for the course "Introduction to Network Analysis in Life Sciences - 3rd edition".

Webpage: <http://www.transmittingscience.org/-courses/syst-bio/networks/>

GRANTS: Thanks to the donations of former participants, this year there is a place for free at the course for PhD students. If you want to apply please send an e-mail to [grants@transmittingscience.org](mailto:grants@transmittingscience.org) including: 1- Full name and country, 2- Short project (maximum 300 words), 3- Letter of your advisor stating if you have any grant to develop your PhD. Deadline: March 31st. Please include the name of the course in the subject line.

INSTRUCTORS: Dr. Diego Rasskin-Gutman (Institut Cavanilles de Biodiversitat i Biologia Evolutiva, Spain) and Dr. Borja Esteve-Altava (Institut Cavanilles de Biodiversitat i Biologia Evolutiva, Spain).

DATES: October 24th - 28th, 2016.

PLACE: Instalaciones de Sabadell del Institut Català de Paleontologia M. C. Sabadell, Barcelona (España).

**COURSE DESCRIPTION:**

In the last decades, network analysis has provided new insights into the organisation and functioning of complex biological systems. A basic knowledge on network modelling and network analysis will provide biologists a better understanding of cutting-edge research in their fields.

This course will introduce participants into the analysis of complex biological systems using network models. Students will learn the basics of network analysis: gathering information, building network models, and interpret the outcomes of their analysis.

This course combines theoretical introduction and computing practices using the free software environment R (previous knowledge in R is not required)

Participants are encouraged to bring their own data for practicing. Emphasis is placed on offering participants a wide overview of network modelling in biology and the many available software tools to do it.

Organized by: Transmitting Science and the Institut Catalá de Paleontologia Miquel Crusafont.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Sole

Soledad De Esteban-Trivigno, PhD.  
soledad.esteban@transmittingscience.org Trans-  
mitting Science [www.transmittingscience.org](http://www.transmittingscience.org)  
soledad.esteban@transmittingscience.org

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## Budapest ConservationGenetics May30-Jun10 Deadline

Recent Advances in Conservation Genetics Course (ConGen2016) Lake Balaton

Early Registration Deadline Approaching.

Dear Conservation Genetics Community:

Please note that the deadline for the Early Registration for ConGen2016 is approaching (February 29), and scholarships are available.

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 more 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
- Augostinho Antunes: CIMAR, Centro Interdisciplinar de InvestigaçãŁo Marinha e Ambiental, Laboratory of Ecotoxicology, Genomics and Evolution, University of Porto, PORTUGAL
- Alfred Roca: Associate Professor, Department of Animal Sciences,

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## Debrecen Hungary

### SexRolesAdultSexRatios Apr15-17

Workshop: Sex roles and adult sex ratios

15-17 April, 2016, University of Debrecen, Debrecen, Hungary

Sexual selection, mating systems, parental care and sex roles attract considerable interest in evolutionary biology, behavioural ecology and beyond. One of core ideas is that the environment imposes specific pressures that select for particular breeding system, mating behaviour and patterns of parental care. Recent works are shifting the emphasis from the abiotic environment to the social environment, of which an important indicator is the adult sex ratio (ASR). ASR varies widely in nature, and understanding the causes and consequences of this variation is an important goal because ASR impacts behaviour and reproduction, and ultimately population fitness. The causes and implications of ASR variation in wild populations, however, remain obscure. The objectives of this workshop are to overview recent studies in sex roles and sex ratios, and to evaluate the use of phylogenetic comparative methods for the analyses of sex roles and sex ratios. This workshop will be relevant to postgraduate students, young scientists and established scholars with an interest in evolutionary biology, behavioural ecology and population demography.

Confirmed invited speakers will include Professor Robert Freckleton, University of Sheffield, UK Professor Jan Komdeur, University of Groningen, The Netherlands Dr Vladimir Remes, Palacky University, Czech Republic Professor Zoltán Varga, University of Debrecen, Hungary Professor Tamás Székely, University of Bath, UK Dr Veronika Bókonyi, MTA Plant Protection Institute, Hungary Dr László Zsolt Garamszegi, Doñana Biological Station, Spain

The Workshop will start on Friday (15 April), and continue all day Saturday (16 April). For Sunday (17 April) we plan a full-day excursion to Hortobágy National Park, a UNESCO World Heritage site.

For further details on University of Debrecen, please see <https://www.unideb.hu/portal/en> Information on the city of Debrecen can be found at <http://eng.debrecen.hu/> Information on Hortobágy National Park can be found at <https://www.hnp.hu/en> Workshop organizers: Dr Balázs Vági, University of Debrecen



Dr Zsolt Végvári, University of Debrecen and Hortobágy National Park Professor András Liker, University of Pannonia

In addition to the presentations by invited speakers, we will accept a limited number of contributed talks.

The conference will be held at Life Science Building of University of Debrecen. There is no registration fee. Attendees are expected to book their own accommodation (for accommodation, see <https://revngo.com/kossuth-kollegiumok-debrecen> (on campus); [www.campushotel.hu](http://www.campushotel.hu); or visit [www.booking.com](http://www.booking.com)). The prices vary between 10 EUR and 50 EUR per night per person. Meals will be at the university Canteen on campus (approx.10 EUR per meal).

