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# E v o l D i r

April 1, 2015

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.



Foreword .....	1
Conferences .....	2
GradStudentPositions .....	23
Jobs .....	47
Other .....	66
PostDocs .....	75
WorkshopsCourses .....	117
Instructions .....	135
Afterword .....	135

---

## Conferences

Amsterdam PlantGenomeEvolution Sep6-8 ..... 2	SaoPaulo Evolution Jun26-30 MinorityAirfare ..... 13
Berkeley EvoDevo Aug5-9 ..... 3	SaoPaulo Evolution Jun26-30 MinorityStudentTravel 13
Bologna ItalianSocEvolutionaryBiol Aug31-Sep3 ..... 3	Saskaton CanSocEcoEvol May22-24 EarlyBird ..... 14
Cairns Birdsong Aug9-14 ..... 4	Scotland EMPSEB StudentEvolutionaryBiology Sep8- 12 ..... 14
Cairns MatingConflict Mar16 ..... 4	StAndrews DrosophilaEvolution May8 ..... 14
Cambridge EvolutionaryGenomics Mar17 ..... 4	Stockholm MammalBiol Aug16-22 Registration .... 15
Crete EvolutionaryBiol Oct7-11 ..... 5	Sydney Hawkesbury BiologyTephritidFlies Apr2 ... 15
Dublin Bioinformatics Jul10-11 ..... 5	Tours France EukaryoticGenomes Jul8-10 ..... 16
Edinburgh QuantitativeGenetics Mar18 ..... 6	Tubingen PopBio May14-16 ..... 16
Germany IBAC2015 VocalisingFemales Sep7-12 ..... 7	Turkey EcolEvolutionaryBiol Aug6-7 Registration . 17
Guelph Barcoding Aug18-21 ..... 7	UBrno PlantGenetics Sep7-10 ..... 17
KansasStateU ArthropodGenomics Jun17-19 Deadline- Mar9 ..... 8	UCalifornia Berkeley EvoDevo Aug5-9 ..... 18
Krakow Poland EvolutionaryPhysiology Aug23-28 .. 9	UCalifornia Berkeley EvoDevo Aug5-9 Deadlines .. 18
Montreal PopulationCohorts Apr16-17 ..... 9	UHuddersfield ProtistEvolution Apr15-17 ..... 19
NESCent BiodiversityDisease May4-6 CallApplicants 10	ULisbon ReticulateEvolution Jul17 ..... 19
Paris EvolutionaryAdaptation Jul8-10 ..... 10	UMichigan AnnArbor PopGenet Jul25-26 ..... 19
Paris MathModelsEcolEvol Jul8-10 Registration ... 11	UMichigan ECSS Microbiome Ecol Evol Mar28 ... 20
Paris MMEE AdaptationInAChangingEnvironment Jul08-10 ..... 11	UMichigan SocSystematicBiol May20-22 ..... 21
Paris MMEE LinkageAndTheLimitstoSelection Jul08-10 12	Vienna SSMBE2015 Jul12-16 EarlyBird ClosingThisSun- day ..... 22
Peru Biodiversity Oct15-18 ..... 12	Zurich EvolMed Jul30-Aug1 ..... 22

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### Amsterdam PlantGenomeEvolution Sep6-8

\*Plant Genome Evolution 2015\* A Current Opinion Conference Amsterdam, The Netherlands 6-8 September 2015

For full conference details visit <http://www.plantgenomeevolution.com> \*Submit abstracts by 3 April 2015\*

It is our pleasure to announce the third Current Opinion Conference on Plant Genome Evolution, to be held in Amsterdam, 6-8 September 2015. We are delighted to be holding this (now biannual) event again after a very successful first and second meeting in 2011 and 2013 where renowned plant researchers gave inspiring talks and where many discussed their latest research in the field.

For the 2015 meeting, we are even more ambitious than the previous years and are trying to put together an even more exciting programme focused on (new) plant genomes, natural variation, domestication, epigenetics,

and systems biology, of course all with a strong emphasis on evolution and evolutionary aspects.

This third meeting will present the unique opportunity to meet and discuss with colleagues, get updated on the newest developments and insights in plant genome evolution, and will provide unique possibilities to network and discuss collaborations. We are delighted to announce that Prof. Gerald A. Tuskan (Oak Ridge National Laboratory and JGI, USA) has agreed to deliver the plenary lecture on Sunday, opening the meeting.

Topics

- (Novel) Genome projects - Genome and epigenome evolution - Gene and genome duplication - Genomic views on hybridization, heterosis, domestication, and speciation - Genomic variation and population genomics
- Bioinformatics, systems and synthetic biology

Mary McAdam <mary@2market2market.co.uk>

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### Berkeley EvoDevo Aug5-9

Registration for the inaugural meeting of the Pan American Society for Evolutionary Developmental Biology <<http://www.evodevopanam.org/>> is open! Mark your calendars for the meeting dates, 5-9 August, 2015. Only a few spots left!!!

\*The registration deadline is April 1, 2015. Click **\*\*here\*** <<http://www.evodevopanam.org/meetings-events.html>> **\*\*to register.\***

Follow us: @EvoDevoPanAm

Join Us: #EvoDevo15

A few meeting highlights:

- **\*Confirmed speakers:** \*Chris Amemiya, Alexa Bely, Sean Carroll, Rachel Collin, Kim Cooper, Tamara Franz-Odenaal, Matt Gibson, Angela Hay, Vivian Irish, Catherine Linnen, Mark Martindale, Jose Xavier Neto, Natalia Pabón-Mora (Early Career Award Recipient), Richard Palmer, Rudy Raff (Pioneers Award recipient), Bob Reed, Matt Rockman, Neelima Sinha, Stacey D. Smith, Ralf Sommer, Mansi Srivastava, James Umen

- Published abstracts
- Posters on display throughout the entire meeting
- Poster prizes for PhD students and postdocs
- Child Care reimbursement available!! Bring the whole family.

All details about registration, accommodation options, child care services, and the conference program are available at the following website: <http://www.evodevopanam.org/meetings-events.html> Support the Society and Become a Member!! To learn more about PASEDB, visit the following website: <http://www.evodevopanam.org/> The Organizing Committee and the PanAm SEDB Executive Council look forward to welcoming you to Berkeley in August!

Chelsea Specht <cdspecht@berkeley.edu>

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### Bologna ItalianSocEvolutionaryBiol Aug31-Sep3

The University of Bologna, the Department of Biological Geological and Environmental Sciences and the Molecular Zoology Lab (MoZoo Lab) invite you at the 6th Congress of the Italian Society of Evolutionary Biology that will be held in Bologna (Italy) from August 31 to September 3, 2015.

You can find all the informations at the Conference website [www.evoluzione2015.net](http://www.evoluzione2015.net) The 6th SIBE congress wants to specifically promote exchanges and discussion among Italian and non-Italian evolutionary Biologists, with particular attention to young researchers. Symposia will cover different topics, including the most up-to-date thematic areas of Evolutionary Biology. A particular attention will also be given to the dissemination of the nature and social role of evolutionary biologists to general public.

The Conference is organized into 7 thematic symposia covering most of the fields of Evolutionary Biology. The Conference warmly welcomes all professional and non-professional Evolutionary Biologists, as well as teachers and science writers. It is also particularly addressed to young students and scientists and, through an informal and easy going atmosphere, wants to promote exchanges and synergies among scientists and/or amateurs.

The Congress venue is conveniently located in the University Area, which is close to the historic part of the beautiful city of Bologna, the house of the oldest University in the world.

We hope to see you in all in Bologna

The Organizing Committee of the 6th Congress of the Italian Society of Evolutionary Biology

Marco Passamonti <marco.passamonti@unibo.it>

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## Cairns Birdsong Aug9-14

REMINDER: ABSTRACT DEADLINE APPROACHING!

As a part of the Behaviour 2015 conference that will be held in Cairns, Australia, on 9-14 August 2015, we are pleased to announce a symposium on the topic "Female song: fitness costs and benefits".

Symposium summary:

Bird song, traditionally regarded as primarily a male trait, is in fact widespread among female songbirds and was likely present in the ancestor of modern songbirds. These recent findings challenge the view that sexual dimorphism in the expression and complexity of song is largely the outcome of sexual selection on males. It is now clear that understanding the evolution of bird song requires explaining variation within and among species in the expression and complexity of female song. To do this, we need a better understanding of the nature of variation in female song in different contexts and systems, as well as the fitness costs and benefits of variation in the expression and complexity of female song. The aim of this symposium is to draw together current research on female song with the goal of understanding the fitness costs and benefits of the diversity of female singing behaviour apparent among songbirds.

Abstract submissions for oral presentations can be submitted until 16 March 2015:

<http://www.behaviour2015.org/symposium-details/>  
For more details, please don't hesitate to contact us:

Michelle L Hall - hall.mATunimelb.edu.au

Naomi E Langmore - naomi.langmoreATanu.edu.au

The conference is a major international meeting and a great opportunity to meet and interact with other scientists in the field, as it will be a joint meeting of the International Ethological Conference (IEC < <http://www.ethologycouncil.org/> >), Australasian Society for the Study of Animal Behaviour (ASSAB < <http://www.assab.org/> >), Australasian Evolution Society (AES < <http://australasianevolutionsociety.com/> >), and International Society for Applied Ethology: Australasia, New Zealand and Africa Region.

naomi.langmore@anu.edu.au

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## Cairns MatingConflict Mar16

For those of you interested in the role of conflict in mating and reproduction, please consider registering for the "Costs and Conflict in Reproduction" symposium at this year's Behaviour 2015 in Cairns (<http://www.behaviour2015.org/>). If you wish to submit an abstract, follow the instructions under "Symposium Details" (<http://www.behaviour2015.org/symposium-details/>). Please note that abstracts are due by March 16.

id #19662 Costs and Conflict in Reproduction Conflict between individuals is ubiquitous in nature, and stems from costs incurred by one or more players in an interaction when their optima do not align. Self-promotion and cost avoidance help to shape all manner of behavioural interactions - including those associated with reproduction. Conflict can manifest among members of the same sex (e.g., male-male sperm competition, queen/worker conflict), or between the sexes, where the reproductive optima of females and males differ (sexual conflict). Additionally, when species with poor mate recognition systems occur sympatrically, interspecies interactions may also impose significant costs to one or both players (reproductive interference). This symposium aims to focus on different facets of antagonism in the context of reproduction, to gain insights into conflict and conflict resolution gleaned from different perspectives and across hierarchical levels (i.e., within sexes, between sexes, between populations, between species).

Thank you,

Nikolai Tatarnic & Leigh Simmons

Nikolai Tatarnic <Nikolai.Tatarnic@museum.wa.gov.au>

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## Cambridge EvolutionaryGenomics Mar17

Conference: Evolutionary Genetics and Genomics, 17th March 2015, Cambridge UK

The meeting will be taking place in Cambridge (UK) on Tuesday 17th March 2015. The meeting is free to

attend and no registration is required. The meeting aims to bring together people working on all aspects of evolutionary genetics.

We have a fantastic line up of talks including three invited speakers:

-Josephine Pemberton, University of Edinburgh “Genomic analysis of body size in a free-living population” <http://pemberton.bio.ed.ac.uk/josephine-pemberton>

-Nathan Bailey, University of St Andrews “Genomic Invasion” <http://www.flexiblephenotype.org/>

-Aoife McLysaght, University of Dublin “Dosage sensitive genes in evolution and disease” <http://www.gen.tcd.ie/molevol/> Details and full programme of talks can be found here: <http://www.evolutionarygenetics.group.cam.ac.uk/eggs/eggs.symp@gmail.com>

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## Crete EvolutionaryBiol Oct7-11

Dear colleagues,

It is my pleasure to announce that the registration and the abstract submission for the 13th International Congress on the Zoogeography and Ecology of Greece and Adjacent Regions that will take place in Irakleio (Crete, Greece) between the 7th and the 11th of October, 2015 will open on April 1st. The deadline for abstract submission and early registration will be July 30, 2015. Visit our congress website (<http://13iczegar.nhmc.uoc.gr/>) for the most current information. The congress' scope includes all issues related to systematic, phylogeny, biogeography, ecology, evolution, and conservation on animal species in the eastern Mediterranean region. Research concerning all aspects of animal biodiversity (terrestrial, subterranean, freshwater and marine) within a geographical region that includes the Balkan and Italian peninsulas, Asia Minor and Anatolia, as well as the Near East and the Mediterranean coasts of north-eastern Africa are welcome. The official language of the 13th ICZEGAR will be English. Sessions will convene in the mornings and afternoons and will include lectures by invited speakers, as well as talks and poster presentations selected from submitted abstracts.

The invited key speakers are: - Dr Adalgisa Caccone, Department of Ecology & Evolutionary Biology, Yale University, New Haven (CT), USA - Dr Neil Davies, University of California, Berkeley, USA - Dr Bella S. Galil, National Institute of Oceanography, Israel - Dr

Katerina Harvati-Papatheodorou, Eberhard Karls Universität Tübingen, Senckenberg Center for Human Evolution and Paleocology, Paläoanthropologie, Tübingen, Germany.

We will appreciate very much if you disseminate this information among your colleagues and encourage them to participate. We hope that you or some of your colleagues will be interested to attend the Congress. I look forward to welcoming you in Irakleio (Crete) for a scientifically stimulating and socially enjoyable meeting.

With best regards,

On behalf of the Organizing Committee Dr Nikos Poulakakis

Communication via e-mail is strongly encouraged (13iczegar@nhmc.uoc.gr).

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## Dublin Bioinformatics Jul10-11

Call for Abstracts for the 16th Annual Bioinformatics Open Source Conference (BOSC 2015) A Special Interest Group (SIG) of ISMB/ECCB 2015

Dates: 10-11 July, 2015 Location: Dublin, Ireland  
Web site: [http://www.open-bio.org/wiki/BOSC\\_2015](http://www.open-bio.org/wiki/BOSC_2015)  
Email: bosc at open-bio.org BOSC announcements mailing list: <http://lists.open-bio.org/mailman/listinfo/bosc-announce> Important Dates: March 24, 2015: Registration opens for ISMB and BOSC (<https://www.iscb.org/ismbeccb2015-registration>) April 3, 2015: Deadline for submitting BOSC abstracts May 3, 2015: Notification of accepted talk abstracts emailed to authors July 8-9, 2015: Codefest 2015, Dublin ([http://www.open-bio.org/wiki/Codefest\\_2015](http://www.open-bio.org/wiki/Codefest_2015)) July 10-11, 2015: BOSC 2015, Dublin ([http://www.open-bio.org/wiki/BOSC\\_2015](http://www.open-bio.org/wiki/BOSC_2015)) July 10-14, 2015: ISMB/ECCB 2015, Dublin

The Bioinformatics Open Source Conference (BOSC) covers the wide range of open source bioinformatics software being developed, and encompasses the growing

movement of Open Science, with its focus on transparency, reproducibility, and data provenance. We welcome submissions relating to all aspects of bioinformatics and open science software, including new computational methods, reusable software components, visualization, interoperability, and other approaches that help to advance research in the biomolecular sciences. We particularly wish to invite those who have not participated in previous BOSCs to join us this year!

Two full days of talks, posters, panel discussions, and informal discussion groups will enable BOSC attendees to interact with other developers and share ideas and code, as well as learning about some of the latest developments in the field of open source bioinformatics. BOSC is sponsored by the Open Bioinformatics Foundation, a non-profit, volunteer-run group dedicated to promoting the practice and philosophy of Open Source software development and Open Science within the biological research community.

We invite you to submit one-page abstracts for talks and posters. As mentioned, any topics relevant to open source bioinformatics and open science are welcome. Here are some potential session topics (but please don't feel limited to these!): Open Science and Reproducible Research Standards and Interoperability Data Science Visualization Translational Bioinformatics Bioinformatics Open Source Libraries and Projects

If your company or organization is interested in being a sponsor for BOSC 2015, please contact us! Sponsors in 2014 included Google, Eagle Genomics, GigaScience, and Curoverse—we thank them for their support.

BOSC 2015 Organizing Committee: Nomi Harris and Peter Cock (co-chairs), Raoul Jean Pierre Bonnal, Brad Chapman, Robert Davey, Christopher Fields, Sarah Hird, Karsten Hokamp, Hilmar Lapp, Monica Munoz-Torres. [http://www.open-bio.org/wiki/BOSC\\_2015](http://www.open-bio.org/wiki/BOSC_2015)  
monica.cecilia@gmail.com

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## Edinburgh QuantitativeGenetics Mar18

The 8th meeting of the Edinburgh Alliance for Quantitative Trait Genetics (E-ACTG) sponsored by the Genetics Society and BBSRC will take place on Wednesday March 18th.

The focus will be on Genomic (and other) Prediction. Details of location, timing and programme below.

The meeting is free but please register to attend by March 10th via Google docs at:

<https://docs.google.com/spreadsheets/d/1uS3GL8jeN0g-LOqmmnTETBMozcFXxh-l1BIF3YBI9QI/edit?usp=sharing>

Chris Haley Josephine Pemberton

\*\*\*\*\*

Edinburgh Alliance for Complex Trait Genetics Eighth meeting - Wednesday March 18th, 2015 Royal College of Physicians, 9 Queen Street, Edinburgh, EH2 1JQ

>From 12.00 Arrival, registration

12.30 Lunch

13.10 Session 1 Chair: David Porteous (MRC IGMM)

13.10 David Porteous (MRC IGMM) Introduction

13.25 Ricardo Pong-Wong (Roslin Institute) The foundations of genomic prediction: Lessons from livestock

13.50 Paul McKeigue (Centre for Public Health Sciences) Using genetic predictions of biomarkers to investigate causal pathways

14.15 Enrique Sanchez Molano (Roslin Institute) Genomic prediction of hip dysplasia in Labrador Retrievers

14.40 Tea

15.10 Session 2 Chair: David Porteous (MRC IGMM)

15.10 Oriol Canela-Xandri (Roslin Institute) From genotypes to phenotypes with massive numbers of individuals

15.35 Riccardo Marioni (Centre for Cognitive Aging and Cognitive Epidemiology) Improving phenotypic prediction by combining genetic and epigenetic associations

16.00 Smaragda Tsairidou (Roslin Institute) Imputation and genomic prediction for bTB resistance in dairy cattle

16.25 Mairead Bermingham (MRC IGMM) Using livestock approaches for genomic prediction in humans

16.35 Isobel Stewart (Roslin Institute) Genomic prediction in colorectal cancer

16.45 Athina Spiliopoulou (MRC IGMM) Future Opportunities

17.00 Refreshments and discussion

18.00 Meeting ends

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Prof. J.M. Pemberton Institute of Evolutionary Biology University of Edinburgh EH9 3FL

Tel: 0131 650 5505 Fax: 0131 650 6564 Web: <http://-wildevolution.biology.ed.ac.uk/>

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

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## Germany IBAC2015 Vocalising Females Sep7-12

Dear Evoldir Members,

Registration is now open for the International Bioacoustics Congress for 2015 to be held in Murnau Germany on 7-12 September 2015 (<http://2015.ibac.info/>).

Abstract submissions are invited for an oral presentation in the symposium: 8. "Vocalizing females: Sexual dimorphism revised". Bird song, traditionally regarded as primarily a male trait, is in fact widespread among female songbirds and was likely present in the ancestor of modern songbirds. If you study female vocalisations or sexual dimorphism in vocalisations, this symposium will be a great opportunity to explore the implications of these findings and identify new directions for research while engaging with others working in the field. Check out the the rest of the conference program here (<http://2015.ibac.info/programme>). Murnau is a popular scenic tourist destination in Bavaria, so it is worth booking accommodation soon. Please submit an abstract before 31 May 2015 at (<http://2015.ibac.info/abstracts-submission>), and also notify me of your interest in participating as soon as possible <hall.m@unimelb.edu.au>.

Look forward to seeing you in Murnau!

Dr Michelle L Hall Research Fellow School of BioSciences University of Melbourne Melbourne, Vic, 3010 Australia Email: [hall.mATunimelb.edu.au](mailto:hall.mATunimelb.edu.au) Web: <http://michellehall.wordpress.com/> [hall.m@unimelb.edu.au](mailto:hall.m@unimelb.edu.au)

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## Guelph Barcoding Aug18-21

Dear Colleagues,

It is our pleasure to announce that the 6th International Barcode of Life Conference will be held at the University of Guelph, Canada, from August 18-21, 2015.

This biannual conference series showcases the latest scientific achievements and socio-economic implications of work conducted by the DNA barcode research community. The theme of the 6th Conference, Barcodes to

Biomes, signals the ongoing expansion of our community's research agenda from studies on particular sets of species in particular places to investigations of entire biotic assembles at local and global scales.

The conference features internationally renowned plenary speakers on topics ranging from evolution to ecology to conservation. The meeting also features diverse parallel sessions, a poster session, and social events that are included in registration. Eligible delegates may apply for a Travel Award as well as Student and Postdoctoral Prizes.

Plenary Speakers include:

Yves Basset, Louis Bernatchez, Mark Blaxter, David Castle, Melania Cristescu, Thibaud Decaens, Eduardo Eizirik, Brock Fenton, Dawn Field, Rosemary Gillespie, Charles Godfray, Mehrdad Hajibabaei, Illka Hanski, Paul Hebert, David Hik, Michael Hofreiter, Monte Hummel, Dan Janzen, Peter Kevan, Karl Kjer, Nancy Knowlton, John Kress, John La Salle, Thomas Lovejoy, Laurence Packer, Rod Page, Naomi Pierce, Stuart Pimm, David Posada, Sujeevan Ratnasingham, Paul Snelgrove, Bridget Stutchbury, Derek Tittensor, Jana Vamosi, Wolfgang Wagele, Tetsukazu Yahara

Registration for the 6th International Barcode of Life Conference is now open and will continue throughout the conference. Further details can be found at: <http://dnabarcodes2015.org/>. Abstracts will be accepted until April 15, 2015.

Please be so kind as to forward this announcement and the conference poster to others who may find this conference of interest. We hope to welcome you to Guelph in August!

Conference poster: <http://dnabarcodes2015.org/wp-content/uploads/2015/03/conferenceFlyer.pdf> Yours sincerely,

The Conference Operating Committee,

Sarah Adamowicz Mehrdad Hajibabaei Robert Hanner Paul Hebert

[info@dnabarcodes2015.org](mailto:info@dnabarcodes2015.org)

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## KansasStateU ArthropodGenomics Jun17-19 DeadlineMar9

\*-\* Ninth Annual Arthropod Genomics Symposium \*-\*  
June 17, 2015 to June 19, 2015 K-State Alumni Center,  
Kansas State University Manhattan, Kansas Symposium  
Website: [www.ksu.edu/agc](http://www.ksu.edu/agc) ABSTRACT DEADLINES  
IN 2015 Monday, March 9 - If you DO wish your ab-  
stract to be considered for an oral presentation/General  
Session talk. Monday, March 9 - If you DO wish your  
abstract to be considered for a poster presentation at  
the IGTRCN pre-meeting workshop. Wednesday, May  
20 - If you do NOT wish for your poster abstract to be  
considered for oral presentation and DO want to present  
a poster.

TRAVEL GRANTS AVAILABLE Two separate travel  
grants are available to attend the meeting: 1) IGT-RCN  
- sponsored by the Insect Genetic Technology Research  
Coordination Network.

Deadline: March 9, 2015 2) Eck Institute Travel Grants  
for Vector Biologists - sponsored by the Eck Institute  
for Global Health.

Deadline: March 30, 2015 Additional information is  
available on the Travel Grants page of the symposium  
website.

REGISTRATION Please register online at the Sym-  
posium website, <http://www.k-state.edu/agc>! Early  
bird deadline for reduced fees is April 10. Deadline for  
general registration is June 5.

SPEAKERS Keynote Speaker: David A. O'Brochta,  
Institute for Bioscience and Biotechnology Research  
& Department of Entomology, University of Maryland  
College Park

Featured Speakers: +Michelle Cilia, USDA-ARS, Boyce  
Thompson Institute for Plant Research, Cornell Uni-  
versity, USA +Martin J. Donnelly, Liverpool School  
of Tropical Medicine and the Wellcome Trust Sanger  
Institute, UK +Rosemary G. Gillespie, University of  
California, Berkeley, USA +Sijun Liu, Iowa State Uni-  
versity, USA +Frank Lyko, German Cancer Research  
Center, Heidelberg, Germany +Duane McKenna, Uni-  
versity of Memphis, USA +Armin P. Moczek, Indiana  
University, USA +Amanda J. Moehring, Western Uni-  
versity, Ontario, Canada +Daniel E. Neafsey, Broad  
Institute of MIT and Harvard University, USA +Greg  
Ragland, Kansas State University, USA +Anne-Nathalie

Volkoff, INRA (UMR1333), Montpellier 1 University,  
France

The symposium focuses on new insights gleaned from  
analyzing arthropod genomes and is designed for scien-  
tists interested in genomic studies of Arthropods, both  
model organisms and those of agricultural or health  
relevance. The program will include platform presenta-  
tions, welcome reception, Genome Train Workshop, An-  
notation Café, and arthropod genomics-related poster  
sessions. A few poster abstract submissions will be  
selected for platform presentations. Postdoctoral, grad-  
uate, and undergraduate students are also encouraged  
to attend. Sessions conclude Friday evening, followed  
by an optional evening at Konza Prairie Biological Sta-  
tion < <http://kpbs.konza.k-state.edu/> > with dinner  
and live music by the Red State Blues Band < [http://-  
www.redstatebluesband.com](http://www.redstatebluesband.com) >.