Application deadline: Friday 11 March 2016 Applications (max 5 pages that may include a CV, motivation letter and the title and abstract of the proposed contribution) should be emailed as a single PDF to Dr Balázs Vági ([bi.vagi@gmail.com](mailto:bi.vagi@gmail.com))

Balázs Vági, PhD research fellow Department of Evolutionary Zoology, University of Debrecen, Debrecen, Egyetem ter 1., 4032, Hungary Phone: +36 52 316 666 ext. 62356 <%2B36%2052%20316%20666%20ext.%2062334> | Fax: +36 52 512 941

[bi.vagi@gmail.com](mailto:bi.vagi@gmail.com)

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## Faro Portugal Statistical Genetics Bruce Weir

ADVERTISEMENT WEBSITE: [http://att.ccmар.ualg.pt/statistical\\_genetics\\_2016](http://att.ccmар.ualg.pt/statistical_genetics_2016) WORKSHOP IN STATISTICAL GENETICS - taught by BRUCE WEIR - Professor of Biostatistics, and Director of the Institute of Public Health Genetics at the University of Washington. Bruce Weir is the author of the textbook "Genetic Data Analysis" (3rd edition in preparation) and he has directed the Summer Institute in Statistical Genetics since 1996. <http://www.gs.washington.edu/faculty/weir.htm>, <http://www.ncbi.nlm.nih.gov/pubmed/?term=Bruce+Weir> DESCRIPTION: A unified treatment for the analysis of discrete genetic data, starting with estimates and sample variances of allele frequencies to illustrate genetic vs statistical sampling and Bayesian approaches. A detailed look at Hardy-Weinberg and linkage disequilibrium, including the use of exact tests

with mid-p-values and a new look at X-chromosome Hardy-Weinberg testing. A new characterization of population structure with F-statistics, based on allelic matching within and between populations with individual relationship estimation as a special case. Analyses illustrated with applications to forensic science and association mapping, with particular reference to rare variants.

VENUE: Centre of Marine Sciences, University of the Algarve, Faro, Portugal. <http://ccmar.ualg.pt> - Google maps: <https://goo.gl/cM78fp>

DATE: 8th-9th September 2016

FORMAT: 2-day workshop, lectures and hands-on practical sessions (attendees will need 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: 240 euro

Registration does not include travel and lodging. Faro has an international airport located 4 km from the Gambelas Campus of the University of Algarve where the course will take place.

HOW TO APPLY: Applications in the form of a CV and motivational letter should be sent to [ccmaratt@ccmar.ualg.pt](mailto:ccmaratt@ccmar.ualg.pt) by 31st March 2016. Applicants will be selected on merit and successful applicants will be informed by 10th April 2016.

SCHOLARSHIPS: At least 2 scholarships to cover registration fees will be awarded to PhD students; applicants should indicate if they would like to be considered and must send proof of student status.

ACCOMMODATION: Recommended: Hotel Aeromar at Faro beach ( <http://www.aeromar.net/en>) has temporarily reserved (until 31st May) and discounted 8 double rooms, priced 62.5 euro and 80 euro , double and single occupancy, respectively (mention CCMAR reservation when booking). Additional accommodation at the beach and in Faro centre: <http://goo.gl/mgG85g>. A minibus service will run between the beach, town centre, and campus.

CONTACTS: Ester Serrão - Assistant Professor, UALG/CCMAR - [eserrao@ualg.pt](mailto:eserrao@ualg.pt) Cymon J. Cox - FCT Coordinating Researcher, CCMAR - [cymon@ualg.pt](mailto:cymon@ualg.pt)

Advanced Technologies and Training programme @ CCMAR 2016 [ccmaratt@ccmar.ualg.pt](mailto:ccmaratt@ccmar.ualg.pt), [att.ccmар.ualg.pt/statistical\\_genetics\\_2016](http://att.ccmар.ualg.pt/statistical_genetics_2016)

The Centre of Marine Sciences (Centro de Ciências do Mar, CCMAR) is an independent multidisciplinary, non-profit institute located on the Gambelas cam-

pus of the University of the Algarve in Faro with ~250 members and a mission to promote research and education in the marine sciences. Faro (<http://www.algarve-tourist.com/Faro-portugal-guide.html>) is the capital city of the Algarve region of southern Portugal and borders the Ria Formosa National Park (<http://www.formosamar.com/en>). The Algarve (<http://www.visitalgarve.pt/?idioma=uk>) boasts > 300 days of sun per year, stunning beaches and mountain vistas, opportunities for diving, golf, and other sporting activities, and a unique traditional regional cuisine (esp. seafood). A variety of optional social activities will be organised to coincide with the course and special events can be organised upon request for participants and/or accompanying persons (diving, surf, stand-up paddle, windsurf, kayaking, horse-riding, tennis, bird-watching, nature walks, boat guided tours, fishing, etc).

Bruce Weir - Recent Publications:

Zhu ZH, Bakshil A, Vinkhuyzen AAE, Hemani G, Lee SH, Nolte IM, van Vliet-Ostapchouk JV, Snieder H, The LifeLines Cohort Study, Esko T, Milani L, MÃÄgi R, Metspalu A, Hill WG, Weir BS, Goddard ME, Visscher PM, Yang J. 2015. Dominance genetic variation contributes little to the missing heritability for human complex traits. *American Journal of Human Genetics* 96:377-385.

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## Friday Harbor Washington Comparative Embryology Jun13-Jul15

Applications are open for the Comparative Invertebrate Embryology course at the Friday Harbor Labs (June 13 - July 15, 2016). \*Applications are needed by Feb. 29th\*.

It is a great course for anyone interested in the evolution of development, developmental mechanisms, animal evolution, or the ecology or physiology of early life stages. The focus of the course is hands-on observation of living embryos and larvae from over a dozen animal phyla. The Friday Harbor Labs gives access to an extraordinary variety of organisms from diverse marine habitats,

all in a beautiful setting, and provides opportunities to interact with a broad community of biologists.

We aim to bridge cell and molecular approaches with ecological and evolutionary approaches to provide an integrated view of animal development. Depending on student interests, students may learn techniques such as: - Spawning and culture of embryos and larvae from diverse phyla. - Confocal microscopy and SEM - Microinjection - Methods for measuring cell/embryo mechanical properties

Instructors include Dr. Sally Leys and myself. Dr. Leys is an expert on sponge development and the evolution of animal body plans. My research focuses on the roles of biomechanics in development-environment interactions. We will also have guest lectures from experts on diverse topics and taxa, including Drs. Brad Shuster, Richard Strathmann, Sophie George, Tony Pires, and others TBD.

For the course description, please see: <http://depts.washington.edu/fhl/studentSummer2016.html#SumA-2> .

Please share with students who might be interested.

Thank you.