\*-\* Pre-Symposium Workshop \*-\* INSECT GENETIC  
TECHNOLOGY workshop June 17, 2015 (Wednesday  
morning and afternoon) Robust protocols to manipulate  
genes and genomes have not yet been developed for most  
insects other than *Drosophila melanogaster*, and this  
shortfall is limiting research progress in many aspects of  
arthropod genomics. The NSF-RCN on Insect Genetic  
Technologies (IGTRCN: 2014-2019; [igtrcn.org](http://igtrcn.org)) seeks to  
remedy this problem by facilitating the communication  
of best practice and new techniques among arthropod  
genomicists.

This IGTRCN-sponsored workshop will comprise (1)  
talks that showcase the latest genetic technologies, (2)  
discussion sessions for exchange of ideas and solutions  
for effective insect genetic engineering, and (3) posters.  
Proposals from the workshop will be integrated into  
the IGTRCN program of hands-on practical workshops,  
fellowships, and the IGTRCN KnowledgeBase. Early-  
career researchers are particularly encouraged to present  
their research at this workshop. A limited number of  
travel grants to attend the workshop are available for  
early stage investigators. For more information on poster  
abstract and travel grant submission for the workshop,  
go to [http://www.k-state.edu/agc/symposium\\_level-  
workshop/index.html](http://www.k-state.edu/agc/symposium_level-workshop/index.html) . ANNOTATION CAFÉ The  
i5k Workspace@NAL and the Web Apollo development  
team are hosting an Annotation Café during poster ses-  
sions where both experienced and novice annotators  
can ask questions to an expert, share curation advice  
with other annotators, or chat with scientists from the  
National Agricultural Library and Web Apollo teams  
about the annotation services they provide.

TENTATIVE PROGRAM for SYMPOSIUM & WORK-  
SHOPS



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>

“UrodziÅem siÄ z rodziców ubogich, od dziecka pociÄg  
czujÄc do myÅlenia byt penetrujÄcego” StanisÅaw  
Lem, Cyberiada

marcin.czarnoleski@uj.edu.pl

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## Krakow Poland Evolutionary Physiology Aug23-28

International Congress of Comparative Physiology and Biochemistry has been organized every four years since 1983. ICCPB 2015 in Krakow, Poland puts emphasis on the integrated view of organisms “From Molecules to Macrophysiology”.

The meeting will be held in 23-28 August 2015 at the Jagiellonian University, where Nicolaus Copernicus started academic education that led him to revolutionizing ideas about the Universe. The deadline for early registration is 14<sup>th</sup> April.

Go to: [www.iccpb2015.confer.uj.edu.pl](http://www.iccpb2015.confer.uj.edu.pl) < <http://www.iccpb2015.confer.uj.edu.pl> >

Thirty thematic Symposia, including an Open Session will cover a wide range of topics:

Molecular and integrative physiology: homeostasis, hormones, genomes, trade-offs, telomeres, longevity

Neurophysiology: olfaction, chemical ecology, photoreception, enteric nervous system, monoamines

Physiology of biological rhythms: circadian clocks, photoperiodism

Energetics and temperature: avian flight, cardiorespiratory functions, endothermy, performance, metabolic scaling, body size, cell size, oxygen limitation, phenotypic plasticity, seasonality

Stress physiology: cellular stress, oxidative stress, life history, innate and acquired immunity  
Miscellaneous: fatty acids, actin and actin-binding proteins, statistical analysis of physiological data, biosensors\*\*

Dr. Marcin Czarnoleski

Jagiellonian University Institute of Environmental Sciences Gronostajowa 7, Krakow 30-387 Poland phone: (+48)126645203 email: [marcin.czarnoleski@uj.edu.pl](mailto:marcin.czarnoleski@uj.edu.pl)

Dr hab. Marcin CzarnoÅski

Instytut Nauk o Årodowisku Uniwersytet JagielloÅski ul. Gronostajowa 7, Kraków 30-387 tel: 126645203 email: [marcin.czarnoleski@uj.edu.pl](mailto:marcin.czarnoleski@uj.edu.pl)

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## Montreal Population Cohorts Apr16-17

Registrations < <http://www.symposium.cartagene.qc.ca/> > are now open for CARTaGENEs < <http://symposium.cartagene.qc.ca/> > Workshop and Symposium on Cohorts, Big Data and Genomics and Medicine.

Population cohorts are created with significant public or private investment and, in some countries, are the primary resource for research and health. Studies with increasingly larger numbers of individuals reflecting the changing population demographic and environment are deemed necessary to draw meaningful and actionable conclusions about the underlying genetic and environmental determinants of phenotypes and chronic diseases. Issues around genomic, phenotypic and clinical data acquisition, data storage, and managing access from population cohorts have been, in part, addressed by many of the existing large regional and national population research programs. Currently, data integration, interoperability, harmonization and data sharing are recognized as important goals.

To highlight these programs, the research opportunities and address challenges, CARTaGENE will host a symposium dedicated to Population Cohorts, Big Data and Personalized Genomics. Leaders and representatives of large regional, national and international cohorts from Europe, the US and Canada will present and discuss findings, analyses, and challenges associated with discovery, data integration, analysis, management and implementation.

The Symposium will take place at the historic Windsor Hotel in downtown Montreal, the 16-17 April, 2015.

Speakers include: Sonia Anand, Director, The Alliance for Healthy Hearts and Minds, McMaster University Philip Awadalla, Director CARTaGENE and the Canadian Data Integration Centre, OICR, Montreal Rex Chisholm, Vice-Dean Northwestern University and eMERGE Christine desRosiers, Director of the Metabolomics Laboratory, The Montreal Heart Institute, University of Montreal Emily Drabant-Conley,

Director Business Development 23&Me Alan Evans, Director Ludmer Institute, McGill University Tom Hudson, President Ontario Institute for Cancer Research, University of Toronto Eimear Kenny, Asst. Professor of Genetics and Genomic Sciences, Mt. Sinai NY Daniel Levy, Director of the Framingham Heart Study, Boston University Gil McVean, Director, Big Data Institute, WTCHG, Oxford University Jonathan Marchini, Professor Statistical Genomics, WTCHG, Oxford University Stephen Montgomery, Professor The Sardinia Project, Stanford University Charles Rotimi, Chief and Director, Metabolic Cardiovascular and Inflammatory Disease Genomics Branch, Centre for Research on Genomics of Global Health, NIH Michael Schull, CEO, Institute for Clinical Evaluative Sciences, University Hospital Network Toronto John Spinelli, Director BC Cancer Agency, BC Generations and Canadian Partnership for Tomorrow Project

This is an excellent opportunity to hear and discuss novel research from large population programs and establish collaborations in an interactive and engaging environment. Please register at <http://-symposium.cartagene.qc.ca> “Philip Awadalla, Prof” <philip.awadalla@mcgill.ca>

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### NESCent BiodiversityDisease May4-6 CallApplicants

On May 4-6, 2015, the Triangle Center for Evolutionary Medicine (TriCEM), the National Evolutionary Synthesis Center (NESCent) and the Duke Tropical Conservation Initiative (DTCI) will be hosting a Catalysis Meeting on “Biodiversity, Conservation and Infectious Disease.”

The goal of the meeting is to understand how conservation and changes in biodiversity impact infectious disease risk in humans and wildlife. The meeting will be composed of approximately 10 researchers from Research Triangle universities (Duke, UNC-Chapel Hill, NC State, and NC Central), with another 25 participants from outside the Triangle. All travel expenses will be covered for non-Triangle participants. In building the participant list, we seek a wide range of interests, approaches, and experience levels. Thus, we welcome modeling approaches, field biologists, and those with expertise in meta-analysis, and graduate students, post-docs, and faculty. At the meeting, we will work toward specific outputs, which will include a special “theme”

issue in a high-impact journal that synthesizes diverse views on this important topic, and development of future working groups to investigate specific questions in greater depth.

For those wishing to participate in the Catalysis Meeting - including scientists from the Research Triangle Universities - we ask that you fill out a brief application at this link: <http://goo.gl/forms/LuCWB5Vhgm> - Hillary S Young Noble Hall 2116 Department of Ecology, Evolution, and Marine Biology University of California, Santa Barbara Santa Barbara, CA Phone: 805-893-4681 <http://www.eemb.ucsb.edu/people/faculty/young> Hillary Young <hillary.young@lifesci.ucsb.edu>

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### Paris EvolutionaryAdaptation Jul8-10

Dear all,

I am pleased to announce that the mini symposium “Trade-offs and adaptive syndromes in evolution < <https://mmee2015minisymposium.wordpress.com/> >”, will be held during the - MMEE 2015 - Mathematical Models of Ecology and Evolution < <http://-www.biologie.ens.fr/mmee2015/index.html> > Conference in Paris Jul 8th- 10th 2015. Conference pre-registration < <http://www.biologie.ens.fr/mmee2015/-registration.html> > Deadline is on May 1st. Payment and registration deadline is June 1st.

Symposium description: Many models of evolution have focused on single traits ignoring covariation and co-evolution of them. The joint evolution of several morphological, behavioural or life-history traits that share evolutionary history, needs to be investigated to be able to draw conclusions about syndromes which result from different proximate and ultimate causes. Trade-offs and feedbacks are expected to shape the strength of adaptive syndromes and studying them will greatly improve our understanding of closely related trait changes in evolution.

Confirmed speakers: François Massol (Université des Sciences et Technologies de Lille 1 Bâtiment SN2) Title: Joint evolution of dispersal and the allocation of dispersal cost in heterogeneous landscapes;

Claus Rüdfler (University of Uppsala) Title: Does Organismal Complexity Favor the Evolution of Diversity?

If you are interested in contributing a poster or talk to this symposium, please indicate so (select

mini-symposium 8. Trade-offs and adaptive syndromes) during abstract submission. < <http://wwwabi.snv.jussieu.fr/achaz/mmee/submission.html> >

Bests, Helene Weigang

Helene Weigang PhD Candidate

Biomathematics Group Department of Mathematics and Statistics University of Helsinki P.O. Box 68 (Gustaf Hällströmin katu 2b) Kumpula campus, EXACTUM, room B418 [helene.weigang@helsinki.fi](mailto:helene.weigang@helsinki.fi)

[helene.weigang@helsinki.fi](mailto:helene.weigang@helsinki.fi)

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## Paris MathModelsEcolEvol Jul8-10 Registration

Dear friends,

We are very pleased to announce that registration and submission are now open for the \*MMEE 2015 Paris Conference\*, Mathematical Models in Ecology and Evolution, to be held at Collège de France from 8 to 10 July 2015. \*<http://www.biologie.ens.fr/mmee2015/>\*  
Registration

\*Deadline for preregistration (compulsory): May 1st <http://dr02.azur-colloque.cnrs.fr/preinscription.php?colloque4&lang=en>\* (please make sure to select your category in the 'tarification' table)

\*Deadline for registration and payment: June 1st.\*

The conference fee is 200 euro for full-time faculty. It includes coffee breaks, 3 buffet lunches and the Thursday cocktail. Discounted fees (PhD students 100 euro, ESMTB members 130 euro, postdocs 150 euro) are available upon registration before May 15.

Submission

You can now submit the abstract and title of your poster or talk (20') on the website of the conference \*<http://www.biologie.ens.fr/mmee2015/>\* You will be able to indicate if you would like your talk to be considered for inclusion in one of the 13 minisymposia (each minisymposium will welcome 3 contributed talks in addition to the 2 invited talks). Acceptance of talks will be notified by email from June 1st.

Please do share this information with interested colleagues and relevant emailing lists.

Looking forward to seeing you in Paris,

The organisers,

Amaury Lambert (UPMC, Collège de France) Guillaume Achaz (UPMC, Collège de France) Minus van Baalen (CNRS, ENS) Silvia De Monte (CNRS, ENS) Todd Parsons (UPMC, CNRS, Collège de France) Emmanuel Schertzer (UPMC, Collège de France)

PS. You may receive this e-mail because you subscribed to the newsletter of an earlier MMEE conference. If you do not wish to receive further announcements from MMEE2015, please send an e-mail to [sympa@list01.biologie.ens.fr](mailto:sympa@list01.biologie.ens.fr) with "unsubscribe mmee2015 <your e-mail address>" in the subject line.

PS2. If you are not yet part of the MMEE list, you can check <http://www.biologie.ens.fr/mmee2015/-information.html> to find out how to receive regular information about the conference (no more than approx. 5 emails per year). You can also follow us on twitter using @MMEE2015Paris.

Amaury Lambert, professeur UPMC <http://www.proba.jussieu.fr/pageperso/amaury> SMILE group <http://www.proba.jussieu.fr/~smile> Stochastics & Biology group <http://www.proba.jussieu.fr/~psb> [amaury.lambert@ens.fr](mailto:amaury.lambert@ens.fr)

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## Paris MMEE Adaptation In a Changing Environment Jul08-10

Dear evolDir community,

we would like to draw your attention to the upcoming conference 'Mathematical Models in Ecology and Evolution' (MMEE 2015), to be held at Collège de France from 8 to 10 July 2015 (for more details see <http://www.biologie.ens.fr/mmee2015/>) and invite you to submit an abstract to a mini-symposium on 'Adaptation in a changing environment'. Please note that the deadline for pre-registration (compulsory) is May 1st (pre-register here: <http://dr02.azur-colloque.cnrs.fr/preinscriptions.php>) and the deadline for registration and payment is June 1st. Abstracts can be submitted here: <http://www.biologie.ens.fr/mmee2015/-registrationSymposium> description: Adaptation lies at the heart of Darwinian evolution. Natural populations are constantly faced with environmental changes that force them to either adapt or go extinct – a problem that is aggravated by human-induced global change. Therefore, increasing our understanding of the adaptive process is important for both basic and applied research,

and both empirical and theoretical studies have made important progress in the past two decades. Empirically, it has become clear that evolutionary change can be fast enough to be directly observable and to affect the demography of populations and communities. This has led to a flurry of research on “eco-evolutionary dynamics” and the possibility of “evolutionary rescue” of endangered species. Other work has focussed on the genetic basis of the adaptive process. While genomic approaches often aim at identifying quantitative-trait loci under selection, other studies have proceeded to measure key aspects of the genotype-phenotype map, such as the degree of pleiotropy and epistasis. Finally, previously elusive concepts such as the adaptive landscape are becoming increasingly empirically accessible, and experimental evolution allows the direct observation of adaptive trajectories. Accommodating these new data and results requires the development of theoretical models that go beyond traditional population- and quantitative-genetic approaches by focusing on adaptation in high-dimensional phenotype- and genotype spaces in a specific ecological context. The aim of this symposium is to present recent theoretical advances in the study of adaptation in a changing environment and discuss how these connect and help to explain the phenomena observed in natural populations. The invited speakers will present results about evolutionary rescue in a stochastic environment and how epistasis and natural selection shape the mutational architecture of complex traits. Contributed talks and posters are invited that include (but are not limited to) studies of adaptation using Fisher’s geometric model and similar approaches, studies of the nature of genetic variation and the evolution of the G-matrix, and models of eco-evolutionary dynamics and evolutionary rescue. Confirmed invited speakers: Reinhard Bürger University of Vienna (Vienna, Austria) Luis-Miguel Chevin CNRS (Montpellier, France) Organized by: Sebastian Matuszewski University of Vienna (Vienna, Austria) & EPFL (Lausanne, Switzerland) sebastian.matuszewski@epfl.ch and Michael Kopp (Aix Marseille U) Aix-Marseille University (Marseille, France)

Looking forward to seeing you in Paris!

Sebastian Matuszewski  
<sebastian.matuszewski@epfl.ch>

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## Paris MMEE Linkage And The Limits to Selection Jul08-10

If you are headed to SMBE this summer, then you might want to make an early stop in Paris on your way to Vienna. Henrique Teotónio and I are organizing a symposium on “Linkage and the limits to selection” as part of the Mathematical Models in Ecology and Evolution meeting, July 8-10 at the Collège de France in Paris.

Nick Barton and Dimtri Petrov are our featured speakers, and there will be contributed talks as well. Our symposium is scheduled for the last day of the meeting for extra convenience for those heading to SMBE.

<http://www.biologie.ens.fr/mmee2015/-minisymposium10.html> There are several other symposia on adaptation at the meeting that should be of interest to this group as well, in addition to keynote talks by Michael Doebeli, Maria Servedio, Josh Plotkin, Régis Ferrière, and others.

Hope to see you there.

Patrick C. Phillips, Ph.D. Professor of Biology Institute of Ecology and Evolution Email: pphil@uoregon.edu Phone: (541) 346-0916 | FAX (541) 346-2364 Address: 5289 University of Oregon Eugene, OR 97403-5289 USA Web: Lab <http://www.uoregon.edu/~pphil> IEE <http://evolution.uoregon.edu>

pphil@uoregon.edu

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## Peru Biodiversity Oct15-18

Conference: Peru.Andes.Amazon.Meeting.Oct15-18

The Peruvian NGO “Centro de Ecología y Biodiversidad” (CEBIO) invites you to join us at the International Meeting: Biodiversity and Conservation of the Tropical Andes and the Amazon Rainforest < <http://andesamazonmeeting.org/> >

Registrations < <http://andesamazonmeeting.org/-meeting-registration/> > are now open. The meeting

will be held from October 15 to October 18, 2015 at Lima, Peru.

The objective of the conference is to bring together foreign and Peruvian scientists involved in biodiversity research and conservation of flora and fauna in the Tropical Andes and the Amazon Rainforest. The conference will include plenary talks, symposia, oral and poster presentations < <http://andesamazonmeeting.org/scientific-program/plenary-speakers/> >.

Meeting themes: Biodiversity, conservation, biogeography, systematics, climate change, tropical ecology, DNA barcoding, bioinformatics, next generation sequencing.

Abstract submission closes on May 1, 2015. < <http://andesamazonmeeting.org/submit-an-abstract/> >

Please be kind and forward this announcement to others who may find this conference of interest.

Yours sincerely,

The Conference organizing Committee,

bioconperu@cebioperu.org

“Frank Azorsa (CEBIO)” <fazorsa@cebioperu.org>

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### SaoPaulo Evolution Jun26-30 Minority Airfare

DEADLINE APPROACHING! NESCent/SSE 2015 MSI Faculty Travel Award - Evolution 2015 (Brazil)

The National Evolutionary Synthesis Center (NESCent) and the Society for the Study of Evolution (SSE), are teaming up to provide airfare and conference registration for faculty from Minority Serving Institutions (MSIs) to attend the Evolution 2015 conference in Guarujá, São Paulo, Brazil from June 26-30, 2015. Please note that all other expenses (food, lodging, ground transportation, costs associated with visa procurement) are the responsibility of the traveler.

If you are a faculty member at an MSI, HBCU or other institution with significant enrollment of under-represented minority students, you are encouraged to apply.

This award is intended to provide MSI faculty with an opportunity to present original research in evolution, systematic biology, evolutionary genomics/informatics, evolution education/outreach or other disciplines typically represented at the Evolution meetings. As such,

your application must include a talk/poster title and abstract. In addition, you will be asked to provide a brief (1 page) statement describing how this award will contribute to your professional/scientific development, as well as provide benefit to your students and institution.

Depending on your nationality and immigration status, A VISA MAY BE REQUIRED TO ENTER BRAZIL. More information can be found at the conference website (<http://www.evolution2015.org>). ALL AWARD RECIPIENTS ARE RESPONSIBLE FOR OBTAINING AND PAYING FOR THEIR OWN VISA, and the conference organizers advise that it could take up to a month (or possibly longer) to obtain a visa.

For more information, or to apply, please visit <http://bit.ly/1vsYWYt>. If you have any questions about this program, please contact Jory Weintraub ([jory@nescent.org](mailto:jory@nescent.org)).

APPLICATION DEADLINE: MARCH 15TH, 2015, 5:00 PM PST

AWARDS WILL BE ANNOUNCED BY MARCH 20TH, 2015

Jory P. Weintraub, PhD Assistant Director, Education & Outreach National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200, Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: [jory@nescent.org](mailto:jory@nescent.org) Skype: jory.weintraub

“Weintraub, Jory P” <[lviscrst@live.unc.edu](mailto:lviscrst@live.unc.edu)>

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### SaoPaulo Evolution Jun26-30 Minority Student Travel

APPLICATION DEADLINE APPROACHING! Evolution 2015 (Brazil) - Minority Graduate Student Travel Award

The National Evolutionary Synthesis Center (NESCent) and the Society for the Study of Evolution (SSE), are teaming up to provide airfare and conference registration for minority graduate students attending the Evolution 2015 conference in Guarujá, São Paulo, Brazil from June 26-30, 2015. Please note that all other expenses (food, lodging, ground transportation, costs associated with visa procurement) are the responsibility of the traveler.

Applicants must be graduate students at the time of the conference (June 26-30, 2015), working towards a Masters or PhD in evolutionary science, evolutionary ecology, biogeography, evolutionary informatics, evo-

lution education or some other field appropriate for the focus of the Evolution 2015 conference (<http://www.evolution2015.org>).

Applicants must be members of under-represented/under-served racial/ethnic groups, as defined by the National Science Foundation (<http://www.nsf.gov/statistics/wmpd/>).

Applicants must be US citizens, permanent residents, or foreign nationals currently enrolled in US-based graduate programs. All applicants must be free of any restrictions which would prevent them from traveling out of the US, to Brazil over the dates of the conference.

The application package consists of basic information, a one-page Statement of Academic Interests and Career Goals, a brief biosketch, and a Letter of Recommendation from your academic advisor.

APPLICATION DEADLINE: MARCH 15TH, 2015, 5:00 PM PST

AWARDS WILL BE ANNOUNCED BY MARCH 20TH, 2015

For more information and to apply, please visit <http://bit.ly/16hefaq>. If you have questions, please contact Jory Weintraub ([jory@nescent.org](mailto:jory@nescent.org)).

Jory P. Weintraub, PhD Assistant Director, Education & Outreach National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200, Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: [jory@nescent.org](mailto:jory@nescent.org) Skype: jory.weintraub

“Weintraub, Jory P” <[lviscrst@live.unc.edu](mailto:lviscrst@live.unc.edu)>

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### Saskatoon CanSocEcoEvol May22-24 EarlyBird

We invite you to the 10th Annual Meeting of the Canadian Society for Ecology and Evolution (CSEE) to be held in Saskatoon (SK, Canada) on 22-24 May 2015. This year, the theme of the conference is: 'Ecology and Evolution of Managed Landscapes'. We have an exciting program of symposia, invited speakers, and field trips. Please see the conference website for details: <http://csee2015.usask.ca/index.php>. Conference registration and the call for presentations are now open. Early bird fees and the presentation call end March 15th!

Nous vous invitons à Saskatoon (SK, Canada), du 22 au 24 mai 2015 pour la 10e rencontre annuelle de la CSEE

tenue par l'Université de la Saskatchewan. Cette année, le thème de la conférence est : «*Écologie et évolution des paysages aménagés*». Une gamme passionnante de symposia, conférenciers invités et excursions sur le terrain ont été organisés. Pour plus de détails, veuillez consulter le site internet de la conférence : <http://csee2015.usask.ca/fr/>. L'inscription à la conférence et l'appel de présentations sont maintenant ouverts. Les frais d'inscription hôte et l'appel de présentations se terminent le 15 mars 2015!

[Ciee-Icee@uregina.ca](mailto:Ciee-Icee@uregina.ca)

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### Scotland EMPSEB Student Evolutionary Biology Sep8-12

Registration is now open for EMPSEB21: The 21st European Meeting for PhD Students in Evolutionary Biology

Organised by the University of Edinburgh

Location: University of Stirling - Stirling, UK Date: September 8-12th, 2015

To register, please visit the following link: [http://www.epay.ed.ac.uk/browse/extra\\_info.asp?compid=-1&modid=2&deptid=24&catid=16&prodid=-1886&searchresults=1](http://www.epay.ed.ac.uk/browse/extra_info.asp?compid=-1&modid=2&deptid=24&catid=16&prodid=-1886&searchresults=1) For more information on the conference please visit our website: <http://empseb21.bio.ed.ac.uk> We look forward to seeing you in Stirling in September!

– R. Eileen Butterfield Postgraduate Student, University of Edinburgh - Edinburgh, UK

“I have long felt that biology ought to seem as exciting as a mystery story, for a mystery story is exactly what biology is.” - Richard Dawkins, *The Selfish Gene*

[rebecca.eileen.butterfield@gmail.com](mailto:rebecca.eileen.butterfield@gmail.com)

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### St Andrews Drosophila Evolution May8

ScotFly 2015

Any Drosophilists in Scotland or nearby are warmly invited to attend the 4th 1-day “Scottish Fly Meeting”,

which will take place at St Andrews on Friday 8th May. This is a very informal meeting of researchers with any interest in *Drosophila* and is relatively unusual in bringing together people from a broad range of backgrounds including evolution, development, neurobiology and physiology. New synergisms have emerged from previous meetings.

Invited speakers are Barry Denholm (development), Alistair McGregor (morphology), Megan Neville (behaviour), Darren Obbard (immunology) & Stefan Pulver (neurogenetics).

Contributed talks and posters, from researchers at all career stages, are welcomed.

To register and submit an abstract please send an e-mail to [scotfly@st-andrews.ac.uk](mailto:scotfly@st-andrews.ac.uk). Please send abstracts as one page using font Arial 12 pt. The closing date is 24 April 2015.

Please visit our website for further information: <http://synergy.st-andrews.ac.uk/drosophila/> The organisers, Mike Ritchie and Marcus Bischoff

Mike Ritchie Centre for Biological Diversity, School of Biology, University of St Andrews, Fife. Scotland KY16 9TH UK Phone: 0 (44 outside UK) 1334 463495 Some websites: Lab: <http://biology.st-andrews.ac.uk/ritchie/lab/> Uni: <http://www.st-andrews.ac.uk/profile/mgr> Google: <http://scholar.google.co.uk/citations?user=JSkvwMsAAAAJ&hl> CBD: <http://biodiversity.st-andrews.ac.uk/> Michael Ritchie <[mgr@st-andrews.ac.uk](mailto:mgr@st-andrews.ac.uk)>

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## Stockholm MammalBiol Aug16-22 Registration

Dear everyone,

Registration is now open for the 7th European Congress of Mammalogy in Stockholm (to be held 16-22 August 2015).

To register and pay the conference fee, please follow the instructions at this page: [www.zoologi.su.se/ecm7/-registration.php](http://www.zoologi.su.se/ecm7/-registration.php) Early Registration is until the 15th of April, and Late Registration will be between 16th of April and 16th of June.

The aim of the European Congresses of Mammalogy is to foster communication between researchers working on issues of mammalian biology in the European arena, as

well as providing a venue for the broad dissemination of European mammal research. The relaxed and friendly atmosphere of these congresses provides an excellent opportunity to hear the latest developments in various fields of mammalogy, to share research experience and expertise, and to develop new and closer contacts with colleagues from different countries.

The conference will cover a broad range of topics in mammal biology, including Species Interactions, Population Genetics, Conservation Biology and Ecology & Landscapes.

Please visit the conference website for further information: [www.zoologi.su.se/ecm7](http://www.zoologi.su.se/ecm7) Love.Dalen@nrm.se

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## Sydney Hawkesbury Biology Tephritid Flies Apr2

Dear colleagues,

From: [http://www.uws.edu.au/hie/-events\\_and\\_seminars/biology\\_of\\_tephritid\\_fruit\\_flies](http://www.uws.edu.au/hie/-events_and_seminars/biology_of_tephritid_fruit_flies)

Researchers from the Australian Tephritid fruit fly community (e.g. CSIRO, QUT, Macquarie, Murdoch, SARDI, UNSW, UWS) are gathering for an inaugural semiannual workshop to discuss scientific advances on the biology of this species group.

Topics can include ecology, chemical ecology, physiology, genetics, genomics, molecular biology techniques (e.g. RNAi/CRISPR) and any other discipline that may be of interest to our stakeholders.

The meeting is free and open for anyone interested in networking with scientists working in this species group.

Date: 2nd of April 2015 Time: 10am to 15:30  
Venue: Hawkesbury Institute for the Environment, Building R2, Eucalyptus Seminar Registration required: <https://www.eventbrite.com.au/e/the-biology-of-tephritid-fruit-flies-tickets-15969523274>

Queries to: <http://pubapps.uws.edu.au/teldir/-personprocess.php?14437>

Registrations: If you'd like to give a talk, please let the organiser know by the 20th of March 2015. Otherwise, for catering reasons, please register before the 25th of March 2015.

Accommodation can be provided at the Best Western Colonial Motel for \$118 per room per night (up to 2 people per room), please contact Dr Alexie Papanicolaou for details.

thank you, a

Dr. Alexie Papanicolaou Lecturer in Bioinformatics |  
Hawkesbury Institute for the Environment University  
of Western Sydney | Hawkesbury Campus Postal ad-  
dress: Locked Bag 1797, Penrith, NSW 2751, Australia  
[www.uws.edu.au/hie](http://www.uws.edu.au/hie) A.Papanicolaou@uws.edu.au

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## Tours France Eukaryotic Genomes Jul8-10

Dear Colleagues,

LE STUDIUM, Loire Valley Institute for Advanced Studies, is extremely excited to announce the \*Analysis and Annotation of DNA Repeats and Dark Matter in Eukaryotic Genomes Conference\*, the premiere event of the year for researchers to meet, discuss and share ideas on genic repeats and genomes classification! International leaders in the genomic research will gather in Tours, France, for the first time during a two-day conference over 3 days (\*8-10 July 2015\*) to discuss, learn and share ideas on a number of areas (click here to visit the conference page and announcement < <http://www.lestudium-ias.com/#%21analysis-and-annotation-of-dna-repe/c412> >).

The \*Analysis and Annotation of DNA Repeats and Dark Matter in Eukaryotic Genomes Conference\* aims to shine light on current and emerging research trends for genomes classification by providing a platform for discussion with a peloton of internationally acknowledged leaders.

Please note there are opportunities for poster sessions. For more information, please visit the conference page < <http://www.lestudium-ias.com/#%21analysis-and-annotation-of-dna-repe/c412> >

This one-off conference organised with \*Dr Yves Bigot, Research Director (CNRS - INRA Centre Val de Loire, France) and Dr Peter Arensburger (California State Polytechnic University, Pomona - USA)\* offers a unique opportunity to meet like-minded researchers, build new collaborations, visit the INRA Centre Val de Loire site in Nouzilly near Tours and enjoy the famous local gastronomy and scenery of the Loire Valley region!

We look forward to welcoming you to Tours, Loire Valley, France in next July 2015 and invite you not to miss the 15th May 2015 early bird registration deadline. The conference is open to a hundred participants (academics, post-doctorants, students and R&D scientists,

enterprises).

Sincerely,

On behalf of the scientific committee,

Nicola Fazzalari Scientific Director

\*LE\* \*STUDIUM\* \*Â\* Loire Valley Institute for Advanced Studies Tél. 33 (0)2 38 21 14 85 - e-mail : [nicola.fazzalari@lestudium-ias.fr](mailto:nicola.fazzalari@lestudium-ias.fr) <http://www.lestudium-ias.com> Sophie Gabillet General Secretary LE STUDIUMÂ Loire Valley Institute for Advanced Studies 1 Rue Dupanloup - 45000 Orléans - FRANCE [www.lestudium-ias.com](http://www.lestudium-ias.com) Tel: + 33 (0)2 38 21 14 81 - Portable: + 33 (0)6 67 00 32 22

Sophie Gabillet <[sophie.gabillet@lestudium-ias.fr](mailto:sophie.gabillet@lestudium-ias.fr)>

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## Tübingen PopBio May14-16

Dear Colleagues,

\*\*\* NOTE: Registration closes April 6 \*\*\*

Registration and Abstract submission are now open for the 28th PopBio Conference on plant ecology and evolution, which will take place on 14-16 May 2015 in Tübingen, Germany. <http://www.popbio2015.uni-tuebingen.de/> Keynote Speakers: >>Eric Allan<< (University of Bern, Switzerland) [http://www.ips.unibe.ch/content/biodiversity/index\\_eng.html](http://www.ips.unibe.ch/content/biodiversity/index_eng.html) >>Spencer Barrett<< (University of Toronto, Canada) <http://labs.eeb.utoronto.ca/BarrettLab/> >>Yvonne Buckley<< (Trinity College Dublin, Ireland) <http://www.tcd.ie/Zoology/research/research/buckley/> >>Sinead Collins<< (University of Edinburgh, UK) <http://www.smallbutmighty.bio.ed.ac.uk/> >>Detlef Weigel<< (MPI for Developmental Biology, Tübingen) <http://www.weigelworld.org/> The PopBio conference is hosted by the Plant Population Biology Section (PopBio) of the Ecological Society of Germany, Austria and Switzerland (GfA). Conference activities include oral and poster sessions, an informal welcome mixer on Wednesday evening (May 13), and a post-conference excursion Saturday afternoon (May 16) to the beautiful Schwäbische Alb.

Additional information including registration, abstract submission, and payment information is available on the PopBio 2015 Website: <http://www.popbio2015.uni-tuebingen.de/> \*\*\* IMPORTANT: We strongly encourage you book accommodation as soon as possible! \*\*\* Tübingen is a popular destination for tourists



and other conferences, and affordable rooms are already running low in several places. A small block of rooms is reserved for most of the following hotels: Krone, Am Bad, Fortuna (Reutlingen), Katarina Garni, Garni Sand. Please mention POPBIO when you make a reservation.

Other places that have vacancies: Garni Metropol, Meteora, Am Kupferhammer, GZT Gastehaus, Alte Krone. Alternatively, you may rent a room/flat from private owners.

We hope to see you there! The Tübingen Team: Mark Bilton, Michal Gruntman, Madalin Parepa, Niek Scheepens, Sara Tomiolo, Oliver Bossdorf and Katja Tielbörger

<http://www.popbio2015.uni-tuebingen.de/>-  
popbio2015@uni-tuebingen.de

rob.colautti@botany.ubc.ca

## **Turkey EcolEvolutionaryBiol Aug6-7 Registration**

Dear Colleagues,

The 2nd Ecology and Evolutionary Biology Symposium Turkey 2015 (August 6-7, Ankara) is now accepting abstract submissions at <https://survey.metu.edu.tr/-78885>. Please find more information at <http://eebst2015.bio.metu.edu.tr/Home.html>. We invite talks and poster presentations in all areas of evolutionary biology and ecology. All presentations will be in English and we heartily welcome international participation.

This year's keynote speakers will be Resit Akcakaya (Stony Brook U.), Sergey Gavrilets (U. Tennessee), Rasmus Nielsen (U. California, Berkeley), and Daniel Simberloff (U. Tennessee).

Deadline for abstract submissions is May 15. Registration closes by July 15.

A Cappadocia Tour will be organized following the meeting, for those interested.

We look forward to seeing you in Ankara!

On behalf of the Organizing Committee

Aysegul Birand (birand@metu.edu.tr) and Mehmet Somel (somel.mehmet@googlemail.com)

somel.mehmet@googlemail.com

## **UBrno PlantGenetics Sep7-10**

Mendel Museum of Masaryk University would like to invite you to the conference

Research in plant genetics (From Mendel's peas to the present)

which will be take place 7th september - 10th september 2015 in Mendel Museum of Masaryk University in Brno, Czech Republic.

Conference website: <http://www.mendelgenius.com/en/the-conferences/research-in-plant-genetics-from-mendels-peas-to-the-present> Sections/Topics: Mendel's factors today >From Mendel to population genomics Where is the message? - Genome structure Non-Mendelian genetics Reproduction without sex >From genes to phenotypes The impact. Plant breeding and agriculture

Invited/keynote speakers: Ueli Grossniklaus, University of Zurich, Swiss Edward Buckler, Cornell University, USA Peter van Dijk, KeyGene, Netherlands Catherine Rameau, INRA, Versaille, France Jonathan Wendel, Iowa State University, USA Dani Zamir, Hebrew University, Jerusalem, Israel Burstin J., INRA Dijon, France Ellis N., CGIAR, India Varshney R., ICRISAT, India

Important dates: Registration deadline: 30th April 2015 Abstract submission deadline: 30th April 2015

Registration and Call for Papers: Through attached registration form or website <http://www.mendelgenius.com/en/the-conferences/research-in-plant-genetics-from-mendels-peas-to-the-present>

Contact: Mendel Museum of Masaryk University Mendlovo nám. 1a 603 00 Brno Czech Republic e-mail: [info@mendelmuseum.muni.cz](mailto:info@mendelmuseum.muni.cz) <<mailto:info@mendelmuseum.muni.cz>>

phone: 00420 549 496 669  
[www.mendelmuseum.muni.cz](http://www.mendelmuseum.muni.cz) <<http://www.mendelmuseum.muni.cz>>  
[www.mendelgenius.com](http://www.mendelgenius.com) <<http://www.mendelgenius.com>>

We are looking forward to see you in Brno, Czech Republic!

"Wendel, Jonathan F [EEOBS]" <[jfw@iastate.edu](mailto:jfw@iastate.edu)>

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## UCalifornia Berkeley EvoDevo Aug5-9

Get new Ideas, learn new techniques, form new collaborations: 2015 Meeting of PanAm EvoDevo

REGISTRATION NOW OPEN for the inaugural meeting of the Pan American Society for Evolutionary Developmental Biology < <http://www.evodevopanam.org/> >! Mark your calendars for 5-9 August, 2015,

Register NOW before all 350 slots are filled!

\*The registration deadline is April 1, 2015. Click **\*\*here\*** < <http://www.evodevopanam.org/meetings-events.html> >\* to register.\*

Join us in Berkeley, California for the first EvoDevo meeting in the Americas sponsored by a new professional society dedicated to supporting the EvoDevo field!

A few meeting highlights:

- \*Confirmed speakers: \*Chris Amemiya, Alexa Bely, Sean Carroll, Rachel Collin, Kim Cooper, Tamara Franz-Odenaal, Matt Gibson, Angela Hay, Vivian Irish, Catherine Linnen, Mark Martindale, Jose Xavier Neto, Natalia Pabón-Mora (Early Career Award Recipient), Richard Palmer, Rudy Raff (Pioneers Award recipient), Bob Reed, Matt Rockman, Neelima Sinha, Stacey D. Smith, Ralf Sommer, Mansi Srivastava, James Umen
- \*Contributed papers \*selected from submitted abstracts: submit now to ensure you have a chance to present your work.
- Small, friendly symposia with focused breakout groups and workshops
- Engaging posters on display throughout the entire meeting
- Poster awards and prizes for students and postdocs

All details about registration, accommodations, child care, and the conference program are available at the following website: <http://www.evodevopanam.org/meetings-events.html> Support the Society and Become a Member!! To learn more about PASEDB, visit the following website: <http://www.evodevopanam.org/>

Chelsea D. Specht, PhD Associate Professor; Departments of Plant and Microbial Biology & Integrative Biology Curator of Monocots; University and Jepson Herbaria University of California, Berkeley

111 Koshland Hall, MC 3102 Berkeley, CA 94720  
510.642.5601

cdspecht@berkeley.edu <http://spechtlab.berkeley.edu/>  
Chelsea Specht <cdspecht@berkeley.edu>

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## UCalifornia Berkeley EvoDevo Aug5-9 Deadlines

Secure your spot now at the EvoDevo Event of the Year!

- 1) Join PanAm EvoDevo.
- 2) Register and submit an abstract - NOW.
- 3) Attend the meeting “ August 5th in Berkeley, CA.

Registration for the inaugural meeting of the Pan American Society for Evolutionary Developmental Biology is open! Register and Submit your Abstract by April 1 to secure your spot. Mark your calendars for the meeting dates, 5-9 August, 2015.

There are only a few spaces left to attend, and a few days left to submit your abstract!!!

The registration deadline is April 1, 2015. Click here to register.

Follow us: @EvoDevoPanAm Join Us: #EvoDevo15

A few meeting highlights:

- Invited speakers: Chris Amemiya, Alexa Bely, Sean Carroll, Rachel Collin, Kim Cooper, Tamara Franz-Odenaal, Matt Gibson, Angela Hay, Vivian Irish, Catherine Linnen, Mark Martindale, Jose Xavier Neto, Natalia Pabón-Mora (Early Career Award Recipient), Richard Palmer, Rudy Raff (Pioneers Award recipient), Bob Reed, Matt Rockman, Neelima Sinha, Stacey D. Smith, Ralf Sommer, Mansi Srivastava, James Umen
- Selected abstracts chosen for presentations by members; faculty, postdocs and students encouraged to apply.

- Posters on display throughout the entire meeting

- Poster prizes for PhD students and postdocs

- Child Care reimbursement available!! Bring the whole family.

All details about registration, accommodation options, childcare services, and the conference program are available at the following website: <http://www.evodevopanam.org/meetings-events.html> Support the Society and Become a Member, and enjoy the benefits of being part of the fast-growing and intellectu-

ally invigorating EvoDevo community!! To learn more about PASEDB, visit the following website: <http://www.evodevopanam.org/> The Organizing Committee and the PanAm SEDB Executive Council look forward to welcoming you to Berkeley in August!

Ehab Abouheif Karen Sears Nipam Patel Chris Lowe  
cdspecht@berkeley.edu

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## UHuddersfield ProtistEvolution Apr15-17

BSPB 2015 Registration Open

The 2015 British Society For Protist Biology Spring Meeting will be held between 15-17th April 2015 at the University of Huddersfield. The conference will host two mini-symposia - Experimental Evolution in Protists and The Evolution of Multicellularity - as well as sessions for posters, student talks and contributed talks.

A limited number of student bursaries will be allocated to Society members who are presenting at the conference and will be offered on a first come-first served basis.

Reduced rate Early Bird registration will be open until the 28th March 2015. Full price registration will remain open after this date.

The following speakers will be presenting in the symposia: Experimental Evolution In Protists Will Ratcliff (Georgia Tech) - Plenary Mike Brockhurst (York) Duncan Cameron (Sheffield) Ville Friman (Imperial) Oliver Kaltz (Montpellier) Kai Lohbeck (Kiel) Chris Lowe (Exeter) Peter O'Toole (York)

Evolution of Multicellularity Iñaki Ruiz-Trillo (Barcelona) - Plenary Mark Cock (Roscoff) Frank Nitsche (Cologne) Daniel Richter (Roscoff) Pauline Schaap (Dundee)

BSPB Meeting Webpage: <http://www.protist.org.uk/meetings.html> Martin Carr BSPB Treasurer British Society for Protist Biology <http://www.protist.org.uk> Martin Carr <martcarr74@gmail.com>

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## ULisbon ReticulateEvolution Jul17

CFA: Thematic Session on Reticulate Evolution Before and After the Modern Synthesis: Historical and Epistemological Perspectives and Wider Applications Beyond Traditional Fields -Organized by Nathalie Gontier & Jan Sapp

\*\*\*DEADLINE APRIL 1st, 2015\*\*\*

University of Lisbon, 17th of July, 2015 Website <http://iss-symbiosis.org/Symposia> INVITED SPEAKERS Eric Bapteste, Vitor G. Faria & Élio Sucena, Ricardo Guerrero, Frank Kressing, and Laura Weyrich. Abstracts are now online at: <http://appeel.fc.ul.pt/sub/eve/dir/iss/iss.html> CALL FOR ABSTRACTS & POSTERS We welcome Senior and Junior Researchers to submit poster or regular talks (20 minutes). The full call can be read at <http://appeel.fc.ul.pt/sub/eve/dir/iss/iss.html> ABSTRACT SUBMISSION If you would like to participate in the session, then submit your talk or poster abstract before April 1st, 2015 at <http://iss-symbiosis.org/page-1805892> Be sure to select the specific thematic session: "Reticulate Evolution Before and After the Modern Synthesis"

### REGISTRATION

You can register for the specific symposium or the full conference, and please note that becoming an ISSmember reduces the registration fee. ISS will also provide a limited amount of travel awards to students. Registration procedures are detailed by the International Symbiosis Society at <http://iss-symbiosis.org/>. [appeelannouncements <appeelannouncements@fc.ul.pt>](mailto:appeelannouncements@fc.ul.pt)

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## UMichigan AnnArbor PopGenet Jul25-26

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Dear Colleagues,

The field of population genetics has a remarkable tradition of being a tight-knit and nurturing community. In order to better foster that sense of community for the

popgen groups in the Midwest, we thought it would be fun to organize a short scientific conference to which we could bring our labs and have meaningful introductions and interactions. After a successful first trial last year (Evidence on <https://midwestpopgen.wordpress.com/>), we are excited to run this meeting again.

Thus, we'd like to invite you to come and bring your group to the meeting of the MidWest Population Genetics group, which will be held on July 25-26th at the University of Michigan. The meeting will begin Saturday and continue to Sunday with a BBQ on Saturday evening.

The keynote speaker will be Goncalo Abecasis, chair of Biostatistics at the University of Michigan. Thirteen 25 minute talks will be selected from submitted abstracts. Students are especially encouraged to attend and present their work. There will be a small prize for best poster and best talk by a student or postdoctoral fellow.

Space is limited, so if you do plan to attend, please RSVP to [szoellne@umich.edu](mailto:szoellne@umich.edu) or sign up on <http://tinyurl.com/kv3vtx4> by June 1, and submit your abstracts by June 1 to [dconrad@genetics.wustl.edu](mailto:dconrad@genetics.wustl.edu) so we can finalize our program. There is no registration fee.

The tentative schedule follows below. We do hope that you can make it and help establish this as an important meeting for the population geneticists in our region!

All the best,

Don Conrad, WashU

John Novembre, Chicago

Bret Payseur, Wisconsin

Sebastian Zollner, Michigan

Draft Agenda:

Saturday

12:00-1:30pm Registration and light lunch

1:30-3:30 Four 25 minute talks

3:30-4:30 Posters

4:30-5:30 Keynote

7:30-11 BBQ

Sunday

8-9 Breakfast

9-10:30 Three 25 minute talks

10:30-10:45 Break

10:45-12:15 Three 25 minute talks

12:15-1:30pm Lunch

1:30-2:25pm Three 25 minute talks

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## UMichigan ECSS Microbiome Ecol Evol Mar28

Dear Colleagues,

We are pleased to announce this year's Early Career Scientist Symposium, to be held Saturday, March 28, 2015 in East Hall on the campus of the University of Michigan, Ann Arbor. The theme this year is "Ecosystems within organisms: ecology and evolutionary biology of the microbiome."

Our outstanding lineup of keynote speakers and emerging leaders will address topics such as the role of the microbiome in disease processes, micro-evolution, and development, meta-community theory in host-associated communities, multi-host multi-parasite systems, and eco-immunology. The research focus ranges from bacteria to metazoans and from fitness effects on host organisms or their microbiota to the downstream effects of microbiomes on ecosystems.

We are delighted to announce our keynote speakers: Seth Bordenstein, Associate Professor, Departments of Biological Sciences and Pathology, Microbiology, and Immunology, Vanderbilt University

Georgiana May, Professor, College of Biological Sciences, University of Minnesota.

The following series of talks and interaction time have been scheduled:

Seth Bordenstein (Vanderbilt U.): The microbiome and Darwin's mystery of mysteries

Katherine Amato (U. Colorado): Into the wild: exploring the influence of gut microbes on host ecology and behavior

Kevin Kohl (National U. San Luis): Friends for life: gut microbes allow herbivores to consume toxic plants

Andrea Jani (U. Hawaii): Microbial ecology of an infectious disease: Do symbiotic bacteria protect frogs from the fungal pathogen *Batrachochytrium dendrobatidis*?

Kelly Weinersmith (Rice U.): Parasite manipulation of host phenotype: mechanisms, behavior, ecology, and evolution

Lunch and poster session, East Hall, third floor terrace

Rachel Vannette (Stanford U.): Community assembly and function of the floral microbiome

Justine Garcia (Emory U.): Animals in a microbial world: partner fidelity and of horizontal bacterial symbioses in true bugs

Angela Poole (Cornell U.): Human salivary amylase gene copy number impacts the gut microbiome and its function

Georgiana May (U. Minnesota): Microbial interactions drive the evolution of virulence in pathogens

Dinner reception, Museum of Natural History, Hall of Evolution, second floor

Register to attend : <http://sites.lsa.umich.edu/ecss/>  
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.

Lunch will be provided at the poster session and a dinner reception will follow the symposium.

Looking forward to your participation,

2015 Early Career Scientists Symposium organizing committee

Tim James (chair) Chelsea Wood Kevin Theis Marian Schmidt Thomas Jenkinson

For further information, contact

Kimberly Fonville <kimafon@umich.edu> Kimberly Fonville <kimafon@umich.edu>

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## UMichigan SocSystematicBiol May20-22

\*Society of Systematic Biologists Stand-alone meeting 2015\*

Please join us for the upcoming meeting of the Society of Systematic Biologists, May 20-22, 2015, to be held at the University of Michigan. This meeting, joint with iEvoBio, features a series of software demos, workshops and panels designed to encourage to one-on-one interactions and in depth discussions. Participants are invited to give lightning talks. Grants-in-aid are available for attending the meeting, and housing will be available via dorm-rooms on the campus of the University of Michi-

gan. Details about the schedule, grants, and registration is available at <http://ssb2015standalone.weebly.com/> Note that attendance will be capped at 300 participants so register early.