Mickey

[mvondass@gmail.com](mailto:m vondass@gmail.com)

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## Hafjel Norway Selection Jun6-10

Dear colleagues,

The Nordic Genetic Resource Center (NordGen) is arranging a workshop\* "Optimal Contribution Selection"\* in Hafjell (Åyer municipality north of Lillehammer), Norway 6th-10th of June 2016.

The main goals of the workshop are:

- to introduce the theory and implementation of Optimal Contribution Selection in sustainable management of breeding and conservation programs

- to promote the independent use of EVA (EVolutionary Algorithms) software with hands-on exercises

To maximize the learning experience of all participants, the workshop is divided into two parts. Participants may choose to register for \*both\* \*or only one\* of the consecutive parts: "Part I - Introductory"\* and "Part II - Advanced"\*. The maximum number of participants

in Part I and Part II are 20 and 25, respectively.

For a more detailed description of the workshop program, registration and practical information please follow the link below:

<https://sites.google.com/a/nordgen.org/workshop-optimal-contribution-selection/> Feel free to distribute this invitation amongst your colleagues and other institutions.

Best regards

Anne Kettunen

Dr. Anne Kettunen Senior Scientist NordGen - Nordic Genetic Resource Center P.O. Box 115, NO-1431 Ås, Norway Street address: Raveien 9, NO-1430 Ås, Norway Phone: +47 9036 5249, mobile: +47 9778 0903 [anne.kettunen@nordgen.org](mailto:anne.kettunen@nordgen.org) [www.nordgen.org](http://www.nordgen.org) Anne Kettunen <[anne.kettunen@nordgen.org](mailto:anne.kettunen@nordgen.org)>

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## LANGEBIO Mexico Drosophila May25-28

### 2016 Drosophila Species Workshop

Applications are being accepted for the 2016 Drosophila Species Workshop held at LANGEBIO in Guanajuato, Mexico. Workshop dates are Wednesday, May 25th - Saturday, May 28th. Please email a one-page summary of research interests to Maxi Richmond ([mrichmond@ucsd.edu](mailto:mrichmond@ucsd.edu)) by March 20th, 2016. Registration is \$350 and will include workshop materials and several meals. The registration fee does not include lodging or airfare.

The main goal of the workshop is to teach participants how to incorporate non-melanogaster Drosophila species into their research program. Participants are introduced to Drosophila systematics, rearing and husbandry techniques, how to design and conduct mating experiments, how to collect flies from wild populations, and analysis of polytene chromosomes. In addition, workshop participants learn the key morphological traits necessary for identifying Drosophila species, and work in depth with the *D. melanogaster*, *D. obscura*, and *D. repleta* species groups along with instructors that specialize in each of these groups to facilitate the process of keying out specimens.

Workshop participants include domestic and international Drosophila researchers that use a variety of techniques pertaining to studies in genomics, proteomics,

systems biology, microbial genetics, developmental biology, chromosome biology, and ecological genetics.

More information: <https://stockcenter.ucsd.edu/info/-workshops> Please email Maxi Richmond ([mrichmond@ucsd.edu](mailto:mrichmond@ucsd.edu)) with any questions.

Maxi Polihronakis Richmond <[mrichmond@ucsd.edu](mailto:mrichmond@ucsd.edu)>

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## MalhamTarn Yorkshire UsingR May2-6

“Advancing in Statistical Modelling using R” We have a limited number of places left for this popular course.

<http://prstatistics.com/course/advancing-in-statistical-modelling-using-r-advr/> Delivered by Dr. Luc Bussiere and Dr. Tom Houslay

This course will run from 2<sup>nd</sup> - 6<sup>th</sup> May 2016 at Malhamtarn Field Station, North Yorkshire, England

This is an introduction to model selection and simplification, mixed effects models, generalised linear models and non-linear models.

The course is aimed at biologists with a basic to moderate knowledge in R. The course content is designed to bridge the gap between basic R coding and more advanced statistical modelling. This five day course will consist of series of modules, each lasting roughly half a day and comprised of lectures and practicals designed to either build required skills for future modules or to perform a family of analyses that is frequently encountered in the biological literature.

Course content is as follows

#### Day 1 Course introduction

Techniques for data manipulation, aggregation, and visualisation; introduction to linear regression. Packages: {tidyr}, {dplyr}, {ggplot2}

#### Day 2 Linear models

Diagnostics, collinearity, scaling, plotting fitted values); fitting and interpreting interaction terms; model selection and simplification; general linear models and ANCOVA.

Packages: {stats}, {car}

#### Day 3 Generalized linear models

Logistic and Poisson regression; predicting using model objects and visualizing model fits.

Packages: {broom}, {visreg}, {ggplot2}

Day 4 Mixed effects models

Theory and practice of mixed effect models; visualising fixed and random effects.

Packages: {lme4}, {broom}, {ggplot2}, {sjPlot}

Day 5 Fitting nonlinear functions

Polynomial & Mechanistic models; brief introduction to more advanced topics & combining methods (e.g., generalised linear mixed effects, nonlinear mixed effects, and zero-inflated and zero-altered models)

Packages: {nlstools}

Afternoon to discuss own data if time permits

Please email any inquiries to [oliverhooker@prstatistics.com](mailto:oliverhooker@prstatistics.com) or visit our website [www.prstatistics.com](http://www.prstatistics.com) Please feel free to distribute this material anywhere you feel is suitable

Upcoming courses - email for details [oliverhooker@prstatistics.com](mailto:oliverhooker@prstatistics.com)

SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R (April)

TIMES SERIES DATA ANALYSIS FOR ECOLOGISTS AND CLIMATOLOGISTS (May)

INTRODUCTION TO PYTHON FOR BIOLOGISTS (May)

ADVANCES IN DNA TAXONOMY USING R (August)

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](mailto:oliverhooker@prstatistics.com)

STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR USING R

INTRODUCTION TO R AND STATISTICS FOR BIOLOGISTS

PHYLOGENETIC DATA ANALYSIS USING R

BIOINFORMATICS FOR GENETICISTS AND BIOLOGISTS

Oliver Hooker

PR Statistics

“[oliverhooker@prstatistics.co.uk](mailto:oliverhooker@prstatistics.co.uk)”  
<[oliverhooker@prstatistics.co.uk](mailto:oliverhooker@prstatistics.co.uk)>

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## North Carolina State U Quantitative Biol Jun19-24

2016 National Academies Special Topics Summer Institute on Quantitative Biology

Lowering the Activation Energy: Making Quantitative Biology More Accessible

June 19-24, 2016

North Carolina State University, Raleigh

Biology requires a rapidly expanding set of quantitative skills including data analysis, statistics, modeling, computational reasoning, and visualization. If you are interested in developing your biology students' quantitative skills, this is the summer workshop for you!