The panel discussions include:

- - \*Species concepts are outmoded and hinder progress in evolutionary biology\* (Chris Simon and James Mallet)

- - \*Molecular dates are reliable and provide a robust foundation for interpreting the history of life\* (Charles Marshall and Blair Hedges)

- - \*More data or better models\* (David Hillis and Antonis Rokas)

- - \*Accurate inference with comparative methods? The field isn't paying enough attention to learning the limits of what we can know\* (Wayne Maddison and Cécile Ané)

The workshop topics include:

- - \*Computational Macroevolution: Analysis and Visualization of Complex Evolutionary Dynamics on Phylogenies (Dan Rabosky)\*

- - \*Publishing digital phylogenies: choosing content, formats, repositories and licenses that make trees useful for future work (Karen Cranston)\*

- - \*Comparative methods in R (Brian O'Meara)\*

- - \*Model-based Biogeographical Analyses: Principles and Practice\*\* (\*Jeet Sukumaran)

- - Species-tree estimation from SNPs to sequences (Laura Kubatko)

- - Interrogating transcriptomic data from processing to analysis (Stephen Smith)

- - \*Bayesian methods for estimating divergence times (Tracy Heath)\*

Note that these workshops are in addition to a Symposium and Software School that will be offered as a pre-meeting workshop (May 18-19) by Tandy Warnow. The symposium will cover new methods for multiple sequence alignments, genome-scale species tree estimation, phylogenetic network estimation, and metagenomic taxon identification. The software school will include hands-on tutorials in new methods, and taught by the developers of the software. No fee will be charged, and travel awards of up to \$500 per person are available. Please see <http://tandy.cs.illinois.edu/symposium-2015.html> for more information.

dewitt832@gmail.com

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## Vienna SMBE2015 Jul12-16 EarlyBird ClosingThisSunday

Hello evoldir community,

last chance for early bird registration: register by Sunday, March 1, to save up to 30% on the registration fee for SMBE 2015, held in one of the most beautiful cities at the spectacular Imperial Palace (Hofburg) in the heart of Vienna!

A few meeting highlights:

- All posters will be on display throughout the entire meeting.
- At least four poster sessions
- 27 symposia on cutting edge topics suggested by SMBE members and one Open Symposium for which 5 featured speakers will be selected through the Local Organising Committee (LOC).
- Plenary speakers: Doris Bachtrog (UC Berkeley), Joe Felsenstein (Univ. of Washington), Johanna Schmitt (UC Davis) and Diethard Tautz (MPI for Evolutionary Biology).
- Heavily subsidized child care
- many awards (<https://www.smbe.org/smbe/-AWARDS.aspx>): — Poster prize for postdocs and PhD students — Fitch prize — Young investigator travel awards — Junior and mid career research awards — Child Care Travel Awards
- affordable accommodation (starting from euro 19,-/night. Also many double rooms are available for euro 60,- /night incl. breakfast)

All details about registration, accommodation options and travel discounts are available at the conference website: [www.smbe2015.at](http://www.smbe2015.at) The Local Organising Com-

mittee is looking forward to welcome you to Vienna in July!

julia.hosp@gmail.com

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## Zurich EvolMed Jul30-Aug1

“Dear Colleagues,

Just as a gentle reminder: The abstract deadline for the ”Evolutionary Medicine Conference: Interdisciplinary Perspectives on Human Health and Disease“ (Juli 30-August 1 2015 in Zurich, Switzerland) is approaching now:

- Abstract Deadline: March 30, 2015 - Early registration Deadline: May 31, 2015

Find all relevant information (abstract submission, registration, accommodation, etc.) on our official conference webpage: <http://www.iem.uzh.ch/-evolmedconf2015.html> Please get in contact with us if you have questions: [evolmedconf@gmail.com](mailto:evolmedconf@gmail.com)

Thanks for sharing the event and the call for abstracts among your colleagues!

We would be happy to welcome you in Zurich soon...

Best wishes

Frank Rühli, Nicole Bender and Kaspar Staub (Conference Organisers)”

Dr. Kaspar Staub Institute Manager, Senior Research Assistant Morphology/Imaging Group Institute of Evolutionary Medicine (IEM) University of Zurich Winterthurerstrasse 190 CH-8057 Zurich, Switzerland Office Y42 G88a Phone +41 44 635 05 13, Mobile +41 79 473 83 55, Fax: +41446355702 [kaspar.staub@iem.uzh.ch](mailto:kaspar.staub@iem.uzh.ch) <http://www.iem.uzh.ch/people/kasparstaub.html> Kaspar Staub <[kaspar.staub@iem.uzh.ch](mailto:kaspar.staub@iem.uzh.ch)>

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## GradStudentPositions

Austria EvolutionGenomeSize .....	23	QUT Brisbane Australia MammalEvolution .....	35
Berlin ConservationFisheries .....	24	Rennes UWuerzburg FishEvolutionSex .....	35
BielefeldU MarinePopulationGenetics .....	24	TulaneU EvolutionaryBiol .....	36
BournemouthU HumanComparativePhylogeography	25	UAberdeen InsectNicheEvolution .....	36
CurtinU Australia MarinePopulationGenetics .....	26	UAdelaide GenomicEvolutionAncientDNA .....	37
CzechRepublic MontaneSpeciation .....	27	UAmsterdam MiteGenomics .....	38
Europe 15 WineEvolution .....	28	UBern PlantHerbivoreInteractions .....	39
Groningen 3PhD PDF OriginSpecies .....	28	UBristol MolecularConvergence .....	39
IMPRS UKiel EvolutionaryBiology .....	28	UBritishColumbia ConservGenetics .....	40
IZW Berlin 2 EvolutionaryDiseaseDynamics .....	29	UExeter CellEvolutionPhylogenomics .....	41
Kaust SaudiArabia UVBRadiation .....	30	UFlorida InsectEvolution .....	41
KLIVV Vienna FishBreedingSystems .....	31	UHuddersfield 5 EvolutionaryGenetics .....	41
LaurentianU 2 WildlifeEvolution .....	32	UMelbourne Insecticide Adaptation .....	42
LeibnizInst Berlin PleistoceneImmunoDiversity ...	32	UNewSouthWales LizardEvolution .....	43
LundU Sweden SocialEvolution .....	32	UQueensland SexBiasedGeneExpression .....	44
MichiganTechU Watermilfoil PopulationGenetics ..	33	UStAndrews Adaptation .....	44
NewcastleU 2 PlantAdaptation .....	34	UTulsa ComparativeTranscriptomics .....	45
NewcastleU PlantAdaptation .....	34	UZurich OrchidSpeciation .....	46
Portugal Biodiversity .....	34		

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### Austria EvolutionGenomeSize

PhD position: Evolutionary ecology of genome size

Despite an explosive increase of genomic information during the last decade the ultimate causes of genome size variation in eukaryotes are still controversial. At the core of this controversy is the puzzling genome size variation across eukaryotic taxa, which spans approximately five orders of magnitude. The goal of this project is to investigate the mechanisms and significance of genome size variation at short evolutionary timescales, such as variation among closely related species, among populations, and among individuals within a population. Our model system is the facultative asexual rotifer *Brachionus plicatilis*, a cryptic species complex consisting of at least 14 closely related species. Within this complex we focus on a lineage that has undergone a 1.9-3.5 fold increase in genome size relative to its sister-species (e.g., <http://www.biomedcentral.com/1471-2148/11/90/abstract>). Within this lineage we also study a population that exhibits a remarkable 25% continuous variation in genome size. The project aims are: (1) to elucidate the mechanisms of genome size variation by comparative genome sequencing (2) to experimentally determine how variation in genome size is maintained

within populations and inherited during sexual reproduction, and (3) to test assumptions and predictions of general hypotheses on genome size evolution using intra-population genome size variation, e.g., that clones with small genome size are favored by selection for maximum population growth rates under nutrient limitation, that clones with large genome size accumulate deleterious mutations faster than clones with small genome size, or that genome size variation at the population level significantly co-varies with cell size, body size and egg development time.

The PhD candidate will be involved in all three project aims, in particular aims (1) and (3). On the methodological level, the PhD project will include experimental work with rotifer cultures, genome size measurements using flow cytometry, basic molecular genetic techniques (e.g., PCR), genome sequencing and bioinformatics. The latter will be done in close collaboration with Dr. David Mark Welch at the Josephine Bay Paul Center (MBL, Woods Hole, USA). This will involve a stay at the MBL for a training in genomic analysis of approximately two weeks duration. The main work will be done at the research institute for limnology in Mondsee (<http://www.uibk.ac.at/limno/>), which is part of the University of Innsbruck. The PhD candidate will be expected to enroll at University of Innsbruck. The project is funded by the Austrian Science Funds (FWF) and salary is according to their regulations (<https://www.fwf.ac.at/>

[en/research-funding/personnel-costs/](#)).

The Institute for Limnology is located in Mondsee, a small town in the Salzkammergut lake district, which lies approximately 30 km east of the City of Salzburg and 200 km east of the City of Innsbruck. The Salzkammergut area is among the most popular regions in Austria. It offers a high quality of life and exceptional opportunities for all kinds of outdoor activities. The Institute has a staff complement of approximately 30, including 8 research scientists, who work on various areas in evolutionary ecology of aquatic organisms.

Applicants should have a M.Sc. degree and a good background in evolutionary biology. Previous experience in experimental work is also advantageous. To apply for this position, please provide: (i) a letter of motivation (in English) including a statement of your research interests, relevant skills and experience; (ii) a short CV including publications (if applicable); (iii) the names of at least two independent referees. All materials should be emailed as a single PDF to [claus-peter.stelzer@uibk.ac.at](mailto:claus-peter.stelzer@uibk.ac.at) with the subject heading EVOL\_GS\_PHD±. Application deadline is the 04 Apr 2015. The University of Innsbruck is an equal opportunity employer and particularly encourages applications from women.

For more details, please contact: Dr. Claus-Peter Stelzer ([claus-peter.stelzer@uibk.ac.at](mailto:claus-peter.stelzer@uibk.ac.at))

“Ri©¬, Simone”<sub>i</sub>[Simone.Riss@uibk.ac.at](mailto:Simone.Riss@uibk.ac.at);

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## Berlin Conservation Fisheries

Graduate position: Berlin.ConservationFisheries

A three-year Early Stage Researcher (ESR), preferably a doctoral (PhD) student, in the field of “Economic and Social Value of Conservation of Endangered Migratory Fishes” is sought within a newly funded EU Marie Skłodowska-Curie Initial Training Network (ITN) entitled IMPRESS. IMPRESS (Improved production strategies for endangered freshwater species, [www.impress-itn.eu](http://www.impress-itn.eu)) is coordinated by the Norwegian University of Life Sciences (NBUM) in Oslo, Norway, and involves 15 ESRs hosted by 9 different organizations in Europe. The candidate sought here will join the Fisheries Research group of Prof. Dr. Robert Arlinghaus in the Department of Biology and Ecology of Fishes at the Leibniz-Institute of Freshwater Ecology and Inland Fisheries in Berlin, Germany and shall be recruited by June, 1, 2015. More details on the position and how to apply can be

found here: <http://www.igb-berlin.de/stellenangebote-details/items/515.html> Robert Arlinghaus

Prof. Dr. Robert Arlinghaus Leibniz-Institute of Freshwater Ecology and Inland Fisheries Department of Biology and Ecology of Fishes Müggelseedamm 310 12587 Berlin

and

Laboratory for Integrative Fisheries Management Faculty of Life Sciences Albrecht-Daniel-Thaer-Institute of Agriculture and Horticulture Humboldt-Universität zu Berlin

For running projects: [www.besatz-fisch.de](http://www.besatz-fisch.de) [www.btypes.igb-berlin.de](http://www.btypes.igb-berlin.de) [www.bioenv.gu.se/english/-salmoinvade](http://www.bioenv.gu.se/english/-salmoinvade) For further information and publication download: [www.agrar.hu-berlin.de/-fakultaet/departments/dntw/jp\\_bfm/publ.html](http://www.agrar.hu-berlin.de/-fakultaet/departments/dntw/jp_bfm/publ.html) [www.besatz-fisch.de](http://www.besatz-fisch.de) [www.researchgate.net/profile/-Robert\\_Arlinghaus?ev=hdr\\_xprf](http://www.researchgate.net/profile/-Robert_Arlinghaus?ev=hdr_xprf) [www.besatz-fisch.de/-adaptfish](http://www.besatz-fisch.de/-adaptfish) News on twitter: <https://twitter.com/-RARlinghausFish> Kate Laskowski <[laskowski@igb-berlin.de](mailto:laskowski@igb-berlin.de)>

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## BielefeldU Marine Population Genetics

Early stage fellowship: Marine population genetics

Supervisors: Dr. Joe Hoffman (Bielefeld University, Germany), Dr Liz Harper (Cambridge University, UK) and Dr Melody Clark (British Antarctic Survey, UK)

Funding is available for an early stage fellowship as part of a Marie Curie Initial Training Network. The fellow will be based in the Hoffman lab at Bielefeld University ([www.thehoffmanlab.com](http://www.thehoffmanlab.com)) and will have the opportunity to register for a PhD. The fellowship will provide training in cutting-edge population genomic approaches and offers excellent opportunities for networking plus individually tailored training and industrial placements. The fellow should therefore be in a strong position afterwards to pursue a career in either academia or industry.

There is mounting concern over the acidification of the World's 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. As a member of the network, the fellow will be expected to work cooperatively within the network, participate in European training events and spend up to 30% of their training with another network partner. Full details of the network can be found at [www.cache-ITN.eu](http://www.cache-ITN.eu). The fellow will use population genomic approaches including RAD sequencing and transcriptomics 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 fellow to explore their own related interests within the framework of this project and in collaboration with the other partners.

We seek a bright and highly motivated candidate who holds an M.Sc. or equivalent in a relevant topic (e.g. marine biology, population or evolutionary genetics, bioinformatics). The ideal candidate will have strong quantitative skills and ideally some experience of programming, although training can be provided. Experience of RAD sequencing would also be advantageous but is not necessary. 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 fellow will join the Hoffman lab, a young and dynamic group comprising five PhD students and a post-doc. 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 post-

docs 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 fellowship offers a generous stipend of at least £43700 per month, including a mobility allowance, for a period of 2.5 years. Funding is also available for the fellow to attend annual meetings and training workshops in Portugal and elsewhere. The fellow will be encouraged to register for a PhD at Bielefeld University.

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## BournemouthU HumanComparativePhylogeography

PhD position at Bournemouth University:

Project Title

Human Biogeography: Comparative Phylogeography of Modern Humans and Other Organisms

Project Summary

**Aims and Rationale** - We will compare the published phylogeographies (genetic biogeographies) of modern humans with those of other vertebrates to elucidate the patterns of population movement in the past. The science of phylogeography provides an understanding of the population dynamics of species in relation to landscape, climate and human related processes over the last 50 thousand years. Species respond to these processes individually, for example using different refugia at different times. The location of these refugia is also determined by the geography and topography of the landscape. Phylogeography can be used to identify the location of these species refugia and/or the place of origin of domestic / commensal species.

**Methods** - Phylogeographic studies have been performed

on organisms as varied as red deer, trout, snails, oak trees, ferns and bacterial and viral pathogens like Black Death and Rabies. Studies have also been done on domestic (sheep, cattle, wheat) and commensal (house mouse, black rat) plants and animals. The data from most of these studies are deposited on GenBank (a freely accessible online database). The project will analyse such data to look at the various patterns seen in each species which can then be grouped by similarity according to geographical and genetic diversity indices. These will include the likely divergence dates of the diversity as well as the topology of the species' phylogenetic tree or network diagrams. The data will also be analysed using GIS and associated geospatial statistics to help identify the place of origin and source of spread of populations.

**Hypotheses:** Human phylogeographic patterns in Europe that relate to Upper Palaeolithic distribution change will generally have a North/South distribution similar to wild species coming out of ice age climate refugia. Those patterns with an East/West distribution will be similar to taxa whose climate refugia was in the East (or South East) or to that of domestic/commensal plants and animals whose origins lay in the South East, representing Neolithic or later distribution change.

**Clearly defined outputs -** The outputs would include a paper submitted to a high impact journal (Nature, Science, PNAS) summarising the general results of the project. A further three papers are envisaged in subject specific journals like Molecular Ecology, Journal of Human Evolution and the Journal of Biogeography. The results of the work will also be presented at international meetings such as that of the Society of Molecular Biology and Evolution, the European Society of Human Evolution etc.

#### Academic Impact

Stewart's paper in Science which looks at Late Pleistocene Humans outside of Africa in relation to the biogeographical patterns of other organisms suggests that there would be an appetite amongst the people in the human evolution community for such an analysis. The research will have an impact on biological anthropology (human evolution), biogeography and molecular ecology thanks to the production of a minimum of 4 publications as well as the participation at international conferences (see above).

The evolution and population genetics (phylogeography) of humans receives a disproportionate amount of attention. Other organisms, although they do not receive the same depth of attention as humans represent the breadth of possible patterns and corresponding processes that can exist in organisms over these time scales. Comparing the genetic patterns in humans with those

in other organisms will help identify similarities and differences between them. The ecological and general biological characteristics of similar and differing species' patterns will help reduce the possible explanations for those patterns. For example humans are widespread geographically similar to wolves, ravens and pike but their phylogeographic patterns are different which may be driven by different limitations on their dispersals or the length of time since dispersal.

#### Societal Impact

The evolution of humans receives a lot of media coverage and Stewart is regularly interviewed by the media on this topic, both relating to his own research and that of other scientists (e.g. New Scientist, BBC World Service). The response of organisms to climate change is also of great interest to the public and receives a corresponding amount of media attention in light of current climatic changes and species' range shifts. The proposed project will undoubtedly have a significant impact due to the public interest it generates.

The understanding of population dynamics in species is important to future conservation of biotas, so the proposed project will have an important contribution to make to conservation planning. Stewart was involved in a Natural England consultancy project looking at the identification of

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## CurtinU Australia MarinePopulationGenetics

'Population Connectivity of Reef Fish in Tropical north-western Australia'

Application Closing Date: until filled

PhD Project with Curtin University, Perth Australia

This project will employ state of the art genotype-by-sequencing methodologies to generate a large volume of single nucleotide polymorphism (SNP) and microsatellite DNA genetic data to provide the first comprehensive investigation of ecological connectivity in the Kimberley marine environment in NW Australia. The research

outcomes will inform the management of fish and other exploited resources and also the design of marine protected areas and off-reserve assets in this remarkable yet understudied region. We anticipate that the approach used in this project will serve as a template for investigating ecological connectivity in other regions of Western Australia.

The project is a partnership between Curtin University, the Western Australian Marine Science Institute (WAMSI) and the Department of Fisheries, WA. We are seeking an Australian or International postgraduate student to develop and deploy contemporary and next generation genomic markers for various fish species along the tropical coast of north-western Australia with the remote and environmentally extreme Kimberley region comprising the main focal area.

One of the major aims of the PhD research will be to infer the routine distances of dispersal and patterns of connectivity among populations of key fish species along the NWA coast (e.g. stripey snapper, blue tuskfish and the range restricted Miller's damselfish). Through the genetic analyses of key taxa with contrasting dispersive life histories the techniques utilised in this project will provide species-specific estimates of realised connectivity at reef-scale (hundreds of metres), inter-reef scale (kilometres-tens of kilometres) and inter-region scale (tens-hundreds of kilometres).

Eligibility criteria: Students must have a First Class Honours or equivalent to be eligible for an Australian Postgraduate Award (APA), or if an international student have 1-2 publications in high quality, peer-reviewed journals and have lead or co-ordinated a significant research project to be eligible for a Curtin International Postgraduate Scholarship (CIPRS). Interested candidates should contact Dr Jennifer McIlwain (jennifer.mcilwain@curtin.edu.au) for further information and send a cover letter outlining their research interest and experience along with their CV.

Dr Jennifer McIlwain Ph.D (Marine Ecology) Head of Department Department of Environment and Agriculture School of Science Curtin University Tel | +61 8 9266 9041

Email | jennifer.mcilwain@curtin.edu.au Web | <http://curtin.edu.au> jennifer.mcilwain@curtin.edu.au

## CzechRepublic MontaneSpeciation

\*PhD: BCCeskeBudejovice.MontaneSpeciation\*

We are seeking a highly motivated postgraduate student to join our international team studying speciation in plants and insects along tropical altitudinal gradients. We are based at the Laboratory for Tropical Ecology at the Institute of Entomology, Biology Centre Academy of Sciences, Ceske Budejovice, Czech Republic,

The successful applicant will have strong background in:

Entomology

Botany

Bioinformatics

Molecular ecology

Population genetics

And/or biostatistics

He/she will be supervised by Simon Segar and expected to develop a research programme on speciation in \*Ficus\*, their pollinating wasps and symbiotic microbes of the wasps along a continuously forested altitudinal gradient in Papua New Guinea (PNG). The project will involve field work in PNG and the use of next generation sequencing to study the population genetics of plant/insect/microbe networks. The successful candidate will be expected to work closely with our collaborators at the University of Minnesota (USA) and the Hawkesbury Institute for the Environment at the University of Western Sydney (Australia).

The position is fully funded (tuition, research and living expenses) for EU applicants only (but candidates from all countries are eligible). The duration of the position is four years and a completed MSc degree is required as is the equivalent of a 1st or 2.1 undergraduate degree in biology, ecology or a related field. The successful candidate will have to conduct field work in a tropical forest in often challenging conditions. They will be able to work independently and have experience with the collection and analysis of population genetic data.

For further details of the project please and group see:

<https://www.dropbox.com/s/ot87ffj4keilszs/PhD%20Project%20Description.docx?dl=0> <http://www.entu.cas.cz/png/cv-novotny-vojtech-lab.html>

To apply please send a CV, contact details for three references, and cover letter stating qualifications, previous work and motivation to Simon Segar (simon.t.segar@gmail.com). The deadline for applications is April 20th 2015, with a preferred start date of June 1st.

Simon Segar <simon.t.segar@gmail.com>

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### Europe 15 WineEvolution

Applications are now invited for 15 PhD positions ('Early Stage Researchers') to be funded by the Marie-Sklodowska-Curie Innovative Training Network 'MICROWINE-Microbial Metagenomics and the Modern Wine Industry', a multidisciplinary study on Viticulture and Wine Microbiology within the Horizon2020 programme of the European Union. Each PhD position is fully funded for 3 years. The positions are based at 13 institutions, in 8 countries, and cover a wide range of disciplines including microbial metagenomics, wine genetics, bioinformatics, geology, chemistry and mathematical modeling. ESR's must commence no later than 1st September 2015. For full details on the network, sub-projects, host institutions, eligibility requirements, and how to apply please go to the project website at <http://www.microwine.eu/recruitment> Please note that applications are welcomed from any qualified applicants, regardless of gender, ethnicity or country of origin, but will only be considered if eligibility requirements are met and the application guidelines are strictly adhered to. For further information please contact the project administrator, Lea Ellegaard-Jensen at: [info@microwine.eu](mailto:info@microwine.eu)

Tom Gilbert Professor of Palaeogenomics Natural History Museum of Denmark

[tgilbert@snm.ku.dk](mailto:tgilbert@snm.ku.dk)

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### Groningen 3PhD PDF OriginSpecies

Three PhD student or postdoc position are available at the Groningen Institute for Evolutionary Life Sciences (formerly the Centre for Ecological and Evolutionary Studies), at the University of Groningen, The Netherlands. The positions are part of the VICI project 'On

the origin of species assemblages' awarded to prof. Rampal S. Etienne ([r.s.etienne@rug.nl](mailto:r.s.etienne@rug.nl)). The aim of this program is twofold: 1. developing a fully stochastic, dynamical, eco-evolutionary and data-friendly theory of community assembly, and 2. testing and informing this theory with model-oriented evolutionary experiments and field studies of both macro-organisms and micro-organisms. The details of the positions can be found here:

PhD position Theoretical eco-evolutionary assembly of ecological communities < <http://www.rug.nl/about-us/work-with-us/job-opportunities/overview?details=00347-02S0004E9P&cat=phd> >

Postdoc position Theoretical eco-evolutionary assembly of ecological communities < <http://www.rug.nl/about-us/work-with-us/job-opportunities/overview?details=00347-02S0004EAP&cat=wp> >

PhD or Postdoc position Simultaneous Estimation and Selection of Species Diversification Models < <http://www.tangram-tis.nl/10378/Vacatures/00347-02S0004EMP/Vacature-PhD-or-Postdoc-Simultaneous-Estimation-and-Selection-of-Species-Diversification?category=-Groepspecifiek%5FRUG%5FCategorie%2CGroepspecifiek%5FRUG%5F> >

"Rampal S. Etienne" <[r.s.etienne@rug.nl](mailto:r.s.etienne@rug.nl)>

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### IMPRS UKiel EvolutionaryBiology

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

The graduate school is dedicated to highest level of research and training in all areas of contemporary Evolutionary Biology. It is a joint initiative of the Max Planck Institute for Evolutionary Biology, the University of Kiel and the Helmholtz Center for Ocean Research Kiel (GEOMAR). The school offers an internationally competitive research environment with state of art facilities. The participating groups are working on a broad variety of scientific topics including molecular, behavioral, theoretical and organismal approaches.

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

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

The deadline for applications is April 19, 2015. The selection week will be held from June 22 - 26 and the program itself starts on September 21, 2015.

Contact: Dr. Kerstin Mehnert, August-Thienemann-Str. 2, 24306 Plön, Germany email: [imprs@evolbio.mpg.de](mailto:imprs@evolbio.mpg.de) phone: +49(0)4522 763 233

The coordinator Kerstin Mehnert

The steering committee Diethard Tautz, Hinrich Schulenburg, Manfred Milinski and Thorsten Reusch

Natascha

Natascha Hasenkamp <[hasenkamp@evolbio.mpg.de](mailto:hasenkamp@evolbio.mpg.de)>

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## IZW Berlin 2 EvolutionaryDiseaseDynamics

Advertisement of vacancy

The Leibniz Institute for Zoo and Wildlife Research (IZW) in the Forschungsverbund Berlin e. V. ([www.izw-berlin.de](http://www.izw-berlin.de)) together with the Research Institute of Wildlife Ecology (FIWI) at the University of Veterinary Medicine, Vienna ([www.vetmeduni.ac.at/fiwi](http://www.vetmeduni.ac.at/fiwi)), the Weierstraß Institute for Applied Analysis and Stochastics (WIAS, [www.wias-berlin.de](http://www.wias-berlin.de)), the Institut for Virology of the Freie Universität Berlin (FU, [www.vetmed.fu-berlin.de](http://www.vetmed.fu-berlin.de)) and the Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB, [www.igb-berlin.de](http://www.igb-berlin.de)) have formed a consortium to implement the AQUAVIR project funded by the Leibniz Association.

Water is required for life. We have accumulated evidence suggesting it may be an overlooked viral vector. In climatic zones with seasonally limited precipitation such as east Africa and central Asia, animals congregate at high densities at scarce water sources. We hypothesize that viruses shed in water in this ecological setting would gain a fitness advantage if they evolved traits permitting the retention of their infectivity in water and

a reduction in host specificity. The AQUAVIR project will determine whether water is a significant viral vector and how viruses behave mechanistically in such settings, and develop mathematical models to understand the epidemiology and evolution of this phenomenon. We therefore seek to fill the following positions:

- 2 doctoral positions in evolutionary disease ecology - 1 postdoc in molecular virology - 1 postdoc in mathematical modeling in epidemiology

Specifically:

1 doctoral student in evolutionary disease ecology: African waterholes (05/15) - IZW

1 doctoral student in evolutionary disease ecology: Asian waterholes (06/15)

- IZW/FIWI Specific tasks: Determine the distribution, persistence and species usage of water sources; determine the effect of water source characteristics on virus presence; non-invasively determine if physiological stress is correlated with virus excretion in potential host species; analyse environmental DNA of water samples to compare genetic diversity of potential viral host sequence diversity obtained directly from animals compared to their drinking sources.

Requirements: Veterinary degree or completed master's / diploma degree in biological sciences; clean driver's licence; competence in statistical methods; ability to work independently in challenging environments and to interact with scientists from a wide variety of fields; strong interest in wildlife, conservation and evolutionary biology; a background in ecology, previous experience with wildlife, experience in field research and off-road driving experience would be highly advantageous.

Position 05/15 will be supervised by Prof Alex Greenwood (IZW Dept of Wildlife Diseases) and Dr Marion L East (IZW Dept of Evolutionary Ecology), position 06/15 by Prof. Alex Greenwood and Prof. Christian Walzer (FIWI).

1 Postdoc in molecular virology (07/15) - IZW/ FU

Specific tasks: Serological analysis of mammalian samples using species-specific viral peptide-based ELISA; next generation sequence characterization of equine herpesviruses from water and animal samples; evolutionary analysis of viral sequences obtained to determine phylogenetic affiliations and estimate evolutionary dynamics of viral populations, including evaluation for positive selection on sequences relevant to virulence or stability in water and/or novel recombination events that might influence viral phenotype; viral mutagenesis to determine whether positively selected sites or recombination events identified in field samples alter viral phenotype, e.g. vir-

ulence or stability; coordinate with two field doctoral students and a postdoc mathematical modeller.

Requirements: The successful candidate will have a completed doctoral degree, extensive experience in molecular virology, a strong interest in wildlife, conservation and evolutionary biology and interact with scientists from a wide variety of fields. Previous experience in evolutionary biology and next generation sequencing analysis will be considered a major advantage.

The postdoc will be supervised by Prof. Alex Greenwood (IZW) and Prof. Nikolaus Osterrieder (FU).

1 Postdoc in mathematical modeling in epidemiology (08/15) - IZW/WIAS

Specific tasks: Develop and analyze epidemiological models incorporating water as a viral vector, temporal changes of water sources and interactions between different species; simulate individual-based models in the ecological setting of the project.

Requirements: The successful candidate should have a completed doctoral degree and be experienced in epidemiological modeling using probabilistic concepts. Candidates with a strong background in mathematical modeling

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## Kaust SaudiArabia UVBRadiation

Ph.D. and M.Sc. Fellowships Offered at KAUST Red Sea Research Center

Ph.D. fellowships offered

Impacts of UVB Radiation on Red Sea biota

Ph.D. Thesis to be co-supervised by Profs. Susana Agusti, Carlos M. Duarte and Christian R. Voolstra

The Red Sea is an ultraoligotrophic environment characterized by highly transparent waters to damaging UVB radiation along with very high temperatures. Recent evidence suggests that Red Sea biota is highly vulnerable to UVB radiation, which is exacerbated by high temperature. However, UVB impacts has yet been assessed only for zooplankton and picoautotrophs. This project will characterize the impacts of UVB radiation on key

Red Sea biota, encompassing keystone species in benthic (such as seagrass and corals) and pelagic (such as phyto and zooplankton and meroplankton) habitats. It will do so through field observations and field and laboratory experiments assessing impacts of UV radiation at multiple levels: molecular, cellular, physiological, organismal, holobiont and population levels. The project will also assess complex interactions mediated by UV for selected model species, including UV-driven constraints on organismal life history mediated by ontogenetic variability in their vulnerability to UV radiation as well as possible benefits of UV radiation on Red Sea biota driven by antagonistic effects resulting from UV impacts on pathogens, parasites and predators.

Key qualifications (in addition to general KAUST requirements, see below): Prior research experience ideally including publications in international journals, SCUBA diving, solid underpinnings in marine and molecular ecology.

Impacts of dust deposition on Red Sea microbial communities Ph.D. Thesis to be co-supervised by Profs. Carlos M. Duarte and Dr. Jesus M. Arrieta

The Red Sea is an ultraoligotrophic environment characterized by blooms of the nitrogen-fixing cyanobacteria *Trichodesmium* sp.. These blooms appear to be associated to events of dust deposition. However, dust deposition, a major feature of the Red Sea, is expected to have profound consequences on Red Sea biota, as it also delivers nutrients, organic carbon, pollutants and air-borne microbes. This project will characterize the inputs of elements and microorganisms associated with dust deposition and will assess their impacts on Red Sea microbial communities and the biogeochemical dynamics of this ecosystem.

Key qualifications (in addition to general KAUST requirements, see below): Prior research experience ideally including publications in international journals, solid underpinnings in marine biogeochemistry and molecular ecology.

Seagrass ecology and ecosystem functions in the Red Sea Ph.D. Thesis supervised by Prof. Carlos M. Duarte

Seagrass are angiosperms adapted to life in the sea, forming productive and valuable ecosystems across the world. The Red Sea contains, in particular, dense multispecific seagrass meadows. However, there has been remarkably little research effort focused on Red Sea seagrass, largely restricted to the species composition and some aspects such as their value as sources of natural products and photosynthetic rates. Yet, seagrass represent arguably the most abundant higher plant vegetation in the Kingdom of Saudi Arabia. This Ph.D. project aims at filling

the current gap in the ecology of seagrass meadows in the Red Sea while, at the same time, contributing to further our understanding of seagrass ecology in general. In particular, the goals of this research project include: (a) assessing patterns in the distribution and community structure of seagrass meadows in the Saudi coast of the Red Sea; (b) quantifying primary production of Red Sea seagrass meadows and the flux of carbon supporting their role as sources of carbon to the food web, carbon (as well as metal, pollutant, nitrogen and phosphorus) sinks as well as their roles as habitat. In addition we will the effect of seagrass meadows on the carbonate system as well as the rates of carbonate production in Red Sea seagrass meadows as well as their capacity to raise the seafloor, thereby sheltering coastlines from the impacts associated with sea level rise.

Key qualifications (in addition to general KAUST requirements, see below): Prior research experience ideally including publications in international journals, SCUBA diving, solid underpinnings in marine and molecular ecology.

Connectivity and gene flow across Seagrass and Mangrove populations in the Red Sea Ph.D. Thesis co-supervised by Prof. Carlos M. Duarte and Prof. Ester Serrao (Univ. of Algarve, Portugal)

Seagrass and mangroves angiosperms form dense stands along the Red Sea. However, these stands are scattered and often separated by considerable distances, so the extent of gene flow along these system may be restricted and is not know. Moreover, the Red Sea coast spans, along its more than 1,000 Km, a broad range of climatic and productivity regimes. Limited

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**KLIVV Vienna**  
**FishBreedingSystems**

Within the project “Ecological constraints of fish breeding systems” funded by the Austrian Science Fund (FWF) a three-year PhD student position is available at the Konrad Lorenz Institute of Ethology (KLIVV) at the University of Veterinary Medicine Vienna. The PhD candidate will work on the hormonal basis of parental

care behavior, induced polygyny or egg cannibalism. The definite subject of the PhD project will depend on the candidate’s qualifications and interests.

We are looking for a highly motivated, outstanding student with a background in behavioral ecology: experimental design, hands-on work with live animals and good statistical skills (if possible including R) are a prerequisite. Experience in hormone analyses is a plus. Excellent written and oral communication skills in English and the ability to work in a team are a must, a MSc degree (or equivalent) in a related discipline (e.g., zoology, evolution, ecology, biology) is expected.

The PhD candidate will be mainly supervised by Dr. Franziska C. Schädelin and Priv.-Doz. Dr. Richard H. Wagner, but the student is also expected to interact with Prof. Sigal Balshine and her group in Hamilton/Canada, including short visits at the collaborating laboratory abroad.

As a part of the Department of Integrative Biology and Evolution of the University of Veterinary Medicine Vienna, the KLIVV offers an international and stimulating research environment. The successful PhD candidate will join the University’s PhD-program. Vienna is a highly attractive city in beautiful surroundings, with a multicultural population and many educational and recreational opportunities.

The gross salary is at around 28.000 Euro per year before tax (“Bruttogehalt”), including social and health security according to the personal costs provided by the Austrian Science Fund.

Please send your application including motivation for the position, CV, and two reference letters including the contact information of referees to [franziska.schaedelin@vetmeduni.ac.at](mailto:franziska.schaedelin@vetmeduni.ac.at). The PhD project will start in autumn 2015. Applications received until 20<sup>th</sup> April will be given full consideration.

See [www.vetmeduni.ac.at/klivv](http://www.vetmeduni.ac.at/klivv) and <http://www.vetmeduni.ac.at/de/klivv/ueber-uns/-unser-team/lemmel-schaedelin-franziska/>; for more detailed information. Please contact [franziska.schaedelin@vetmeduni.ac.at](mailto:franziska.schaedelin@vetmeduni.ac.at) for any further information and questions.

Franziska Lemmel-Schädelin  
<[franziska.schaedelin@lemmel.at](mailto:franziska.schaedelin@lemmel.at)>

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## LaurentianU 2 WildlifeEvolution

- 1) Ph.D. Position in Boreal Ecology-Moose Ecology, Monitoring & Modelling- Biology, Laurentian University, Sudbury, ON, CANADA-requires solid statistical skills, Contact-Dr. Frank F. Mallory, (fmallory@laurentian.ca).  
 2) M.Sc. Position-Owl Ecology, Biology, Laurentian University, Sudbury, ON, CANADA-requires solid statistical skills, Contact-Dr. Frank F. Mallory, (fmallory@laurentian.ca).

Frank Mallory <fmallory@laurentian.ca>

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## LeibnizInst Berlin PleistoceneImmunoDiversity

Job advertisement:

The Leibniz Institute for Zoo and Wildlife Research (IZW) in Berlin is Germany's premier wildlife research institute, one of eight research institutes in the Forschungsverbund Berlin e. V., a member of the Leibniz Association and jointly funded by the German federal and state governments. The IZW focuses on the life histories and mechanisms of evolutionary adaptations of mammals, their limits and their conservation in natural and anthropogenically influenced environments. The institute operates within the fields of wildlife health and diseases, reproductive biology and medicine, and evolutionary ecology and genetics.

The Department of Wildlife Diseases offers (beginning June 1, 2015) a PhD-Position on "Measuring immunogenetic diversity during the Pleistocene"

This project will utilize novel next generation sequencing approaches to characterize the evolution of immunogenetic loci over a ca. 50,000 year time span in species with contrasting demographic histories (extinct woolly mammoths and muskoxen). We expect to determine the rate of evolution, persistence and replacement of Toll-Like Receptor (TLR) and Major Histocompatibility locus (MHC) alleles for both species which will provide a better understanding of the evolutionary dynamics of the loci that cannot be obtained from examination of modern DNA.

Specific tasks include - Development of hybridization capture assays coupled with next generation sequencing for the MHC and TLRs - Bioinformatic and evolutionary genetic analysis of generated data - Logistical coordination of work between Canada, Denmark and Germany Requirements - Diploma or Master of Science in Biology or related fields; - Strong background in evolutionary biology and phylogenetics; - Preference will be given to candidates with ancient DNA or forensic DNA experience; - Preference will also be given to candidates with next generation sequencing experience; - A background in statistics and bioinformatics would be advantageous; - Organizational skills and ability to work in a team; - Part of the project will take place in Canada. Thus, proficiency in English (speaking and writing) is required

The position is initially limited to two years, June 1, 2015, with the possibility for extension to a maximum of three years. The reimbursement occurs according to TVöD (65%). The IZW is an equal opportunity employer. Applications from women are strongly encouraged. Preference will be given to disabled applicants with the same qualifications. For further information please contact Prof. Alex Greenwood (e-mail greenwood@izw-berlin.de).

Applicants should submit a letter explaining their interests in and particular skills for this position, a CV, copies of relevant degrees and contact details of two people who can provide a reference before April 7th, 2015 via the IZW's online-job-market (button "Apply online").

Von: personal Gesendet: Mittwoch, 4. März 2015 20:59  
 An: Vollberg, Stephanie Betreff: evolDir

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

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## LundU Sweden SocialEvolution

The evolution of sex and society

It is now widely established that selection on sexual behaviour has profound effects on the evolutionary transitions to cooperative societies in which individuals forego the pursuit of selfish reproduction to help others. For example, cooperative breeding and eusociality have been shown to be more likely to evolve when groups are founded by monogamous females. However, it is currently unclear how the evolution of cooperation is influenced by selection on sexual behaviour other than female promiscuity. This PhD position will explore the



relationship between sexually selected behaviour and cooperation using a combination of phylogenetic comparative analyses, field tests, experimental manipulations of social groups, and quantitative genetic and genomic analyses. The comparative component of this project will mainly be focused on birds, but with the potential to examine other taxonomic groups, and the fieldwork will be conducted on populations of ostriches, *Struthio camelus*, in Africa.

#### 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, of which at least 60 credits are from second-cycle courses, or- have acquired largely equivalent knowledge in some other way, in Sweden or abroad.

In particular the candidate should have:

1. A BSc or MSc in Biology, or closely related field, with a background in evolutionary theory and ecology.
2. Practical experience of measuring social behaviour and conducting fieldwork in remote and difficult environments with knowledge of birds being an advantage.
3. Experience of molecular genetics and laboratory work as well as basic skills in bioinformatics.
4. A good understanding of statistics both practically and conceptually.
5. Excellent spoken and written English.

#### Basis of Assessment

The employment of doctoral students is regulated in the Swedish Code of Statues 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.

More specifically, we are looking for a highly motivated candidate with a strong scientific curiosity that has previously demonstrated the ability to conduct high quality scientific research. In line with this, candidates will be evaluated using the following criteria:

1. The ability to work independently, formulate and solve scientific problems.
2. The relevance and quality of qualifications, experience and publications and/or degree projects.
3. The clarity of written and oral communication.
4. The scientific quality and feasibility of the research plan (See below).

To facilitate assessment candidates are required to sub-

mit, together with their application, a motivational letter of why they want to do a PhD in ecology and evolution (1/2 page max), and a brief research plan outlining a topic they are interested in, why this is important and how the ideas presented can be tested (max 1 page).

Informal enquiries are welcome.

Deadline for applying: 30th March 2015

Charlie Cornwallis Lund University

Web: <https://lu.mynetworkglobal.com/en/what:job/-jobID:59750/where:4/> charlie.cornwallis@biol.lu.se

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## MichiganTechU Watermilfoil PopulationGenetics

We have two Graduate Research Assistantships available for two graduate students (MS/PhD) to work on the population genetics and community ecology of invasive watermilfoil in Michigan waterways funded by the Michigan Invasive Species Grants Program. One student will focus on the genetics (microsatellites) and patterns of hybridization with native watermilfoil in relation to herbicide resistance, and one student will focus on understanding the ecology of invaded and treated communities within various waterways to help understand the effects of the invasive and its control, and design and implement management practices to better control invasive watermilfoil. Students will collaborate with each other and other members of a multifaceted team that includes university researchers, community and state agencies, and private and corporate interest groups.

Minimal qualifications include a background in ecology, evolution, invasive species, and/or population genetics (through coursework OR research positions) and a growing interest in these fields. A strong academic record, evidence of excellent written and analytical skills, and enthusiasm for field and laboratory research will be highly favored.

Interested persons should contact Dr. Erika Hersch-Green (eherschg@mtu.edu) and/or Dr. Casey Huckins (\*cjhuckin@mtu.edu\*) by email and include a CV, a statement of interest in the research assistantship and their research interests in general, and the names of three references. Suitable candidates will then be contacted for an interview to discuss projects and reference

letters will be requested. Invited students will need to submit a formal application to the graduate school at Michigan Technological University.

Review of applications will begin immediately and continue until April 15th or until the positions are filled.

Erika Hersch-Green Department of Biological Sciences  
Michigan Technological University 1400 Townsend Drive  
Houghton, MI 49931 Office: 906-487-3351 Fax: 906-487-3167

Erika Hersch-Green <eherschg@mtu.edu>

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## NewcastleU 2 PlantAdaptation

The School of Biology has an exciting opportunity for a PhD studentship, starting Oct 2015. The strongest student applying to any of the eight proposed plant-based projects will be given the RB Cook studentship. The studentship covers fees and maintenance for UK/EU students.

Two of the proposed projects are in the area of evolution and ecology, complementing ongoing research in the research group of Kirsten Wolff.

Living on the edge: can adaptation at the edge of a species range accommodate rapid climatic change in a long-lived species? <http://www.ncl.ac.uk/biology/-study/postgrad/projects/adaptation.htm> Genetic diversity and evolution of nuclear restorer genes in gynodioecious *Plantago* species <http://www.ncl.ac.uk/biology/-study/postgrad/projects/plantago.htm> For how to apply: <http://www.ncl.ac.uk/biology/study/postgrad/-phds.htm> Deadline: 20 March 2015.

Further enquiries about these two projects: please email with [kirsten.wolff@ncl.ac.uk](mailto:kirsten.wolff@ncl.ac.uk)

Dr Kirsten Wolff Reader in Evolutionary Genetics Newcastle University, School of Biology Devonshire Building 5th floor Newcastle NE1 7RU, UK Phone: 0191 2084852 (internally 84852) email: [kirsten.wolff@ncl.ac.uk](mailto:kirsten.wolff@ncl.ac.uk)  
[www.staff.ncl.ac.uk/kirsten.wolff/](http://www.staff.ncl.ac.uk/kirsten.wolff/) <http://research.ncl.ac.uk/tiliageneticsresearch/> Kirsten Wolff <[kirsten.wolff@newcastle.ac.uk](mailto:kirsten.wolff@newcastle.ac.uk)>

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## NewcastleU PlantAdaptation

DEADLINE EXTENDED:

The School of Biology has an exciting opportunity for a PhD studentship, starting Oct 2015. The strongest student applying to any of the eight proposed plant-based projects will be given the RB Cook studentship. The studentship covers fees and maintenance for UK/EU students.

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Living on the edge: can adaptation at the edge of a species range accommodate rapid climatic change in a long-lived species? <http://www.ncl.ac.uk/biology/-study/postgrad/projects/adaptation.htm> Genetic diversity and evolution of nuclear restorer genes in gynodioecious *Plantago* species <http://www.ncl.ac.uk/biology/-study/postgrad/projects/plantago.htm> For how to apply: <http://www.ncl.ac.uk/biology/study/postgrad/-phds.htm> EXTENDED DEADLINE: 27 March 2015.

Further enquiries about these two projects: please email with [kirsten.wolff@ncl.ac.uk](mailto:kirsten.wolff@ncl.ac.uk)

Dr Kirsten Wolff Reader in Evolutionary Genetics Newcastle University, School of Biology Devonshire Building 5th floor Newcastle NE1 7RU, UK Phone: 0191 2084852 (internally 84852) email: [kirsten.wolff@ncl.ac.uk](mailto:kirsten.wolff@ncl.ac.uk)  
[www.staff.ncl.ac.uk/kirsten.wolff/](http://www.staff.ncl.ac.uk/kirsten.wolff/) <http://research.ncl.ac.uk/tiliageneticsresearch/> Kirsten Wolff <[kirsten.wolff@newcastle.ac.uk](mailto:kirsten.wolff@newcastle.ac.uk)>

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## Portugal Biodiversity

APPLICATIONS FOR SCHOLARSHIPS | UNIVERSITY OF PORTO CALL FOR TWO BIODIV PROJECTS

The Doctoral Programme in Biodiversity, Genetics and Evolution (BIODIV) invites applications for two scholarships under the following specific projects:

Project 1: Optimising global biodiversity conservation priorities in a changing world.

Project 2: The genetic basis of divergent vocalizations in singing birds.

The scholarships are funded by FCT (<http://www.fct.pt/index.phtml.en>) - Portuguese Foundation for Science and Technology. The call for applications is open between 10 and 27 of April 2015.

Information about the programme and on 'How to apply' is available at [www.biodiv.pt](http://www.biodiv.pt). Best regards, Maria Sant'Ana E: applications@biodiv.pt T: + 351 252 660 411 F: + 351 252 661 780

CIBIO Divulgaçã

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### **QUT Brisbane Australia MammalEvolution**

PhD Scholarship in mammal evolution, integrating genomics and palaeontology

The vertebrate evolution group at Queensland University of Technology (Brisbane, Australia) is offering a PhD scholarship to combine genomics and palaeontology, to resolve the origins of placentals, marsupials and monotremes. The candidate will be a central part of a project based at QUT that is developing methods for integrating molecular, fossil and ecological data to trace evolutionary history. You will work with an internationally recognized team of researchers, including collaborators in Australia, France and the UK. Depending of the candidate's skills and interests there will be capacity to tailor the project towards genomic, computational or more palaeontological aspects.

\* Starting May-July 2015 and open to Australian & International applicants. \* Annual stipend \$25,849 (tax free). \* Applications close 29 March \* Location: QUT's Gardens Point Campus, which is in the centre of Brisbane, nestled between the Brisbane River and the Botanic Gardens.

Expected outcomes include improved dating of evolutionary events, and a novel statistical framework for analysing morphological data, to more accurately merge fossils into the tree of life. In turn, the PhD project aims to better understand the roles of competition and environmental change in mammalian diversification and extinction.

Eligibility Criteria:

- Bachelor degree with Honours 1 or 2A, or equivalent from a recognised institution. In judging equivalence,

QUT may consider previous study, relevant research and work experience, research publications, and referees' reports. - Strong quantitative skills. - English language fluency. - Non-essential (desirable): experience in either morphometrics, phylogenetics or other bioinformatics. - Non-essential (desirable): experience in computer coding/programming, especially in bioinformatics or phylogenetics.