In partnership with the National Academies Summer Institutes, the Quantitative Biology Summer Institute (QB SI) is presented by BioQUEST, Science Case Net and QUBES. This will be a working meeting during which participants will learn about and use evidence-based teaching strategies such as backward design, active learning, and assessment, as well as methods such as cases and modeling. Hands on sessions at the institute will focus on resources and methods to address the special challenges associated with teaching quantitative biology. The workshop is developed by BioQUEST, which celebrates 30 years of leadership in biology education reform in 2016, and Science Case Network, which brings expertise on using case based pedagogies. The QUBES project will support ongoing collaborations among participants.

We invite applications from individuals and teams at two and four year institutions. Participants from all STEM fields are welcome. As indicated on the application, participants are expected to work collaboratively after the meeting and implement a module or method in their classes during the 2016-2017 academic year. More information and the application for the Quantitative Biology Summer Institute are available at: <https://-qubeshub.org/groups/summer2016> Review of applications will begin March 28 and applicants will be notified regarding their status of their application by April 4.

Please contact the organizers with any questions:

Kristin Jenkins, BioQUEST  
(kristin.jenkins@bioquest.org), Pat Marsteller, Science  
Case Net (pmars@emory.edu), Sam Donovan, QUBES  
(sdonovan@pitt.edu)

Kristin Jenkins <kristin.jenkins@bioquest.org>

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**Roscoff**  
**Marine Evolutionary Genomics**  
**Jun13-24**

Summer course on marine genomics at the Marine Biological Station of Roscoff (F)

First announcement

>From June 13th - June 24th, 2016

the 12<sup>th</sup> Summer Course on Marine Ecological & Evolutionary Genomics

takes place at the Station Biologique de Roscoff, Roscoff, France.

Aims:

Genomic knowledge is crucial for understanding the marine environment and for an efficient use of its resources. State of the art NGS methods have revolutionized the field, spawning applications in basic research and environmental management. The course will give insight into population, environmental, biodiversity, comparative, evolutionary and functional genomics through lectures, case studies and computer labs. It takes place at the Biological Station, a vibrant research community of 273 scientists and support personnel, located in the old town and fishing port of Roscoff, Brittany, France.

The course includes lectures, tutorials and computer based exercises on the following topics.

- Genomics - next generation sequencing, database searching, basic skills in data handling and bioinformatics
- Population genomics - diversity, structure, connectivity and gene flow, assignment, effective population size, population dynamics, adaptive variation, genotyping by sequencing
- Environmental genomics - environment - genome interactions, ecogenomics and metagenetics
- Functional genomics - genome structure, molecular evolution at the functional level, genomic architecture, functional networks

- Comparative genomics - whole genome comparisons, concatenated phylogenies, genome organization, annotating genomic information, co-evolution

- metagenomics

The course covers all aspects of life in the ocean.

Target group:

PhD students (at least in their second year) and junior postdocs with a solid knowledge in phylogenetics and/or population genetics.

18 participants will be selected on the following criteria:

1. Relevance of the course for their PhD or post-doc project
2. Background and experience
3. We aim at training people with different research backgrounds; not more than one person per institute will be considered. We implement a gender policy.

The selected persons will be notified by March 25th and will have to confirm attendance within 7 days. There is a waiting list in case of non-confirmations and cancellations.

Teaching staff :

Jonas Collin, SB-Roscoff, FR

Simon Creer, Univ. Bangor, UK

Yves Desdevises, OO-Banyuls, FR

Jakob Hemmer-Hansen, DTU-Aqua, DK

Erica Leder, Univ. Turku, Fi

François Partensky, SB-Roscoff, FR

Daniel Vaultot, SB-Roscoff, FR

Filip Volckaert, Univ. Leuven, BE

Mathias Wegner, AWI-Sylt, GE

Organizing committee

Jonas Collin, SB-Roscoff, FR

Damien Guiffant, SB-Roscoff, FR

Matthias Obst, Univ. Gothenburg, SE

Sarah Bourlat, Univ. Gothenburg, SE

Nic Blouin, Univ. Rhode Island, USA

Nathalie Turque, EMBRC-France, FR

Daniel Vaultot, SB-Roscoff, FR

Filip Volckaert, Univ. Leuven, BE

For information, a flyer and application please check <http://meeg2016.sciencesconf.org> . The application deadline is March 10 2016.



Filip Volckaert <filip.volckaert@kuleuven.be>

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**SanJuan PR**  
**PhylogeneticComparativeMethods**  
**Jun28-Jul1**

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.

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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](mailto: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](mailto:liam.revell@umb.edu).

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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 discutidos en el curso incluyen: una introducción al ambiente computacional en R, manipulación de árboles filogenéticos, mínimos cuadrados generalizados en un contexto filogenético, reconstrucciones de estados ancestrales, modelos de evolución, análisis de diversificación filogenética, y visualización de filogenias y datos comparativos. Los instructores del curso serán: Dr. Liam Revell (University of Massachusetts Boston), Dr. Luke

Harmon (University of Idaho), Dr. Mike

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## SCENE Glasgow TimeSeriesDataModelling May10-13

“Time Series Models for Ecologists and Climatologists”

<http://prstatistics.com/course/time-series-models-for-ecologists-and-c> limatologist/

There are still some places left on this new course suited to many types of Ecology, Evolutionary and Climatology data

Delivered by Dr. Andrew Parnell and Dr. Doug McNeill

This course will run from 10th - 13th May 2016 at SCENE Field Station, Loch Lomond national park, Scotland

This course will cover model-based time series analysis with a particular focus on applications in ecology and climatology. All methods will be illustrated using the free, open-source software package R. Time Series data are ubiquitous in the physical sciences, and models for their behaviour enable scientists to understand temporal dynamics and predict future values.

Participants will be taught a wide range of suitable time series models for both discrete and continuous time systems. The course takes a foundational Bayesian approach, which will enable participants to have a deeper understanding of the models being fitted, and to estimate all unknown quantities with uncertainty. Participants are encouraged to bring their own data sets for discussion with the course tutors.

Course content is as follows

Day 1 Basic concepts

Class 1: Introduction; some example time series datasets; prediction vs explanation

Class 2: An introduction to Bayesian Statistics.

Class 3: The AR(1) model

Practical: revision on using R to load data, create plots and fit statistical models

Round table discussion: understanding the output from a Bayesian model

Day 2 Arima modelling

Class 1: ARMA models for real data

Class 2: ARIMA and sARIMA modelling

Practical: An introduction to the Bayesian modelling language JAGS

Round table discussion: understanding and running a JAGS model

Day 3 Continuous Time Series Modelling

Class 1: Brownian Motion and its application to real data sets

Class 2: An introduction to Stochastic Volatility Modelling

Practical: Fitting continuous time models in JAGS

Round table discussion: Issues of continuous vs discrete time

Day 4 Advanced Times Series Models

Class 1: Multivariate models

Class 2: Fractional differencing and models using differential equations

Practical: Running advanced models in JAGS

Round table discussion: Bring your own data set

Please email any inquiries to [oliver-hooker@prstatistics.com](mailto:oliver-hooker@prstatistics.com) or visit our website [www.prstatistics.com](http://www.prstatistics.com) Please feel free to distribute this material anywhere you feel is suitable

Upcoming courses - email for details [oliver-hooker@prstatistics.com](mailto:oliver-hooker@prstatistics.com)

SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R (April)

ADVANCING IN STATISTICAL MODELLING USING R (May)

INTRODUCTION TO PYTHON FOR BIOLOGISTS (May)

ADVANCES IN SPATIAL ANALYSIS OF MULTIVARIATE ECOLOGICAL DATA (July)

ADVANCES IN DNA TAXONOMY USING R (August)  
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

PHYLOGENETIC DATA ANALYSIS USING R

BIOINFORMATICS FOR GENETICISTS AND BIOLOGISTS

Oliver Hooker

PR Statistics

Oliver Hooker

PR~Statistics

“oliverhooker@prstatistics.co.uk”

<oliverhooker@prstatistics.co.uk>

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## Stockholm

### AncientEnvironmentalDNA Mar10

Dear colleagues,

Registration is open for the SciLifeLab mini-symposium: Ancient Environmental DNA.

This mini-symposium will be held in Stockholm on March 10 and bring together scientists interested in the field of ancient environmental DNA and will provide an opportunity to present new results and discuss current ideas and techniques for the analysis of DNA data from ancient settings.

Confirmed keynote speakers are Inger Greve Alsos, University of TromsÅ, Francesco Ficetola, University of Grenoble-Alpes and Mikkel Winter Pedersen, University of Copenhagen.

For additional information and registration go to: <https://www.scilifelab.se/events/scilifelab-mini-symposium-ancient-environmental-dna/>

Best regards,

Laura Parducci (laura.parducci@ebc.uu.se)

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## Switzerland TamingTheBeast Jun26-Jul1

Dear colleagues,

We are happy to announce our summer school “Taming the BEAST” and would kindly ask you to forward this email to interested students and PostDocs. We apologize if you receive this email more than once. Phylogenetics and phylodynamics are central topics in modern biology. Phylogenetic inferences reconstruct the evolutionary relationships between organisms, whereas phylodynamic inferences reveal the dynamics that lead to the observed relationships. These two fields have many practical applications in disciplines such as epidemiology, developmental biology, paleontology, ecology and even linguistics. However, phylogenetics and phylodynamics are complex and fast-evolving fields. As such, inference tools are not easily accessible to researchers who are not from a computational background.

Taming the BEAST is a summer school focusing on the BEAST2 software and consisting of a mix of invited talks, lectures and hands-on tutorials by leading and renowned experts in the field (including several of the core developers of BEAST2). The aim of this summer school is to equip participants with the skills necessary to confidently perform their own phylogenetic and phylodynamic inferences in Bayesian settings, while providing them with a firm grasp of the theory behind those inferences. Participants are also highly encouraged to bring their own datasets along and to engage with the organizers and speakers to address any problems specific to their own datasets/analyses. Registration is now open! We welcome applications from graduate students and early-career scientists in the life sciences. Preference will be given to applicants who are not from a computational background and applicants who have already collected/assembled a dataset that they need to analyze.

Invited speakers:

Tanja Stadler (ETH Zurich)

Alexei Drummond (University of Auckland)

Tracy Heath (Iowa State University)

Tim Vaughan (University of Auckland)

Oliver Pybus (University of Oxford)

Dates: June 26th to July 1st (Registration deadline:

March 15th).

Place: Engelberg, Switzerland

Registration Fee: 650 CHF for students and postdocs, 1000 CHF for industry. (Registration fee includes accommodation and meals).

For more information regarding the program, registration, venue, etc, please visit the summer school website: <https://www.bsse.ethz.ch/cevo/taming-the-beast.html>  
We hope to see you there, the Taming the BEAST organizing team

Best regards, Venelin Mitov Department of Biosystems Science & Engineering Mattenstrasse 26 4058 Basel Switzerland Email: [venelin.mitov@bsse.ethz.ch](mailto:venelin.mitov@bsse.ethz.ch) Phone: +41 61 38 73411 Office: 7.48

Mitov Venelin <[venelin.mitov@bsse.ethz.ch](mailto:venelin.mitov@bsse.ethz.ch)>

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## Toulouse Evolution May30-31

Dear colleagues,

We are delighted to invite you to the 4th Toulouse Economics and Biology Workshop, which will take place on May 30-31, 2016.