To Apply, submit your CV, the names and contact details for two referees, and a brief statement addressing the eligibility criteria to Matt Phillips (m9.phillips@qut.edu.au).

enquiries to Matt Phillips m9.phillips@qut.edu.au +61 7 3138 4805 <http://www.mphillipsbiol.com> The vertebrate evolution group at QUT is within the School of Earth, Environmental and Biological Sciences (in the Science and Engineering Faculty).

Further details: <http://www.mphillipsbiol.com/-contacts-vacancies.html> Matthew Phillips <m9.phillips@qut.edu.au>

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### **Rennes UWuerzburg FishEvolutionSex**

Evolution of sex determining regulatory networks

Sex can be determined by a plethora of mechanisms and the different mechanisms do not follow a phylogenetic pattern. Moreover sex determination is highly variable, sometimes even among closely related groups of organisms. The current understanding is that the primary signal, which triggers the genetic sex determination cascade, differs between the various groups of organisms, while the downstream regulatory network remained evolutionarily highly conserved. Our recent results and a detailed re-examination of previous work indicate however, that also downstream of the primary sex determiner a great variety of molecular mechanisms exist. This is in stark contrast to the molecular control of other vertebrate organ systems. So far, no explanation has been offered how such a variety in the molecular pathways of sexual development is possible and why it exists. Teleost fish show a particular wide variety of sex determination mechanisms were even sister species can have totally different modes how the male vs female decision during embryogenesis is made. We use fish of the genus *Oryzias* (medakas and related species) as models to approach three major questions:

- 1.) Are different SD mechanisms triggering the same, related or totally specific molecular pathways during the process of the fate differentiation of the gonad anlage?
- 2.) How stable are SD mechanisms in evolutionary terms?
- 3.) What is the evolutionary meaning of the high variability of sex determination mechanisms?

The PhD project will focus on the identification of chromosomal sex determination mechanisms in different species of the genus and a comparative molecular characterization of regulatory interactions of a known sex determining genetic network from the medaka *Oryzias latipes* in related species with similar or divergent sex determining mechanisms. On the methodological level the project will include up to date new sequencing technologies (RAD-tags, RNA-seq, CHIP-seq) and the tool-box for functional analyses in evolutionary developmental biology (in-vivo bioimaging, conventional transgenesis and genome editing by CRISPR/Cas9). The PhD project is embedded in a binational collaboration between the INRA institute for Fish physiology and Genomics in Rennes, France and the Biocenter of the University in Wuerzburg, Germany. The PhD student will be enrolled at the International Graduate School of Wuerzburg and work at both locations according to the experimental plan during the progress of the project.

For more details and practical information, please contact: Dr. Amaury Herpin (aherpin@rennes.inra.fr) at Rennes and Prof. Dr. Manfred Schartl (phch1@biozentrum.uni-wuerzburg.de) at Wuerzburg.

Amaury Herpin <amaury.herpin@rennes.inra.fr>

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## TulaneU EvolutionaryBiol

The Ecology and Evolutionary Biology Department at Tulane University supports a one year non-thesis Master's degree program designed for students planning to enter more advanced professional degree programs (e.g., law, public health, medicine, veterinary medicine, natural resources management) and for students intent on pursuing additional academic training (e.g., Ph.D. degree programs). The program also will be useful for students interested in seeking employment with environmental agencies of federal, state, and municipal government; non-governmental organizations; and in private industry, including environmental consulting firms.

The Plus One MS degree program is intended to pro-

vide foundational and advanced academic training in Ecology, Evolutionary Biology, Organismal Biology, and related disciplines. The program involves completion of coursework and recommended completion of an independent study with departmental faculty (see: <http://tulane.edu/sse/eebio/faculty-and-staff/faculty/>) or an internship with an approved off-campus organization. The opportunity to undertake independent study or to accrue on-the-job training with a governmental agency or private entity through an internship lends a unique character to this program and may provide students an advantage when seeking employment following graduation.

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

Applications are due May 1. Those interested in the program are encouraged to contact the program adviser (Dr. Richards-Zawacki, cori@tulane.edu <mailto:cori@tulane.edu>) or any faculty member whose research is of interest. More information can be found at <http://tulane.edu/sse/eebio/academics/graduate/plus-one-ms.cfm> Elizabeth Derryberry, Ph.D. Assistant Professor Ken and Ruth Arnold Early Career Professor in Earth & Ecological Science Department of Ecology & Evolutionary Biology Tulane University New Orleans, LA 70118 504-862-8285 (office) 504-862-8706 (fax) elizabethderryberry.tulane.edu

ederrybe@tulane.edu

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## UAberdeen InsectNicheEvolution

Title: Niche Evolution in wild or lab-reared insects (U. of Aberdeen, UK)

I am seeking talented and motivated PhD students to investigate evolutionary causes and consequences of ecological niche divergence during adaptive radiations, range shifts, or in response to anthropogenic habitat modification.

The student may choose to conduct fieldwork with wild or pest insect species in Northeast Scotland, or can apply their ideas in mesocosm experiments using lab-bred insects such as seed beetles (*Callosobruchus maculatus*).

See <http://lancasterlab.weebly.com> for ongoing projects in the laboratory, and contact Lesley Lancaster [lesleylancaster@abdn.ac.uk](mailto:lesleylancaster@abdn.ac.uk) to express interest in joining the lab. Together, we will brainstorm a project idea that fits with the ongoing work in my lab and with your unique research goals.

Research training: The student will be provided with all relevant research training.

Essential background required by the student: First / second undergraduate degree (or equivalent), or masters degree with commendation/distinction.

Link to the project: <http://www.abdn.ac.uk/-clsm/graduate/research-areas/niche-evolution.php>

To apply online: <http://www.abdn.ac.uk/clsm/-graduate/research-areas/biological-and-environmental-sciences.php> APPLICATIONS DUE: 30th April 2015.

It is advised to email Lesley Lancaster ([lesleylancaster@abdn.ac.uk](mailto:lesleylancaster@abdn.ac.uk)) with informal inquiries prior to applying online.

**\*KEY DETAILS\*:** This project advert is for a competitively-funded scheme for a limited number of Elphinstone PhD Scholarships (<http://www.abdn.ac.uk/-clsm/graduate/elphinstone-phd-scholarships.php>).

These scholarships are available to students of any nationality, and will cover all tuition and fees associated with pursuing a PhD at the University of Aberdeen. Living expenses are not covered in the scholarship, however, and thus applicants should be prepared to contribute approximately £45,000 pounds to cover living expenses for the duration of their PhD. It is not advised to take on part time work during an intensive PhD-ship, so ideal candidates are those with sufficient means to cover their expenses for the duration of their studies.

Lesley Lancaster, PhD University of Aberdeen School of Biological Sciences Zoology Building, Tillydrone Ave. Aberdeen AB24 2TZ [lesleylancaster@abdn.ac.uk](mailto:lesleylancaster@abdn.ac.uk) +44 01224 274551 <http://lancasterlab.weebly.com> The University of Aberdeen is a charity registered in Scotland, No SC013683. Tha Oilthigh Obar Dheathain na charthannas clàraichte ann an Alba, Àir. SC013683.

“Lancaster, Lesley” <[lesleylancaster@abdn.ac.uk](mailto:lesleylancaster@abdn.ac.uk)>

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## UAdelaide GenomicEvolutionAncientDNA

PhD positions in animal palaeogenomics and epigenomics at the Australian Centre for Ancient DNA (ACAD), Adelaide, Australia

We are currently conducting a number of projects investigating the genomic evolution of large mammals during periods of rapid environmental change occurring during the late Pleistocene and the Holocene (supported by Australian Research Council grants DP140104233, LP130100646, and FL140100260). Key aims of these projects are to:

- Resolve the evolutionary history of living and extinct megafaunal species
- Characterise demographic responses of animal populations to past environmental change
- Explore hybridisation, extinction and speciation events to better understand how ancestral genetic diversity is distributed among surviving populations
- Study the process of selection through time at the genomic scale, and investigate relationships between the strength and direction of selection and environmental variables
- Examine the role that epigenetic modifications play in facilitating rapid adaptation to environmental changes

Study species include a range of mammals, predominantly ungulates and carnivorans, for which ACAD already possesses a large collection of sub-fossil material. In addition, there is scope within these projects for collecting new specimens from museums and directly from the field. For example, we recently collected deep-frozen bison bones from Canadian gold mines to complement our existing collection of bovid specimens. See blog posts at:

- <http://acadelaide.wordpress.com/2014/08/09/-digging-up-frozen-bones-in-gold-mines/> - <https://acadelaide.wordpress.com/2015/02/05/a-gold-mine-within-a-gold-mine/>
- Multiple positions are available and are open to both international and domestic students. Applicants should have interest and a record of exceptional academic achievement in at least one of the following areas: ancient DNA, evolutionary biology, bioinformatics, or molecular biology. The projects will suit hard-working and motivated candidates who can demonstrate independent thinking and good communication skills. Training will focus on the generation and analysis of Next Generation Sequencing

data, with potential for fieldwork and opportunities to gain skills in both molecular biology laboratory techniques and bioinformatics.

ACAD collaborates with a team of high-profile international researchers from Europe and the USA, and successful applicants will be co-supervised by Prof. Alan Cooper, Dr Bastien Llamas and Dr Julien Soubrier at ACAD, School of Biological Sciences, University of Adelaide. For more information about ACAD, check out <http://en.gravatar.com/acadelaide> for links to Twitter, Facebook, our blog, recent publications and the official website.

Interested applicants are encouraged to send a resume, a cover letter, and the contact details of three referees to Dr Bastien Llamas ([bastien.llamas@adelaide.edu.au](mailto:bastien.llamas@adelaide.edu.au)) and Dr Julien Soubrier ([julien.soubrier@adelaide.edu.au](mailto:julien.soubrier@adelaide.edu.au)). The next application round is in April 2015.

Both the Australian Department of Immigration and University of Adelaide expect international applicants to meet the English Language Proficiency (ELP) requirements. The ELP is based on high scores in IELTS (International English Language Testing System) or TOEFL (Test of English as a Foreign Language). For further information please refer to <http://international.adelaide.edu.au/apply/admission/>. Competitive scholarships are available via the University of Adelaide Graduate Centre for domestic (<https://www.adelaide.edu.au/graduatecentre/scholarships/research/>) and international students (<http://www.adelaide.edu.au/graduatecentre/scholarships/research-international/opportunities/>).

– Bastien Llamas, PhD ARC Senior Research Associate  
Australian Centre for Ancient DNA Department of Genetics and Evolution School of Biological Sciences The University of Adelaide South Australia 5005 AUSTRALIA Ph: +61 (0)8 8313 5565 | Fax: +61 (0)8 8313 4364 | Mob: +61 (0)411 539 426 E-mail: [bastien.llamas@adelaide.edu.au](mailto:bastien.llamas@adelaide.edu.au) Web: <https://www.adelaide.edu.au/directory/bastien.llamas> For more information about ACAD, check out our Gravatar < <http://en.gravatar.com/acadelaide> > web page for links to [image:

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## UAmsterdam MiteGenomics

PhD position in Evolutionary Biology University of Amsterdam - Faculty of Science - Institute for Biodiversity and Ecosystem Dynamics

We have a PhD position available to study the ecogenomics of host race formation in spider mites. Spider mites are important crop pests with a remarkable evolutionary potential to adapt to a vast array of different host plants, including more than 1000 different plant species. However, the factors that determine such an enormous host plant range have not yet been uncovered. The project aims to uncover the genetic determinants of plant adaptation in a generalist mite species by several complementary approaches. Specific detoxification enzyme families recently uncovered in the genome sequences will be studied in silico and in vitro. Using an experimental evolution set-up, mites are allowed to adapt to several novel host plant species and phenotypically characterized. Population-level bulk segregant mapping will be used to uncover genomic regions (genes) associated with adaptation. Adaptation and speciation in a natural habitat will be studied to determine the effects of adaptation in the context of speciation and gene flow in nature.

The Institute for Biodiversity and Ecosystem Dynamics is one of eight research institutes of the Faculty of Science at the University of Amsterdam. The institute covers a wide range of subjects in both fundamental and applied research. Our scientific studies aim at a better understanding of the dynamics of ecosystems at all relevant levels, from genes to climate change, using a truly multidisciplinary approach.

Requirements MSc in biology, biotechnology or agricultural sciences. Experience with experimental approaches relevant to the project, such as current techniques in molecular biology is recommended. Ability to work on a multidisciplinary topic in a multidisciplinary research team.

For additional information, please contact: Dr. Thomas Van Leeuwen (T.B.S.VanLeeuwen@uva.nl) Dr. Hans Breeuwer ( J.A.J.Breeuwer@uva.nl)

Appointment The position will start preferably 01-MAY-2015, but is flexible. The full-time appointment will be on a temporary basis for a maximum period of 4 years. Initial appointment will be for a period of 18 months

and after satisfactory evaluation it will be extended for a total duration of 4 years. The full-time gross monthly salary will range from 2,125 in the first year to 2,717 in the final year, according to the Dutch salary scales for PhD candidates. The Collective Labour Agreement Dutch Universities is applicable. The annual salary will be increased by 8 % holiday allowance and 8.3 % end-of-year bonus.

Job application Applications should include a detailed CV, a motivation letter, and the names and contact addresses of two references from which information about the candidate can be obtained. Applications should be sent before 01-MARCH-2015 to application-science@uva.nl. Please quote vacancy number in the subject field. Interviews will be held 17 and 18 April 2015.

J.A.J.Breeuwer@uva.nl J.A.J.Breeuwer@uva.nl

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## UBern PlantHerbivoreInteractions

PhD in Plant-Herbivore Interactions (Switzerland)

Herbivores and their natural enemies have a profound impact on plant growth and yield. A major aim in plant biology is, therefore, to understand the factors that influence herbivore damage and predation by higher trophic levels in order to improve ecosystem management and pest control strategies. This project investigates the dynamics of plant herbivore natural enemy interactions in the rhizosphere, with a focus on plant toxins and climate change. The successful candidate will work on the interaction between maize, its most important herbivore pest *Diabrotica virgifera* and entomopathogenic nematodes as promising biocontrol agents. Using analytical, molecular and ecological approaches, he/she will investigate how plant secondary metabolites influence the interaction, and how soil abiotic factors that are likely to be altered by climate change affect the different players of the system. The PhD project is closely associated with the Oeschger Centre for Climate Change Research (OCCR), a world-leading institution in climate sciences.

We look for an enthusiastic PhD student with strong interests in plant-herbivore interactions. Applicants should have a firm background in one of the following fields: Molecular biology, biochemistry, plant physiology, analytical chemistry, entomology, ecology. All our projects are highly integrative and require willingness to embrace multiple disciplines within the domain of plant- environment interactions. Excellent University

grades at the MSc. level are expected. Fluent spoken and written English are prerequisites for this position.

We offer an inspiring research environment, including state-of-the art research facilities, intensive supervision and an exciting project of considerable fundamental and applied relevance. The institute of Plant Sciences is located at the shore of the river Aare, close to the vibrant centre of the city of Bern. The PhD student is paid according to University standard rates and will benefit from the courses offered by the Graduate School of the OCCR ([www.climatestudies.unibe.ch/graduate](http://www.climatestudies.unibe.ch/graduate)).

How to apply: Send a single pdf including a letter of motivation, a CV with University grades and the names and addresses of two referees to [matthias.erb@ips.unibe.ch](mailto:matthias.erb@ips.unibe.ch). The position is available immediately and will remain open until filled.

Contact: Prof. Matthias Erb, Institute of Plant Sciences, University of Bern, Altenbergrain 21, 3013 Bern, Switzerland, [matthias.erb@ips.unibe.ch](mailto:matthias.erb@ips.unibe.ch).

Matthias Erb <[matthias.erb@ips.unibe.ch](mailto:matthias.erb@ips.unibe.ch)>

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## UBristol MolecularConvergence

We are seeking PhD candidates for a funded PhD at the University of Bristol.

Measuring and interpreting convergence in molecular data

Supervisors: Davide Pisani (University of Bristol), Matthew Wills (University of Bath), and Mark Wilkinson (The Natural History Museum, London)

Deadline for application: 31st March.

Informal inquiries: [davide.pisani@bristol.ac.uk](mailto:davide.pisani@bristol.ac.uk)

Please Apply Online: <http://www.bristol.ac.uk/-earthsciences/courses/postgraduate/phd-research.html>

In biology, convergent similarity is a form of correspondence (e.g. between morphological features or of molecular sequences/structures from different species) not caused by common ancestry. Two species that display a convergent feature therefore acquired it starting from distinct ancestral features. At the least at the morphological level convergence is generally considered a consequence of evolutionary adaptation, and is generally achieved in species that adapted to a common lifestyle. An example is the evolution of fins in dolphins (mammals) and ichthyosaurs (reptiles). Convergence happens

also at the molecular level and striking examples have been discovered in the prestin gene in bats and dolphins. Prestin plays a key role in echolocation and convergence of this molecule was achieved in these two echolocating lineages. However, the extent to which convergence affect molecular data is not clear, and the forces underpinning molecular convergence are often equally unclear. Further on, how we should measure molecular convergence is not fully clear. Sequence similarity should obviously be included in the equation, but whether this similarity should be weighted, for example based on the phylogenetic distance between the considered species, is not known. Yet this can significantly impact our perception of the pervasiveness of convergence in genomic evolution.

Generally, evolutionary convergence is assumed to be more common and more detailed in more closely related species, simply because closely related species tend to be more similar and tend to have more similar evolutionary constraints and potentialities. Further to that, it is often argued that molecular (i.e. genetic) data tend to be less affected by homoplasy than morphological data. We would argue that these expectations or beliefs are the closest thing we currently have to any 'Law of Convergence' and that a sensible and promising way of investigating the importance of convergence and its broader significance is by testing these expectations. If patterns of convergence are not so constrained and data-dependent, this would provide a powerful novel insight into the nature of evolutionary change.

This PhD project is part of a larger Templeton Foundation funded research programme, the aim of which is investigating the pervasiveness of convergence in biology and its role in the process of adaptation. In specific, the student working on this project will investigate how to measure convergence in molecular data sets, and investigate how common is molecular convergence.

In particular the student will: (1) develop measures to quantify convergence and address the following questions. (2) How common is convergence in molecular datasets? (2) Is molecular convergence more common within specific lineages (e.g. mammals versus birds)? (3) Are specific parts of the genome more prone to convergent evolution (e.g. protein coding genes versus regulatory non-coding sequences like microRNA)? (4) Are alternative forms of the same data (e.g. amino acid versus nucleotide sequences) differently prone to undergo convergent processes? (4) To what extent is adaptive evolution underpinning the origin of molecular convergences?

The project is entirely computational and will fit a mathematically-inclined student with some experience

in computer programming (or the will to learn about computational methods and programming). You will be based at the University of Bristol, in the newly built 'Life Sciences Building', where you will join the Palaeobiology and Biodiversity Research Group. However, more broadly, you will be the member of a diverse, Templeton funded, research group spread between the University of Bristol, Bath, and the Natural History Museum of London, and interactions and visits to Bath and London will be common.

Dr Davide Pisani Reader in Phylogenomics School of Biological Sciences and School of Earth Sciences University of Bristol Life Sciences Building 24 Tyndall Avenue Bristol, BS8 1TG Email: [davide.pisani@bristol.ac.uk](mailto:davide.pisani@bristol.ac.uk) Phone: +44 (0) 117 39 41196

Davide Pisani <[Davide.Pisani@bristol.ac.uk](mailto:Davide.Pisani@bristol.ac.uk)>

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## UBritishColumbia ConservGenetics

I am looking for a MSc student to join my research team at The University of British Columbia (Okanagan Campus) to take part in a conservation genetic study of a mammalian species at-risk. This opportunity recently emerged and I am hoping to find a highly motivated graduate student to join the project in May/June 2015, although I will consider applicants that require a September 2015 start date. The project offers opportunities for both laboratory and field-based research, and direct collaboration with researchers and managers from government and participating universities. Individuals with a population genetics background and strong analytical skills are especially encouraged to apply. Prior experience with molecular laboratory techniques and working in a field setting are desirable.

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

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



michael.russello@ubc.ca

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## UExeter CellEvolutionPhylogenomics

We are seeking PhD candidates for a funded PhD at the University of Exeter working on eukaryotic cell and genome evolution. This award is funded through the generous donation from the Lawrence Charitable Trust and Mrs Carlotta Palmer and from the College of Life and Environmental Sciences.

As a result of philanthropic gifts and with the aim of supporting research into understanding complex systems through interdisciplinary study and analysis of large datasets, the University of Exeter is looking to recruit a student to study for PhD starting in 2015. The appointed graduate researcher will be based in the research team of Tom Richards who use 'omics' technologies to understand the evolutionary history of complex cellular life (i.e. the rise and diversification of the eukaryotes). Due to the nature of this studentship and the unique manner in which it is funded, applicants are encouraged to identify and develop their own line of research within the wider research aims of host laboratory. Currently, the work of the host laboratory covers four areas:

- 1) Using environmental DNA analysis and single cell genomics to understand the diversity of microbial life and how this fits into the tree of life.
- 2) The role of horizontal gene transfer in the evolution of pathogenic traits.
- 3) Understanding the nature and characteristic of the last eukaryotic common ancestor.
- 4) Developing experimental model systems to study cell-cell mutualistic interactions.

Candidates are encouraged to contact the supervisor and discuss project topics of interest prior to making an application at [t.a.richards@exeter.ac.uk](mailto:t.a.richards@exeter.ac.uk)

Further information about the studentship application can be found here: <http://www.jobs.ac.uk/-/job/AKS525/the-lawrence-palmer-phd-studentship/>  
T.A.Richards@exeter.ac.uk

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## UFlorida InsectEvolution

PHD Position in insect systematics and evolution- University of Florida

ASSISTANTSHIP AVAILABLE in the Lucky Lab at the University of Florida. Research Focus: Insect systematics and biodiversity, ecology, population genetics, evolution. Focus on ants is preferred, but not required. Experience with the following is an asset: insect classification, collections management, morphological and molecular systematics, bioinformatics, fieldwork.

Qualifications: \* Demonstrated ability to complete projects and publish results. \* Master's degree in entomology, ecology and evolutionary biology or relevant biological science. Applicants with intellectual interest in ants and evolutionary processes are encouraged to apply. \* Minimum GPA of 3.5 and competitive GRE scores required. \* Demonstrated ability to complete projects and publish results. \* Excellent written and oral communication abilities.

Interested candidates should send CV, statement of interest and names and contact information of three references to [alucky@ufl.edu](mailto:alucky@ufl.edu) with the subject header PHD POSITION. Applications will be considered on a rolling basis until position is filled; suggested submission deadline is April 1. Start date in Fall 2015 or Jan 2016.

Dr. Andrea Lucky. University of Florida Entomology/Nematology. Gainesville, FL 32611-0620, USA. Email: [alucky@ufl.edu](mailto:alucky@ufl.edu). Website: [www.andrealucky.com](http://www.andrealucky.com)

Andrea Lucky, PhD Entomology/Nematology University of Florida Steinmetz Hall, Rm. 2108 970 Natural Area Drive, PO Box 110620 Gainesville, FL 32611-0620 Phone: (352) 273-3952 Email: [alucky@ufl.edu](mailto:alucky@ufl.edu)

[alucky@ufl.edu](mailto:alucky@ufl.edu)

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## UHuddersfield 5 EvolutionaryGenetics

THE UNIVERSITY OF HUDDERSFIELD: DEPARTMENT OF BIOLOGICAL SCIENCES, SCHOOL OF APPLIED SCIENCES

The Leverhulme Trust Doctoral Scholarship Centre in Evolutionary Genomics

Supervisors: Professor Martin B. Richards, Dr Maria Pala, Dr Ceiridwen Edwards, Dr Martin Carr, Dr Stefano Vanin

Five PhD Studentships in Evolutionary Genomics

Closing date for applications: As soon as possible, and no later than April 30th, 2015

Funding availability: Funded PhD projects for UK/EU students

We are seeking the first cohort of five PhD scholars in Evolutionary Genetics for the new Leverhulme Trust Centre at Huddersfield, to begin in October 2015. The scholars will receive training from leading experts in their respective fields and undertake cutting-edge research in archaeogenetics, palaeogenetics, bioinformatics, genomics, next-generation DNA sequencing, phylogenetics, population genetics, human evolution and forensic analysis.

We envision openings this year in the archaeogenetics of Europe, Southeast Asia/ Pacific and Native Americans, in both humans and domestic animals, working with mitochondrial DNA, Y-chromosome and genome-wide variation (including ancient DNA), and in forensic analysis on molecular insect identification from South American and European archaeological burials. In eukaryotic evolution, research work will include the evolution of fungal genomes and transposable element families.

The students will work in the new molecular biology/ancient DNA facilities at Huddersfield, alongside existing students in all of these areas and two research fellows who will provide day to day guidance, along with the academic staff.