The theme is “Evolution: transmission mechanisms and population structure”, and we are thrilled to welcome the following speakers (titles and summaries coming soon):

Yann Algan < <http://econ.sciences-po.fr/staff/yann-algan/> >, Sciences Po, Paris Carl Bergstrom < <http://octavia.zoology.washington.edu/> >, University of Washington Alberto Bisina < <http://www.econ.nyu.edu/user/-bisina/> >, New York University Jean Clobert < <http://www.ecoex-moulis.cnrs.fr/spip.php?article26> >, Station d'Ecologie Théorique et Expérimentale du CNRS à Moulis Gabriella Conti < <http://gabriellaconti.org/> >, University College London Mats Gyllenberg < <http://www.helsinki.fi/~mgyllenb/> >, University of Helsinki Barry Hewlett < <http://anthro.vancouver.wsu.edu/faculty/hewlett/> >, Washington State University, Vancouver Sarah Mathew < <http://www.sarahmathew.net/> >, Arizona State University, Tempe Hisashi Ohtsuki < [http://bio-math10.biology.kyushu-u.ac.jp/~ohtsuki/index\\_e.html](http://bio-math10.biology.kyushu-u.ac.jp/~ohtsuki/index_e.html) >, The Graduate University for Advanced Studies, Hayama David Queller < <https://wubio.wustl.edu/Queller> >, Washington University, St Louis Paul Seabright < <http://paulseabright.com/> >, Institute for Advanced Study in Toulouse, Toulouse

School of Economics Joan Strassman < <https://wubio.wustl.edu/Strassmann> >, Washington University, St Louis

Besides the plenary sessions, there will be a poster session for post-docs and Ph.D. students. Submissions (abstract + C.V.) should be sent to [econbio\\_poster@iast.fr](mailto:econbio_poster@iast.fr) no later than March 31, 2016. 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 to the workshop.

The workshop will take place at the Institute for Advanced Study in Toulouse, Manufacture des Tabacs, 21 Allée de Brienne, 31015 Toulouse, France.

Registration will open in the beginning of March at: <http://www.iast.fr/conference/4th-toulouse-economics-and-biology-workshop> We look forward to welcoming you!

Organizers: Ingela Alger and Jörgen Weibull Co-organizers: Jeanne Bovet and Arnaud Tognetti

The Toulouse Economics and Biology Workshop <[econbio@iast.fr](mailto:econbio@iast.fr)>

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## UBirmingham Environmental Genomics Mar6-11

NERC-MDIBL Environmental Genomics and Metabolomics Course, 2016

Online Registration Site: [www.birmingham.ac.uk/-EnGen](http://www.birmingham.ac.uk/-EnGen) Date: March 6-11, 2016

Location: The University of Birmingham, UK

Number of Places: up to 50

Participation: Open to everyone.

Priority is given to NERC-funded PhD students and early-career scientists.

Bursaries are available covering registration fee. Please send email to [J.K.Colbourne@bham.ac.uk](mailto:J.K.Colbourne@bham.ac.uk) to inquire about eligibility.

Costs for Non-NERC Funded Researchers: Standard £2340.

Course Leaders: John Colbourne, Joseph Shaw, Xin Zhou and Ben Brown (for genomics). Mark Viant and Warwick Dunn plus staff from the NERC Biomolecular Analysis Facility and Birmingham Metabolomics

Training Facility (for metabolomics).

Research Organisations Involved: University of Birmingham (UK), BGI China National GeneBank (Shenzhen, China), Mount Desert Island Biological Laboratory (USA)

Online Registration Site: [www.birmingham.ac.uk/-EnGen](http://www.birmingham.ac.uk/-EnGen) DESCRIPTION This training opportunity is the third European/UK installment of a successful annual course originating from Mount Desert Island Biological Laboratory. The curriculum is expanded to highlight a multi-omics (system biology) approach to research in environmental sciences. It trains PhD students and early career postdoctoral scientists to investigate how gene function and metabolism are influenced by environmental conditions while accounting for variation that exists within and among natural populations. The course is built on the paradigm that this multidisciplinary research field encompassing ecology, evolution, toxicology, biostatistics and informatics will most effectively grow by training early career environmental scientists to properly design comprehensive, large-scale, Next Generation Sequencing and Metabolomics experiments enabled by drastically increased sample-throughput and lower costs. Most importantly, the challenges of manipulating and analysing population-level omics (big) data must be addressed.

The course provides a significant introduction and much hands-on training experience so that participants can initiate their own environmental omics study and network with others in the field to launch Environmental Scientist careers in academia and industry. Case studies using multi-omics data sets collected at the University of Birmingham will be provided so that you can gain practical experience of analysing and integrating multi-omics data.

Course Details The course will include ~1.5 days of generic environmental omics training and ~3.5 days of specialised genomics or metabolomics training (parallel tracks).

The combined sessions will include: \* Overviews of environmental genomics and metabolomics \* Practical experience of analysing and integrating multi-omics data \* Synthesis sessions to obtaining grant funding \* Question and answer sessions with a panel of experts

The genomics track includes: \* Library construction methods and QC \* Introduction to automation systems and sequence data workflow \* Software solutions for sequence workflows and their application in environmental research \* RNA-seq alignment \* Statistical considerations for analysing genome-scale data \* Practical experience in applying open-source analysis tools

to visualise complex sequence data and explore genome sequence variation, analyse Tuxedo output and perform gene set enrichment analysis \* Synthesis sessions to explore using the most appropriate model organism and maximising outputs from your sequence data

The metabolomics track includes: \* Experimental design \* Quality assurance and quality control in metabolomics \* Hands-on sample preparation \* Analytical technologies including mass spectrometry and NMR spectroscopy \* Data processing, including LC-MS and SIMS stitching procedures \* Univariate and multivariate data analysis approaches \* Metabolite identification

Evening Lecture Series Distinguished visiting academics will provide keynote lectures on each day of the course to highlight environmental omic applications that draw on the expertise of our guest faculty.

Daphnia is used for training because of its growing use as a model system in the environmental sciences and for improving environmental health protection, yet the skills learned during the course will be applicable to all study systems with maturing genomics and metabolomics resources.

[j.k.colbourne@bham.ac.uk](mailto:j.k.colbourne@bham.ac.uk)

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## UMichigan Biostation PlantSystematics Summer

Study the Field Botany of Northern Michigan with two renowned botanists this summer at the University of Michigan Biological Station (UMBS). We welcome back Dr. Charles Davis and Dr. Anton Reznicek as co-instructors for the class.

Dr. Davis is Curator of Vascular Plants in the Harvard University Herbaria and Professor of Organismic and Evolutionary Biology at Harvard. Dr. Anton Reznicek is Curator of Vascular Plants at the University of Michigan Herbarium and a Research Scientist at the University of Michigan.

Davis is a world expert on the parasitic (and remarkably bloomed) plant family Rafflesiaceae. Reznicek is an internationally recognized expert on sedges, especially the genus *Carex*. Both worked alongside legendary botanist, UMBS instructor and Michigan Flora author Edward G. Voss. Reznicek co-authored Field Manual of Michigan Flora with Voss.

Field Botany is a graduate-level course, but we



invite advanced undergraduates to enroll as well. Course information is available at [http://www.lsa.umich.edu/umbs/students/courses/-fieldbotanyofnorthernmichiganeeb556\\_ci](http://www.lsa.umich.edu/umbs/students/courses/-fieldbotanyofnorthernmichiganeeb556_ci).

The University of Michigan Biological Station is one of the premier inland field stations of North America. We are located on Douglas Lake, near Pellston, Michigan at the tip of Michigan's lower peninsula. The Station is situated in the heart of the Great Lakes, with 3 of the lakes within 30-90 minutes' drive. We are also near many unique and sensitive habitats including dunes, alvar, bogs, marshes and old-growth forest.

For more information, please visit our website ([lsa.umich.edu/umbs/](http://lsa.umich.edu/umbs/)) or call the office: 734-763-4461.

– Alicia Farmer, Communications Coordinator University of Michigan Biological Station 734-764-5212

[www.lsa.umich.edu/umbs/](http://www.lsa.umich.edu/umbs/) Alicia Farmer  
<farmeral@umich.edu>

## UParis Diderot LociOfEvolution Sep5-7

The Loci of Evolution Meta-Analysis Workshop 2016 September 5, 9am - September 7, 5pm Université Paris Diderot - Paris 7, France

“To collect and codify the fact of variation is the first duty of the naturalist [???] ; we need a compact catalogue of the known facts, a list which shall contain as far as possible all cases of variation observed ” - William Bateson (1894)

Gephebase is an online database scheduled for public release in Fall 2016 that will integrate our current knowledge of genotype-phenotype relationships in a time of accelerated discovery (GWAS, QTL mapping, reverse genetics). The first version will include no less than 1500 entries, forming an extensive catalogue of the empirical studies that have associated genetic changes to specific phenotypic variations in Eukaryotes.

We are inviting 20 researchers working on different aspects of genetic evolution to join us in Paris next September, and kick-start a community effort on the meta-analysis of the so-called Loci of Evolution. The first day will consist in a presentation of Gephebase contents, and its general potential for meta-analysis. On the second and third day, we will have small discussion groups with the overarching goal of cross-pollinating

opinions and initiate the writing of collaborative reviews. Participants are encouraged to come to the Workshop with a research question in mind. Here are a few possibilities:

- Trait-centered themes: Domestication; Reproductive Isolation; Innate Immunity, Morphological Patterns ; Xenobiotic Resistance; Behavior; Adaptation to Extreme Environments???

- Concept-centered themes: Micro- vs. Macro-evolution; Convergence: mutations in the same vs. different genes; Lateral transfers and Ancestral polymorphisms; Epistasis and complex genetic architectures; Mutational Biases; Optimal Pleiotropy and Mutational Target Size; Structural, regulatory and coding evolution; Balancing selection Vs. Mutation-selection balance; Effects of population size; Loss vs. Gain of function in evolution???

We are looking forward to meeting you and synergizing our efforts to synthesize genetic knowledge. This is an exciting time for evolutionary genetics!

No registration fee, meals and refreshments offered, lodging and travel in charge of the attendants (participants who need assistance to cover these costs are welcome to contact us). Graduate students, post-doctoral researchers and permanent researchers are encouraged to apply before April 15th 2016.

Please contact Dr. Arnaud Martin ([arnaud@gwu.edu](mailto:arnaud@gwu.edu)) for applying or more information.

Dr. Virginie Orgogozo  
[virginie.orgogozo@ijm.fr](mailto:virginie.orgogozo@ijm.fr)

Directrice de Recherche CNRS ???

Institut Jacques Monod (Paris, France)

Dr. Arnaud Martin [arnaud@gwu.edu](mailto:arnaud@gwu.edu) Assistant Professor, Department of Biological Sciences ??? George Washington University (Washington, DC)

Arnaud Martin, Ph.D. Assistant Professor The George Washington University Department of Biological Sciences Mail: 800 22nd St. NW, Suite 6000 Washington, D.C. 20052 USA Office: SEH 6520 ; Lab: SEH 6480a Phone: 202-994-2384 Cell: 949-302-3296 Google Scholar [@evolvwing](https://scholar.google.com/citations?user=evolvwing)

Arnaud Martin <[arnaud@email.gwu.edu](mailto:arnaud@email.gwu.edu)>

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## USheffield UK PopulationGenomics Mar21-23

### POPULATION GENOMICS WORKSHOP

March 21st-23rd 2016 University of Sheffield, UK

This course will be held at the NERC Biomolecular Analysis Facility at the University of Sheffield and introduce participants to a variety of population genomics analyses for large next generation sequencing (NGS) datasets. It will include discussion on single nucleotide polymorphism (SNP) calling and filtering options, an introduction to population genomics statistics using the PopGenome R package, examining genetic structure, Fst-based analyses such as outlier detection/genomic islands of divergence and genome-wide association analysis (GWAS).