Applicants should hold a good first degree (and preferably also an MSc or MA) in Genetics, Molecular Biology, Statistics, Computing, Bioarchaeology, Biological Anthropology, or other relevant subject, and ideally have experience of generic biological lab techniques such as DNA extraction and PCR. For the insect-related project, a general knowledge of general entomology/zoology and invertebrate morphology is required. Although training and hands-on supervision will be provided, it is essential that the candidates can operate independently and take the initiative to direct their research.

The studentship will cover the full cost of tuition fees for UK/EU students, and will pay an annual tax-free bursary of £14,057 for three years (RCUK rates). There are additional funds available for laboratory consumables and travel for conferences, visits to collaborating laboratories and sample procurement.

To apply, please go to: [http://halo.hud.ac.uk/-pgr\\_onlineapps/](http://halo.hud.ac.uk/-pgr_onlineapps/) and complete the on-line application, ensuring you select full-time PhD Biology. Please type 'Leverhulme Trust' in the 'Personal Statement' field. Please then email your CV, transcripts and two letters of recommendation in support of your application to Professor Richards (email: [m.b.richards@hud.ac.uk](mailto:m.b.richards@hud.ac.uk)). Please indicate in your email which supervisor and kind of project you are interested in, and why you believe you are well-qualified for that project.

For informal enquiries please contact:

Archaeogenetics: Professor Richards on +44 (0)1484 471676 (email [m.b.richards@hud.ac.uk](mailto:m.b.richards@hud.ac.uk)) or Dr Maria Pala on +44 1484 472273 ([m.pala@hud.ac.uk](mailto:m.pala@hud.ac.uk))

Eukaryotic evolution: Dr Martin Carr on +44 (0)1484 471608 ([m.carr@hud.ac.uk](mailto:m.carr@hud.ac.uk))

Forensic entomology/funerary archaeology: Dr Stefano Vanin on +44 (0)1484 473179 ([s.vanin@hud.ac.uk](mailto:s.vanin@hud.ac.uk))

Related web links: <http://www.hud.ac.uk/research/-researchcentres/egrg/> <http://www.hud.ac.uk/research/-biologicalsciences/> <http://www.examiner.co.uk/news/-west-yorkshire-news/huddersfield-university-secures-1m-funding-8557938> University of Huddersfield inspiring tomorrow's professionals. [<http://marketing.hud.ac.uk/-HOSTED/EmailSig2014/EmailSigFooter.jpg>] Martin Richards <[M.B.Richards@hud.ac.uk](mailto:M.B.Richards@hud.ac.uk)>

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## UMelbourne Insecticide Adaptation

A PhD project is available at The University of Melbourne - School of BioSciences (Australia) to work with Alex Fournier-Level and Charles Robin on the limit of adaptation to insecticide in *Drosophila melanogaster*. We are seeking highly motivated candidates to carry out original research on the genetic basis of resistance in natural populations at the whole-genome scale. Candidates should have a strong interest in population genetics and a deep curiosity about evolution. Rigor and strong work ethics are essential; interest in quantitative methods would be a plus.

The Project:

Pesticides have imposed a dramatic selective pressure on insect populations, leading to the emergence of numerous sources of resistance. To preserve the efficacy of insecticides against pests and disease vectors, it is critical to understand the genetic basis of resistance

mechanisms and test if resistance can be both general and efficient without cost. The idea is that a resistance alleles might have to be either targeting multiple insecticides or be very efficient at resisting to one class only. This will involve screening multiple natural populations of *D. melanogaster* for multiple classes of insecticides, applying genome-wide association methods and follow-up candidates in functional assays (in collaboration with Phil Batterham) as well as modeling their evolution within and among populations. In particular, we ought to understand the degree of epistasis/functional redundancy between genes of the central nervous system to keep it functioning when accumulating resistance mutations.

#### The Funding:

The successful candidate will apply for a scholarship package through the Faculty of Science, which provides a tax-free annual stipend (current rate of AUD\$25,392 p.a., equaling \$973 per fortnight) and full waiver of tuition fees for the three years of the doctoral program. The successful student can further supplement their annual income by contributing to the undergraduate teaching classes and by acting as laboratory class demonstrators and tutors. All research expenses will be covered, as well as costs associated with all postgraduate coursework and conference attendance.

#### The Environment

The University of Melbourne is the leading research university in Australasia, and is internationally recognized for excellence in research and teaching. The School of BioSciences is a newly formed institution, proceeding from the merging of the Departments of Botany, Zoology and Genetics; providing a world-class research environment in evolutionary biology, genomics and ecology. The school harbors a collegiate graduate students society, offering a very interactive and vibrant environment for the successful candidate. Further information on the research programs including recent publications, can be found at: [www.adaptive-evolution.org](http://www.adaptive-evolution.org) To apply, please send a cover letter, a CV, academic transcripts, and contact details for two academic references to [afournier@unimelb.edu.au](mailto:afournier@unimelb.edu.au) or [crobin@unimelb.edu.au](mailto:crobin@unimelb.edu.au)

Informal inquiries are also welcome at the same addresses. Applicants must have completed a four-year undergraduate degree, or Bachelors degree with honours, or a masters degree by May 31 2015. Review of applications will begin immediately, and suitable candidates will be contacted for phone interviews.

Alexandre Fournier-Level

School of BioSciences

The University of Melbourne Royal Parade Parkville, VIC 3010, Australia Ph: +61 3 8344 2362

website: <http://www.adaptive-evolution.org> alexandre.fournier@unimelb.edu.au

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## UNewSouthWales LizardEvolution

PhD position studying lizard personality, learning and metabolism at the University of New South Wales

Dr. Daniel Noble and A/Professor Shinichi Nakagawa in the Evolution & Research Centre (E&ERC), at the University of New South Wales (UNSW) are seeking a highly motivated and enthusiastic student to study the covariation between metabolism, personality and learning in a model Australian lizard system. The student will join a newly formed lab group at UNSW and be part of an exciting multidisciplinary team building links between environmentally driven effects on phenotypic variation and the consequences of these effects on fitness. The student will combine theory with extensive experimental work manipulating incubation temperatures, taking behavioural and physiological measures, and establishing controlled semi-natural breeding experiments to obtain multigenerational data. They will use cutting edge molecular (e.g. SNP genotyping) and statistical tools (e.g. meta-analysis, Bayesian and individual-based modeling) during their candidature to address important topical questions in evolutionary and behavioural ecology. The student will also work with collaborators from Macquarie University, Sydney University, and The Australian National University in addition to other research groups at UNSW. We expect the student to travel to both international and national conferences to present the results of their work during their candidature.

If you are interested in joining our exciting project at E&ERC, UNSW please send an email with an expression of interest, why you are interested in joining the lab and your CV to Dan ([daniel.wa.noble@gmail.com](mailto:daniel.wa.noble@gmail.com)) and Shinichi ([s.nakagawa@unsw.edu.au](mailto:s.nakagawa@unsw.edu.au)). High quality applicants will apply for an APA scholarship through UNSW, which covers tuition and provides a stipend (\$25,392/year; more details at: <https://research.unsw.edu.au/domestic-research-candidate-scholarships>). Opportunities exist to make additional income through teaching positions advertised in the department.

Note that to apply for an APA scholarship, the candidate needs to be an Australian or New Zealand citizen

or permanent resident. However, we welcome students who would like to bring their own scholarship to join our project.

Shinichi Nakagawa <s.nakagawa@unsw.edu.au>

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## UQueensland SexBiasedGeneExpression

### Genomics of Sexually Dimorphic Gene Expression

Applications for PhD positions in evolutionary genetics are invited in the lab of Steve Chenoweth at the University of Queensland. Our group uses genomic and quantitative genetic approaches to understand the evolution of sex differences and is currently focused on the evolution of sexually dimorphic gene expression. We use both model and non-model *Drosophila* species and have recently developed significant genomic resources for *Drosophila serrata* including de novo genome and transcriptome assemblies, a panel of 100 re-sequenced lines and multiple sets of evolving populations. Research projects will leverage these new resources to develop innovative approaches to understand the selective processes and constraints that influence the evolution of sexual dimorphism in the transcriptome.

Prior training in the following areas is highly desirable but not essential: quantitative or population genetics, bioinformatics, genomics or evolutionary biology.

#### Qualifications

Applicants require either a Bachelor's degree with Honours, 'Master of Science, MPhil or equivalent degrees. International applicants usually will have published some work in peer-reviewed journals. Australian and New Zealand applicants must have received first class Honours degrees. Scholarship schemes at the University of Queensland are highly competitive. The UQ Graduate School website provides further information on the entry requirements for admission to the PhD program (<http://www.uq.edu.au/grad-school/our-research-degrees>) and scholarship details. Individuals successful in gaining a tuition-fee waiver scholarship usually also obtain a living stipend.

**\*\*Application process\*\*** Interested candidates should send a cover letter describing their motivation and research interests along with a CV to s.chenoweth@uq.edu.au no later than Tuesday April 21st 2015. Short-listed candidates will be asked to provide further information and documentation and

will be interviewed over Skype. Following, the final applicants will be invited to apply for a PhD at UQ. For further information on the UQ application process please contact the Postgraduate Administration Officer Gail Walter [gj.walter@uq.edu.au](mailto:gj.walter@uq.edu.au)

**\*\*UQ and the School of Biological Sciences\*\*** The School of Biological Sciences is a large and research-intensive unit at the University of Queensland, one of Australia's most prestigious Universities. The School has broad expertise across the disciplines of ecology and evolution, molecular and quantitative genetics, developmental biology, behaviour, plant and animal physiology, and conservation biology. Our research programs span all scales of biological organisation, from molecules and cells, to organisms, populations, species and communities, and take advantage of study animal and plant systems in a large variety of habitats (see <http://www.biology.uq.edu.au/> for detailed information on our research programs).

Steve Chenoweth Associate Professor School of Biological Sciences University of Queensland St. Lucia, QLD 4072 Australia

[www.chenowethlab.org](http://www.chenowethlab.org) s.chenoweth@uq.edu.au

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## UStAndrews Adaptation

Project title: Genome-scan methods for identifying genomic regions involved in adaptation to extreme environments

Supervisors: Oscar E. Gaggiotti (School of Biology, University of St Andrews) and Janine Illian (School of Mathematics & Statistics University of St Andrews)

Climate change can lead to extreme climate and weather events with dramatic negative impacts on both natural and domesticated species. Therefore, there is great interest in identifying genetic variants that may allow species to adapt to extreme environmental conditions. The field of population genomics addresses this problem by screening genome-wide patterns of DNA polymorphism to detect the locus-specific signature of positive selection. The objective of the doctoral project is to contribute to this emerging field by developing state of the art statistical methodology and a novel genome scan method to uncover associations between genomic regions and environment variables (e.g. temperature, aridity) from the joint analysis of population genomics and environmental data. The focus will be on spatial and

spatio-temporal Bayesian methods implemented using the Integrated Nested Laplace Approximation (INLA).

We are looking for an enthusiastic, dynamic, and independent student interested in studies at the interface between statistics and population genomics. Candidates must have a strong background in statistics and an interest in population genetics and computational biology. They should also be proficient in English. The focus of the project is on statistical developments and data analysis so it does not include any lab or fieldwork.

Interested candidates should send CV, statement of interest and names and contact information of three references to [oeg@st-andrews.ac.uk](mailto:oeg@st-andrews.ac.uk) with the subject header PHD POSITION.

Oscar E. Gaggiotti Professor, MASTS Chair Scottish Oceans Institute East Sands University of St Andrews St Andrews Fife KY16 8LB UK <http://biology.st-andrews.ac.uk/contact/staffprofile.aspx?sunID=-oeg> <http://www.congressgenetics.eu/-default.aspx> <http://intercrossing.wikispaces.com/-What+is+INTERCROSSING%3F> <http://scholar.google.co.uk/citations?hl=en&user=-tfqcdv0AAAAJ> Oscar Gaggiotti <[oeg@st-andrews.ac.uk](mailto:oeg@st-andrews.ac.uk)>

## UTulsa Comparative Transcriptomics

Graduate research opportunity to study the comparative transcriptomics of extreme phenotypes. Department of Biological Sciences - University of Tulsa

A graduate student at the M.S. or Ph.D level is sought to work with Drs. Warren Booth and Charles Brown in the Department of Biological Sciences at The University of Tulsa, Oklahoma. The successful applicant will develop a research project focused on understanding the evolution of extreme phenotypes examined through a comparative transcriptomic approach. In the Booth-Lab we use cimicid insects as models to study rapid evolutionary processes and the genetics of spatiotemporal metapopulations. Here, we will investigate extreme phenotype evolutionary in the swallow bug (*Oeciacus vicarius*: Cimicidae), a disease vectoring ectoparasite of cliff swallows (*Petrochelidon pyrrhonota*). The PIs have amassed a large collection of swallow bugs exhibiting phenotypes of interest, specifically relating to metabolic quiescence, thermal tolerance, and dispersal, and are in the process of sequencing the transcriptomes of an exploratory set on our inhouse Illumina MiSeq. The

work will draw on a long-term (32-year) study on social behavior and reproductive ecology of cliff swallows in western Nebraska and the student will have opportunities to visit the field site, and collect and sequence the transcriptomes of additional samples should interesting questions arise.

Applicants for this position should have a strong background in population genetics, molecular ecology, or evolutionary biology, and meet the admission requirements for the Department of Biological Sciences graduate program. (<http://www.utulsa.edu/-academics/colleges/college-of-engineering-and-natural-sciences/departments-and-schools/Department-of-Biological-Science.aspx>). If a non-U.S citizen, the applicant must already have a valid VISA permitting them to enter and study in the United States. Funds are not available to cover this as part of this project.

The students stipend, tuition, and medical insurance, is covered as part of the teaching assistantship.

Applications should include the following: 1) A letter of interest (not exceeding two pages). 2) A curriculum vitae. 3) Names and email addresses for at least two academics/researchers willing to provide a letter of recommendation 4) Copies of undergraduate/post-graduate transcripts 5) Electronic copies of published manuscripts, if any.

For more information about this opportunity, contact Drs. Booth ([warren-booth@utulsa.edu](mailto:warren-booth@utulsa.edu)). Anticipated start date is mid-August 2015.

Additional information regarding our research can be found at our current departmental webpages:

Dr. Warren Booth - [www.booth-lab.org](http://www.booth-lab.org) < <http://www.utulsa.edu/academics/colleges/college-of-engineering-and-natural-sciences/departments-and-schools/Department-of-Biological-Science/Our-Faculty-and-Staff/B/Warren%20Booth.aspx> >

Dr. Warren Booth Assistant Professor of Molecular Ecology Department of Biological Sciences University of Tulsa 315 Oliphant Hall Tulsa, OK 74104

Tel. (918) 631-3421 - Office (918) 631-3136 - Lab Web site < <http://www.utulsa.edu/-academics/colleges/college-of-engineering-and-natural-sciences/departments-and-schools/Department-of-Biological-Science/Our-Faculty-and-Staff/B/-Warren%20Booth.aspx> > - TU academic Lab website < <http://www.booth-lab.org/> >

“Booth, Warren” <[warren-booth@utulsa.edu](mailto:warren-booth@utulsa.edu)>

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## UZurich OrchidSpeciation

PhD Position “ Ecological genomics of parallel pollinator-driven speciation in orchids

A PhD position is open for a highly motivated student with a keen interest in evolutionary and ecological questions, and a solid knowledge of genomics and bioinformatics/statistics.

The successful candidate will be part of a team investigating the molecular basis of parallel pollinator-mediated reproductive isolation and ecological speciation between sexually deceptive orchids of the genus *Ophrys*. The project seeks to understand the degree of convergence, at the phenotypic and molecular levels, of two cases of species divergence mediated by the same pollinators. In particular, the successful candidate will investigate (1) the extent of convergence in pollinator-attractive traits and reproductive isolation between species, (2) the extent of similarities in the genomic architecture underlying these adaptive traits, and (3) the evolution of specific metabolic pathways (and their regulation) controlling pollinator attraction. This multidisciplinary project will involve a combination of field work (in the Mediterranean) and state-of-the-art tools for phenotypic, metabolomic and ecological genomic (RNA-Seq and Exome-Seq) characterisation of natural plant populations. For background information on the study system, please see e.g. Schlüter & Schiestl (2008, *Trends Plant Sci.*), Schlüter & al. (2011, *PNAS*) and Sedeek & al. (2013, *PLoS One*; and 2014, *Mol. Ecol.*).

The ideal candidate should be highly motivated and able to articulate her/his motivation for this project clearly.

S/he should be well organised, with a thorough understanding of evolutionary biology, population genetics and molecular biology, and should have an interest in orchid pollination. The candidate is expected to be proficient in statistical data analysis, with a good working knowledge of R and proven experience in bioinformatics, ideally with an ecological genomics background. Programming skills in other languages (e.g. Delphi or C/C++) are an advantage. Since the student will have to prepare libraries for Illumina sequencing, basic laboratory skills are necessary; previous field experience is a plus. Proficiency in English and good communication skills are essential, as is a completed MSc degree (or equivalent) in biology or a related discipline, and the proven ability to carry out research independently.

We offer a 3-year PhD position at the University of Zurich, Switzerland, at a competitive salary (>47kCHF/a before tax) funded by the Swiss National Science Foundation. The student will be part of the Institute of Systematic Botany, located in the beautiful Botanic Gardens and within walking distance of Lake Zurich. The successful candidate will work in a young, active, interdisciplinary and stimulating environment and will have access to state-of-the-art tools and techniques.

Your application should consist of a letter of motivation (1-2 pages), your CV and (if applicable) publication list, and the names and e-mail addresses of three academic referees. The letter of motivation should detail why you think the project is relevant, why you are personally interested in it, and why you think you are well-suited to undertake it. Please send your application (or any requests for further information) electronically to Dr Philipp Schlüter (philipp.schlueter at systbot.uzh.ch). Screening of applications will begin immediately and continue until the position is filled. The preferred start date is 1st of June 2015.

philipp.schlueter@systbot.uzh.ch

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## Jobs

AMNH NewYork Parttime EducationFacilitator ... 47	UBath Tech EvolutionaryGenomicsMicrobes ..... 56
ColoradoC OneYearTeaching EvolBiol ..... 47	UCalifornia Merced SummerAssist ForestAdaptation 56
ColoradoStateU GuppyBehavior SummerREU ..... 48	UConnecticut Bioinformatics ..... 57
EwhaWomansU Seoul EcolEvol ..... 48	UGoettingen 4 GeneticsBreeding ..... 58
ForestService Oregon PlantAdaptation ..... 49	UGroningen MolResTech MarineAdaptation ..... 59
JustusLiebigU Germany 3 Evolution ..... 49	UHawaii Hilo ResTech ..... 60
LakeForestC Chicago LabTech EvoDevo ..... 50	UHelsinki Bioinformatics ..... 60
MasseyU NZ EvolutionaryEcol ..... 51	UKansas Bioinformatics ..... 61
MFPL Vienna ComputationalBiosciences ..... 52	ULausanne parttime EvolutionaryMicrobiol ..... 62
PennsylvaniaStateU CoarIEvolution ..... 52	UMiami MolResTech MarineMammals ..... 62
QueenMaryU ResFellow EvolutionaryGenomics .... 53	UOklahoma ResAssistProf Bioinformatics ..... 63
RiceU HuxleyFellow EcolEvolution ..... 53	UPennsylvania Informatics ..... 63
RutgersU MolLabTech MarineAcclimAdapt ..... 53	USussex ResearchTech 2 SocialBees ..... 63
TempleU AsstDir InstGenomicsEvolMed ..... 54	UVermont LabTech EvolutionaryGenomics ..... 64
TempleU DataAnalyst Genomics ..... 55	WillametteU VisitingProfessorship ..... 65
TempleU Evol GenomicsCompSci ..... 55	
TempleU PopulationGenetics ..... 56	

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### AMNH NewYork Parttime EducationFacilitator

The American Museum of Natural History seeks to hire a part-time Physical Anthropology Facilitator to work in the Sackler Educational Laboratory for Comparative Genomics and Human Origins. Primary responsibilities will be to communicate key concepts in human biology and evolution to the public, and teach middle and high school groups. Facilitation requires comprehensive knowledge of hominin and primate skeletal material, proficiency with fundamental molecular biology techniques (i.e. PCR, restriction digest, gel electrophoresis), and a working knowledge of basic neurobiology. Requirements are a Masters Degree in Physical Anthropology, Forensic Anthropology, Genetics, or Human Biology. The ideal candidate will have informal teaching experience in a museum, zoo, or after school program.

Please see full listing and apply online here: <https://careers.amnh.org/applicants/jsp/shared/position/-JobDetails.css.jsp?postingId=142402> Julia M. Zichello, PhD Manager, Sackler Educational Laboratory for Comparative Genomics and Human Origins American Museum of Natural History Central Park West at 79th Street New York, NY 10024 212.769.5138

Julia Zichello <jzichello@amnh.org>

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### ColoradoC OneYearTeaching EvolBiol

One-year openings in Animal Biology and in Ecology and Biostatistics

The Department of Organismal Biology and Ecology at Colorado College announces two one-year, non-tenure track Assistant Professor positions in Animal Biology and in Ecology and Biostatistics to begin in August 2015. A review of completed applicant files will begin immediately and continue until the position is filled.

Responsibilities for the Animal Biology position includes teaching six courses including one with oversight of student research; the courses include an introductory course in vertebrate biology, an animal physiology course, and either an upper-level or non-majors course in the candidate's area of specialty. The ability to integrate subfields of zoology, physiology, and evolutionary biology is highly desirable. Apply electronically to: <http://employment.coloradocollege.edu/postings/1948> Responsibilities for the Ecology and Biostatistics position includes teaching six courses including one with oversight of student research; the courses include a field-based ecology course, a biostatistics course, and either an upper-level or non-majors course in the candidate's area of specialty. Familiarity with experimental design

in ecology and with Rocky Mountain or Southwestern ecosystems is highly desirable. Apply electronically to: <http://employment.coloradocollege.edu/postings/1949> Colorado College is a private, undergraduate, highly selective liberal arts institution enrolling approximately 2000 students. The college uses the Block Plan calendar in which students take one class at a time, allowing for significant field experiences.

PhD (or near completion) and teaching experience required. Applications will include the following: 1) a description of relevant professional background, 2) statements of teaching philosophy and research interests, 3) curriculum vitae with email address, 4) unofficial copies of undergraduate and graduate transcripts, and 5) 3 letters of recommendation. Information about Colorado College and OBE can be found at our web site: <http://www.ColoradoCollege.edu>. The Colorado College welcomes members of all groups and reaffirms its commitment not to discriminate on the basis of race, color, age, religion, sex, sexual orientation, gender identity, gender expression, national origin, or disability in its educational programs, activities, and employment practices. The College is committed to increasing the diversity of the college community. Candidates who can contribute to that goal are particularly encouraged to apply.

Thanks, Shane Heschel Assoc. Prof. Organismal Biology & Ecology Colorado College

Shane Heschel <Shane.Heschel@ColoradoCollege.edu>

and/or a career in inquiry-based scientific research.

This position lasts for 12 weeks (beginning mid- to late-May) and allows for two weeks off if the student so desires. A stipend of \$2,000/month will be provided to cover housing and other expenses, and additional funds are available for travel to a scientific conference. The student must be a U.S. citizen or permanent resident and should be enrolled as an undergraduate in Fall 2015. Applications from women, underrepresented minorities, and persons with disabilities are especially encouraged.

To apply, please email the following application materials as PDFs to John Kronenberger ([john.kronenberger@colostate.edu](mailto:john.kronenberger@colostate.edu)) by Friday, March 20th: 1) A cover letter including the following: - Why you are interested in this position? - What previous experience do you have that is relevant for this position? - When are you available to start and end this position? - What are your future plans?

2) A resume including contact information for at least two references

3) A transcript (unofficial is acceptable)

For more information about the experiment referred to above, please visit: <http://johnkronenberger.weebly.com/> John A. Kronenberger PhD Student Graduate Degree Program in Ecology Department of Biology Colorado State University 770-355-1855 Check out my website! <<http://johnkronenberger.weebly.com/>>

[j.kro365@gmail.com](mailto:j.kro365@gmail.com)

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## ColoradoStateU GuppyBehavior SummerREU

The Guppy Group in the Dept. of Biology at Colorado State University is seeking applicants for an NSF Research Experience for Undergraduates (REU) position in summer 2015 to study the effects of gene flow on guppy behavior. The successful applicant will work closely with Drs. Lisa Angeloni and Chris Funk and PhD students John Kronenberger and Dale Broder to develop an independent research project centered around our ongoing gene flow experiment. The primary objective will be to assess how our experimental treatments differentially affect behavior and how this, in turn, impacts fitness. This REU will provide invaluable experience in study design, behavioral assays, molecular genetic techniques, data analysis, and dissemination of results, and will thereby prepare the student for graduate school

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## EwhaWomansU Seoul EcolEvol

Faculty position (non-Korean) in ecology at Ewha Womans University, Seoul, Korea

Department of Life Science and Division of EcoScience at Ewha Womans University invites application for a faculty position in ecology (broadly defined). This position is open to candidates without Korean citizenship, with primary language for teaching and research being English. It is a tenure-track full-time (12-month) position at the ranks of either Assistant or Associate Professor starting in September 2016.