The majority of the course will comprise practical computer sessions, giving participants hands-on experience in these analyses. We will perform these on the high performance computing cluster at Sheffield and computers will be provided. No prior experience is required, but familiarity with the Linux environment and basic command line tools would be advantageous (the course will include a short introduction/refresher to Linux).

There is no charge for the course, and successful applicants will be provided with accommodation for two nights and up to £100 towards travel costs to Sheffield.

The application closing deadline is at 5pm on Friday 26th February.

Further details and how to apply can be found at: <http://www.sheffield.ac.uk/nbaf-s/courses/popgen> < <https://www.sheffield.ac.uk/nbaf-s/courses> >

– Dr Helen Hipperson

Data Analyst NERC Biomolecular Analysis Facility - Sheffield <http://www.shef.ac.uk/nbaf-s/home> <https://www.facebook.com/nbafsheffield> “h.hipperson@sheffield.ac.uk” <h.hipperson@sheffield.ac.uk>

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## USouthernMaine ToolsForTreeOfLife Jul7-8

### NEXT GENERATION PHENOMICS Tools for the Tree of Life Workshop

July 7 and 8, 2016 Abromson Community Education Center University of Southern Maine Portland, Maine

A workshop to showcase and further collaborate on new web based programs developed for scientists, educators and students to collect phenomic information for assembling and annotating the Tree of Life. Publically available tools focused on natural language processing, computer vision and crowd sourcing.

For details about the workshop and registration, please go to <https://cms.usm.maine.edu/bio/ngp> . Dr. Lisa Moore Professor Department of Biological Sciences University of Southern Maine Portland, ME 04103 office: Science bldg, room 476B, C wing office phone: 207-780-4261 email contact: lrmoore@maine.edu

Lisa Moore <lrmoore@maine.edu>

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## Volterra Italy SystemsBiol Jul8-14

\* Our sincere apologies if you receive multiple copies of this announcement \* 3rd International Synthetic and Systems Biology Summer School - SSBSS 2016, 8-14 July 2016, Volterra (Pisa) - Tuscany, Italy

ssbss.school@gmail.com <http://www.taosciences.it/ssbss/> <https://www.facebook.com/ssbss.school/> The Synthetic and Systems Biology Summer School (SSBSS) is a full-immersion five-day residential summer school at the Volterra Learning Center (Pisa - Tuscany, Italy) on cutting-edge advances in systems and synthetic biology with lectures delivered by world-renowned experts. The school provides a stimulating environment for students (from Master students to PhD students), Post-Docs, early career researchers, academics and industry leaders. Participants will also have the chance to present their results (with Oral Talks and Posters), and to interact with their peers, in a friendly and constructive environment.

SSBSS 2016 DEADLINES: Application: March 31, 2016  
Notification Acceptance: April 10, 2016 Oral Presentation/Poster Submission: March 31, 2016 Notification of Decision for Oral/Poster Presentation: April 10, 2016

<http://www.taosciences.it/ssbss/#application-form>

SPEAKERS \* Yaakov (Kobi) Benenson, Synthetic Biology Group@Department of Biosystems Science and Engineering, ETH Zurich, Basel, Switzerland Lectures: TBA

\* Leonidas Bleris, Bioengineering Department, The University of Texas at Dallas, USA Lectures: TBA

\* Domitilla Del Vecchio, Department of Mechanical Engineering, MIT, USA Lectures: TBA

\* Diego Di Bernardo, Dept of Chemical Materials and Industrial Production Engineering University of Naples "Federico II", Naples, Italy Lecture 1: "Engineering and Control of Biological Circuits in Yeast" Lecture 2: "Engineering and Control of Biological Circuits in Mammalian Cells"

\* J. Gootenberg, Feng Zhang's Group, Department of Systems Biology, Harvard Medical School, Harvard University, USA Lectures: TBA

\* Markus Herrgard, Technical University of Denmark - Biosustain, Novo Nordisk Foundation Center for Biosustainability, Denmark Lecture 1: "Developing an Integrated Cell Factory Design Tool" Lecture 2: "Using Automated Laboratory Evolution to Optimize Cell Factories?"

\* Shalev Itzkovitz, Department of Molecular Cell Biol-

ogy, Weizmann Institute of Science, Israel Lecture 1: "Single Molecule Approaches for Studying Gene Expression in Intact Mammalian Tissues" Lecture 2: "Systems Biology of Stem Cell-Maintained Tissues?"

\* Francesco Ricci, Dipartimento di Scienze e Tecnologie Chimiche, University of Rome Tor Vergata, Rome, Italy Lecture 1: "DNA Nanotechnology Tools and Reactions for Synthetic Biology" Lecture 2: "Nature-inspired DNA-based Nanodevices"

More speakers will be announced soon!

INDUSTRIAL PANEL \* Speakers TBA

Next Generation Sequencing Workshop ? Afternoon July 12th, 2016

\* ?How fast can we align sequences?? Mario Guarracino, CNR, Italy

\* ?Advanced Bioinformatics tools for NGS? ? TBC Luca Zammataro, Yale University, USA

Tutorials: \* ?Detection and analysis of contaminating sequences in NGS sequencing data? Ilaria Granata, CNR, Italy

\* ?Detection and interpretation of circular RNAs in RNA-seq experiments? Parijat Tripathi, CNR, Italy

MORE INFO [ssbss.school@gmail.com](mailto:ssbss.school@gmail.com) <http://www.taosciences.it/ssbss/> <https://www.facebook.com/ssbss.school/> \* Apologies for multiple copies. Please forward to anybody who might be interested \*

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## Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto: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 L<sup>A</sup>T<sub>E</sub>X 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<sup>A</sup>T<sub>E</sub>X do not try to embed L<sup>A</sup>T<sub>E</sub>X or T<sub>E</sub>X in your message (or other formats) since my program will strip these from the message.