Applicants must have PhD degree in ecology and at least two years of post-doctoral research experience. The candidate will teach about two courses per semester, including graduate classes, and establish a strong research



program leading to publications in major journals in the fields of ecology.

We are especially interested in candidates studying central problems in ecology that have broad impacts and potential to generate productive collaboration with ecologists and evolutionary biologists in Korea. Collaborative research opportunity exists with the National Institute of Ecology in Seochon, Korea. The successful applicant will be a member of the Division of EcoScience at Ewha, faculty research areas of which include acoustic animal behavior and ecology, population genetics of freshwater and marine fish, theoretical population genetics, marine invertebrate animal diversity, plant diversity and systematics, primate (gibbon) behavior and ecology, and microbial metabolism.

For initial consideration and inquiry, send CV, research plan and, if possible, link to candidates' Google Scholar Citation profile by email to Yuseob Kim (yuseob@ewha.ac.kr) by the 2nd of April. Applicants can also directly submit the application material to the faculty recruitment system of Ewha (<https://faculty.ewha.ac.kr>) which will be open for application from March 30 to April 8.

Yuseob Kim <yuseob@ewha.ac.kr>

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### ForestService Oregon PlantAdaptation

This is a reciprocal transplant experiment examining if populations and seed zones (regional groups of populations with similar phenotypes and occur in similar climates) are locally adapted.

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Scientists with the Forest Service stationed at the Pacific Northwest Research Station in Corvallis, OR are looking for two field assistants to travel with us to collect data from a reciprocal transplant experiment at 16 common garden throughout the Interior Northwest US (OR, WA, ID, NV) from May-July. This research project is investigating the efficacy of seed zones (regional groups of populations with similar phenotypes and occur in similar climates) for bluebunch wheatgrass comparing differences in establishment, survival, and reproduction of bluebunch wheatgrass populations from local seed zones compared to non-local seed zones. This study will explore the consequences of changing climates for adaptation by substituting space for time to evaluate

different populations in different climates. Results from this work will aid land managers in maintaining and restoring healthy ecosystems by using locally adapted seeds. Assistants will maintain sites, reduce weeds in study plots, and collect data on the reciprocal transplant experiment of bluebunch wheatgrass (*Pseudoroegneria spicata*) to determine the efficacy of seed zones. Desired skills include the ability to collect precise data, possess a valid driver's license, ability to enjoy long distance driving and scenic views, ability to travel for 5-14 days periods, ability to weed by hand, and hoe and small machines.

Biological Science Technician (Plants) GS-0404-04

Applications must be submitted on USA JOBS:

<https://www.usajobs.gov/GetJob/ViewDetails/-396185400> Send questions to Holly Prendeville

"Prendeville, Holly R -FS" <hollyrprendeville@fs.fed.us>

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### JustusLiebigU Germany 3 Evolution

JOB 1: Early Stage Researcher ESR B3 Biogeography Institute/ Supervisor Giessen - Christian Albrecht

Title Drivers of Pontocaspian biodiversity Rise and Demise: satellite regions as source/sinks of Pontocaspian biota

Summary

The Justus Liebig University Giessen is looking for prospective candidates with a background in phylogenetics and biogeography and an interest in interdisciplinary palaeoenvironmental and biodiversity research in the Pontocaspian region (Black Sea, Caspian Sea and Anatolia and surroundings).

Description

The successful candidate will be employed as researcher without a PhD and enrolled as PhD student to complete a PhD thesis within the contract period of 3 years to assess the role of satellite regions (Anatolian and possibly Balkan lake systems) in the evolution of Pontocaspian biota over the past 3 Ma. Lakes and Quaternary lake deposits in Anatolia and the Balkans contain various groups of Pontocaspian taxa. However, it remains largely unknown whether these satellite areas served as sink or source (cf. refuges) for Pontocaspian biota. Combined molecular phylogenetic analyses of extant Pontocaspian species from Anatolian and Balkan

lakes with a rigorous updated study of fossil occurrences and their depositional/geochemical context in these lake basins will allow testing their role as sinks and/or sources. The environmental context of biotic change in selected lake successions will be determined through sedimentological and geochemical analyses and compared with ostracod data through parallel projects. The successful applicant will test the role of selected satellite regions as sources/sinks of Pontocaspian biota using fossil-calibrated molecular clock approaches and phylogeographical analyses (gene-flow analyses and ancestral area reconstructions). This project will include a combined secondment at Naturalis Biodiversity Center and GiMaRIS in Leiden (NL) to study fossil molluscs and to train for conservation biodiversity assessment techniques. The candidate will enroll in an extensive Network Training Program.

#### Research Fields

Comparative biogeography, phylogeography, biodiversity, paleontology, Biostratigraphy

Career Stage Early stage researcher or 04 yrs (Post graduate)

Research Profiles First Stage Researcher (R1)

Type of contract Temporary employment with the Federal State of Hesse. Full time 40 hrs/wk

Salary a month/year A salary that matches the MSCAITN and local rules, a monthly mobility allowance of 600, gross and a possible monthly family allowance of 500, gross.

Benefits In accordance with Marie Sklodowska Curie Regulations

Information about the Marie Sklodowska Curie actions is available at <http://ec.europa.eu/research/mariecurieactions/> [http://ec.europa.eu/research/mariecurieactions/aboutmsca/quickguide/index\\_en.htm](http://ec.europa.eu/research/mariecurieactions/aboutmsca/quickguide/index_en.htm) Financial and other technical information is available at [http://ec.europa.eu/research/mariecurieactions/aboutmsca/actions/itn/index\\_en.htm](http://ec.europa.eu/research/mariecurieactions/aboutmsca/actions/itn/index_en.htm) [www.pontocaspian.eu](http://www.pontocaspian.eu) Address details of workplace Department of Animal Ecology and Systematics Systematics and Biodiversity Group Justus Liebig University Giessen H.-Buff-Ring 26-32 (IFZ) D-35392 Giessen, Germany

Specific demands from your country/ institute Ability to work in an internationally oriented environment, including fluency in English  $\frac{3}{4}$  M.Sc. in relevant field

Applicants are invited to submit the following documents:

Letter of application (max 2 pages); Resume (Curricu-

lum vitae); The names, position and e-mail addresses of at least two persons that can be contacted for reference; List of publications, including submitted manuscripts or papers in press, if any; Transcript of BSc and MSc diploma.

The required documents should be submitted by email to [sollicitaties@naturalis.nl](mailto:sollicitaties@naturalis.nl) before 16 April 2015.

Job 2: Early Stage Researcher ESR B4 Evolution Institute/ Supervisor Giessen - Tom Wilke

Title Drivers of Pontocaspian biodiversity Rise and Demise: Molecular evolution of Pontocaspian biota

Summary The Justus Liebig University Giessen is looking for prospective candidates with a background in evolutionary biology and an interest in interdisciplinary palaeontological and phylogenetic research in the Pontocaspian region (Black Sea, Caspian Sea and Anatolia and surroundings).

Description The successful candidate will be employed as researcher without a PhD and enrolled as PhD student to complete a PhD thesis within the contract period of 3 years to reconstruct past evolutionary events and diversity changes over ~2 Ma in several Pontocaspian species flocks

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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>

## LakeForestC Chicago LabTech EvoDevo

Lab Tech position in EcoEvoDevo at Lake Forest College, Chicago.

We are looking to appoint a research technician and lab manager to work on an NSF-funded project for at least one year. The major duties of the position are to assist and support undergraduate research in integrative developmental biology in the Shingleton Laboratory at Lake Forest College. The specific focus of the project is to explore the developmental mechanisms by which oxygen influences body size, using *Drosophila* as a model organism. This is an ideal position for individuals wanting to gain additional research experience before applying to graduate school, although more experienced researchers are encouraged to apply.

The Shingleton laboratory explores the developmental mechanisms that regulate body and organ size, and how these mechanisms evolve to generate morphological diversity. We are particularly interested in environmental regulators of body and organ size, including oxygen level, nutrition and temperature. The Shingleton laboratory works closely with collaborators in Arizona, Texas and Australia, and there is the potential to travel to partner institutions to gain additional research experience. More information about the Shingleton laboratory can be obtained here: <http://campus.lakeforest.edu/shingleton/-index.html> Lake Forest College is a small liberal arts college located 30 miles north of Chicago, with a heavy emphasis on research. Faculty in the biology department maintain active research programs and the college has strong connections with other Chicago-based research institutions. The college is easily accessible from the city by train, and many faculty and staff commute daily to campus from Chicago.

Candidates must have a bachelors degree in a biology-related field, excellent organizational and time management skills, and basic computer skills (excel, word processing, etc.). Candidates must also have experience with *Drosophila* genetics and fly pushing. Familiarity with basic molecular biology techniques is preferred but not essential.

#### Principal Responsibilities:

Conduct experiments in support of critical developmental physiology projects in the laboratory.

Maintain *Drosophila* stocks and conduct crosses to generate flies with specific genotypes.

Assist in supervising undergraduate researchers in various laboratory projects.

Provide laboratory-specific training for researchers.

Order laboratory supplies and manage laboratory resources.

#### To apply:

Applicants should send a CV, a covering letter explaining their suitability for the post, and contact details (including email addresses) of 2-3 referees who would be available to provide references before interview. Interviews will be conducted in person for candidates living locally, or via skype. Complete application packages, as well as informal inquiries, should be sent to: shingleton@mx.lakeforest.edu

Review of applicants will begin immediately and continue until position is filled. Ideal start data is 5/1/15.

Lake Forest College embraces diversity and encourages applications from women and members of other histori-

cally underrepresented groups.

Alexander W. Shingleton Associate Professor

Department of Biology Lake Forest College 555 North Sheridan Road Lake Forest, IL 60045

Ph: 847-735-6049 web: campus.lakeforest.edu/shingleton

“Shingleton, Alexander”  
<shingleton@mx.lakeforest.edu>

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## MasseyU NZ EvolutionaryEcol

We seek to appoint a new Lecturer in Ecology within the Institute of Agriculture and Environment (IAE) at Massey University’s Palmerston North campus, New Zealand

<http://massey-careers.massey.ac.nz/8723/lecturer-in-ecology> Closing date is 30 April 2015

Applicants for the position will have excellent academic credentials and a PhD in Ecology or related discipline, a demonstrated track record of high-quality research outputs and success in obtaining research grants. The successful candidate will pursue research of international calibre, attract external research funding, supervise post-graduate students, and teach at all levels, both within the BSc Major in Ecology and also potentially across related fields (e.g., Conservation Biology, Environmental Science, Zoology, Physiology, Biometry), engaging in novel curriculum development for research-led teaching. The successful candidate will also engage in outreach and administrative services to the University and broader academic and professional communities.

We seek candidates whose research programme will complement and enhance the existing Ecology Group research capabilities within IAE, which has strengths in behavioural ecology, population and community ecology, evolutionary ecology, freshwater ecology, plant ecology, conservation biology, zoology, and environmental science and management. The ideal candidates will also establish collaborations with researchers from other disciplines within IAE. Applicants from all fields of Ecology will be considered, but those with expertise in ecosystem ecology, microbial ecology, landscape ecology, behavioural ecology, evolutionary ecology, population ecology, or applied entomology are particularly encouraged to apply.

Level of position and salary will be commensurate with

experience.

For further information please visit; <http://jobs.massey.ac.nz/> Enquiries of a scientific nature should be directed to Prof Murray Potter (telephone +64 6 356 9099 ext: 84836; DDI +64 6 9517836; Fax: +64 6 3505623. Email: [m.potter@massey.ac.nz](mailto:m.potter@massey.ac.nz). Information about the Ecology Group and links to other IAE pages can be found at <http://ecology.massey.ac.nz> . [M.Morgan-Richards@massey.ac.nz](mailto:M.Morgan-Richards@massey.ac.nz)

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## MFPL Vienna Computational Biosciences

The following text can also be found at: <http://www.mfpl.ac.at/about-us/open-positions/-position/news-detail/wwtf-funded-positions-in-the-computational-biosciences-hosted-by-the-mfpl.html>

WWTF-funded positions in the Computational Biosciences, hosted by the Max F. Perutz Laboratories (MFPL), Vienna, Austria

The WWTF Austria has launched a call for applications in the Computational Biosciences.

The “Vienna Research Groups for Young Investigators” call by the City of Vienna and the WWTF will fund promising young scientists starting their first independent research group in Vienna. One to two positions with up to 1.6 Mio. EUR funding per group are available, for 6-8 years, with the possibility during this time of conversion to a tenure track position. See:

<http://www.wwtf.at/programmes/ls/index#c4567h>

The positions need to be hosted by a university or research institute in Vienna, so the MFPL (<http://www.mfpl.ac.at>) is now seeking outstanding candidates from, but not limited to, the following areas:

- Computational Biology - Bioinformatics - Computational Biophysics and Structural Biology - Computational Genomics - Computational Population Biology - Computational Phylogenomics

Interested candidates should send their CV, brief career summary and research proposal, up to three publications, and the names of three referees, preferably as a single PDF, to Graham Warren ([facultyopenings@mfpl.ac.at](mailto:facultyopenings@mfpl.ac.at)). The deadline is April 20th 2015.

This is a two-step procedure. Short-listed applicants will be invited to MFPL for interview in May and successful candidates will then be sponsored by the MFPL

to apply for one of the WWTF positions, the deadline for which is July 15th 2015.

Heiko Schmidt <[heiko.schmidt@univie.ac.at](mailto:heiko.schmidt@univie.ac.at)>

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## PennsylvaniaStateU CoarEvolution

The Baums lab in the Department of Biology at Penn State (<http://bio.psu.edu/directory/ibb3>) is looking for an experienced researcher to conduct NSF-funded experiments on acclimatization of shallow-water corals to increased temperature as a result of the 2014 bleaching event in the Florida Keys. Responsibilities include organizing and conducting a microcosm experiment over three months in the Florida Keys (July -Sep 2015) with little supervision, requiring the researcher to live in the Florida Keys during this time. Experience with aquarium experiments on corals and AAUS SCUBA certification is required. The successful candidate will be proficient in using molecular tools such as gene expression analysis, RADtag sequencing and bacterial 16s tag sequencing as well as analysis of next generation sequencing data. An advanced degree in marine biology or molecular ecology or related fields is needed. This position will be filled at the research assistant or research associate level, depending upon education and experience. Candidate must be able to begin work on 1 June 2015. Position initially funded for 6 months with possibility of continuation. Applications must be submitted electronically at <https://psu.jobs/job/56345> and include a cover letter detailing research interests and experience, a current CV and names and contact information for three references. Review of applications will begin immediately and continue until position is filled.

CAMPUS SECURITY CRIME STATISTICS: For more about safety at Penn State, and to review the Annual Security Report which contains information about crime statistics and other safety and security matters, please go to <http://www.police.psu.edu/clery/>, which will also provide you with detail on how to request a hard copy of the Annual Security Report.

Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to minorities, women, veterans, disabled individuals, and other protected groups.

Job URL: <https://psu.jobs/job/56345> [ibb3@psu.edu](mailto:ibb3@psu.edu)

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## QueenMaryU ResFellow EvolutionaryGenomics

Queen Mary University of London

Research Fellow to develop Bioinformatics / Evolutionary Genomics Facilities

The School is therefore recruiting an exceptional person to help improve our use of computing resources to drive forward Evolutionary Genomics & Bioinformatics research in the School. We are looking for someone who likes to make things happen, who is a problem solver and is passionate about carving themselves a role with a broad range of skills. We need someone who is keen and has a can-do attitude for this exciting and varied role.

The successful candidate might have a background in evolutionary biology, computer science or an informatics discipline. They will be expected to combine evolutionary insight and considerable expertise in High Performance computing and sysadmin and hacking (e.g. BioPython, BioPerl, ruby, shell, R, node/javascript).

For example the successful candidate would be expected to be able to set up a Galaxy server and help new users exploit it for Genomic analysis, proteomics etc.

Closing date 27 March 2015

More information available at: <http://goo.gl/TCIrdu> <http://bit.ly/genehack> <http://www.hr.qmul.ac.uk/jobs/items/148561.html> RA  
Nichols <r.a.nichols@qmul.ac.uk>

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## RiceU HuxleyFellow EcolEvolution

HUXLEY FELLOW in ECOLOGY & EVOLUTION: The BioSciences department of Rice University ([\\*http://biosciences.rice.edu/\\*](http://biosciences.rice.edu)) seeks to fill a Huxley Fellow position in ECOLOGY or EVOLUTION. The position is a two-year appointment with a third year extension possible, with a tentative start date of July 1, 2015. Our prestigious Huxley Fellow Program aims to recruit outstanding researchers with a PhD and postdoctoral experience, who merge excellence in teaching (25%) and

research (75%). The Huxley Fellows receive faculty status, employee benefits, competitive salary, and research funds for independent or collaborative research. Collaborative interests with the existing faculty in the EEB research area are a plus. An application (curriculum vitae, statement of research interests and statement of teaching) and three letters of recommendation should be submitted via e-mail to Diane Hatton, [\\*rdh@rice.edu](mailto:*rdh@rice.edu). Please write "Huxley Fellow Application" in the subject line. Application review will begin March 27, 2015. For further questions and informal inquiries please contact Dr. Julia Saltz ([\\*julia.b.saltz@rice.edu](mailto:*julia.b.saltz@rice.edu)), Huxley Fellow Search Committee Chair. Rice University is an Equal Opportunity/Affirmative Action Employer and values a diverse faculty. Women and minorities are encouraged to apply.

Julia B. Saltz Assistant Professor of Ecology & Evolutionary Biology Department of Biosciences Rice University 6100 Main Street, MS-170 Houston, TX 77005 [julia.b.saltz@rice.edu](mailto:julia.b.saltz@rice.edu) [Saltzlab.wordpress.com](http://Saltzlab.wordpress.com)

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

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## RutgersU MolLabTech MarineAcclimAdapt

Laboratory Technician, Rutgers University, New Brunswick, NJ

The Adams Lab in the Department of Marine and Coastal Sciences is searching for an organized, enthusiastic, and skilled individual to work as a full time laboratory technician. We use developmental and molecular biology techniques coupled with field observations to study the role of the larval stage in the acclimatization and adaptation of marine species around the world.

The technician will assist the PI in managing the molecular lab and conducting research. Specific duties will include ordering and maintaining equipment and supplies, care of invertebrate animals (e.g. sea urchins, corals), preparing DNA and RNA libraries, characterizing gene expression, performing basic data analysis, training students, and maintaining an organized, safe, and productive laboratory environment. Up to 20% travel may be required. We offer an exciting and interdisciplinary work environment, opportunities to be involved in a wide range of ecological, developmental and evolutionary projects, and the potential for co-authorship on scientific manuscripts.

#### Minimum Qualifications

- A bachelors degree in a related scientific field or an equivalent combination of education and relevant experience in molecular ecology, molecular biology, or developmental biology
- Demonstrated understanding and experience in molecular biology procedures (e.g. preparing reagents/buffers, gel electrophoresis, PCR, and cloning)
- Demonstrated ability to execute tasks efficiently and with rigor
- Exceptional organizational skills and strong ability to accomplish tasks independently
- Ability to master detailed laboratory procedures
- Excellent communication in English and proficiency using Microsoft office
- The ability to lift at least thirty pounds

#### Preferred Qualifications

- Previous experience working in a lab characterizing gene expression and/or organismal responses to environmental changes
- Previous experience working with invertebrate larvae, marine or aquatic
- Knowledge of marine biology or ecology
- Familiarity with immunostaining and/or gene perturbation techniques
- A Master's degree or equivalent research experience in a related scientific field will be viewed positively

This is a full-time position, initially appointed for a period of 12 months at a yearly salary of \$36,000 - \$45,000 (depending on qualifications), plus benefits. The position can be extended depending on performance and funding.

To apply, please submit a PDF-format application including (1) a cover letter; (2) a curriculum vitae detailing past research experience and educational training; and (3) contact information for three professional references via e-mail to [diane.adams@rutgers.edu](mailto:diane.adams@rutgers.edu). Please write "Laboratory technician position" in the subject line. Applications will be reviewed on a rolling basis until the position is filled. The position is available to begin as early as May 1<sup>st</sup> and as late as July 1<sup>st</sup>.

More information about the Adams lab can be found at <http://adams.marine.rutgers.edu>. Please contact Dr. Diane Adams, [diane.adams@rutgers.edu](mailto:diane.adams@rutgers.edu), if you have any questions.

Rutgers is an equal opportunity, affirmative action employer, and is committed to providing employment op-

portunities to minorities, women, veterans, disabled individuals, and other protected groups.

Diane K Adams, PhD

Rutgers the State University of New Jersey Institute of Earth, Ocean and Atmospheric Sciences Dept of Marine and Coastal Sciences 71 Dudley Rd, New Brunswick NJ 08901 USA

(w) 848-932-3279 (c) 617-312-8076

[dadams@marine.rutgers.edu](mailto:dadams@marine.rutgers.edu)

Diane K Adams <[dadams@marine.rutgers.edu](mailto:dadams@marine.rutgers.edu)>

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### TempleU AsstDir InstGenomicsEvolMed

iGEM @ Temple University Assistant Director

The Institute for Genomics and Evolutionary Medicine (iGEM) is seeking candidates for the position of the Assistant Director of iGEM (<http://igem.temple.edu>). He/she will assist the Director (Sudhir Kumar) in all matters related to operations, academics, and grants. The duties include assistance with writing grant applications and progress reports, development and management of shared institutional resources, developing and maintaining relationships with stakeholders or potential funding sources, and coordinating institute outreach. They will also be responsible for the coordination of activities such as: implementing systems and procedures, preparing reports and/or financial analyses, managing web presence, and organizing special events, workshops, and meetings.

We are looking for candidates with knowledge of molecular and/or genomic biology, strong interpersonal skills, and excellent oral and written communication abilities. Proficiency with Microsoft word, power point, and excel is a must. While we seek candidates with doctoral degree who do not plan to pursue traditional research careers, applications from highly experienced candidates with bachelors and masters degrees will also be seriously considered.

Interested candidates should send inquiries or their detailed resume to [s.kumar@temple.edu](mailto:s.kumar@temple.edu) (include a cover letter). The application deadline is March 31, 2015.

Temple University is located in the heart of historic Philadelphia, and is the sixth largest provider of graduate school education in the USA. Situated between New

York City and Washington DC, Philadelphia is home to a large biotech industry and has many outstanding academic, research, and cultural institutions. Temple University is an equal opportunity, equal access, affirmative action employer committed to achieving a diverse community (AA, EOE, m/f/d/v).

Sudhir Kumar, Ph.D. Director, iGEM@Temple <http://igem.temple.edu> s.kumar@temple.edu phone: 623-225-5230

s.kumar@temple.edu

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## TempleU DataAnalyst Genomics

### Data Analyst Position

Temple University's Institute for Genomics & Evolutionary Medicine (iGEM; [igem.temple.edu](http://igem.temple.edu)) seeks a Technical Support Specialist Assistant focused on the analysis of large sequence datasets. Responsibilities include data management and archiving, development and implementation of standard workflows and pipelines, and analysis of high throughput data for empirical research conducted by iGEM scientists and collaborators.

### Required Education and Experience:

Associate's (or higher) degree with at least one year of experience in data analysis and/or computer programming. Demonstrated experience programming with standard languages and tools. An equivalent combination of education and experience may be considered. Experience working in an academic research environment is preferred.

The successful candidate will have strong organizational and record keeping skills, clear understanding of DNA and expression data, experience and comfort with file manipulation in a Windows/LINUX environment as well as designing and troubleshooting analysis pipelines using published sequence analysis tools.

Temple University's Main Campus is located in the heart of Philadelphia, the 5th largest city in the United States. Philadelphia is known as a center of history, arts, and culture with a relatively affordable cost of living. Temple University serves a diverse student population with an enrollment of ~38000 students in 2014, and is part of a vibrant educational community of 34 colleges located within the city limits.

Job Posting at Temple Human Resources: [https://hospats.adminsvc.temple.edu/css\\_external/](https://hospats.adminsvc.temple.edu/css_external/)

[CSSPage\\_JobDetail.ASP?T=20150324152430&](http://igem.temple.edu/CSSPage_JobDetail.ASP?T=20150324152430&)

Apply for this position online at: [https://hospats.adminsvc.temple.edu/css\\_external/cssPage\\_Welcome.asp](https://hospats.adminsvc.temple.edu/css_external/cssPage_Welcome.asp) (USE job# TU-18850).

For additional information or enquiries, contact Sudhir Kumar (s.kumar@temple.edu)

Sudhir Kumar <s.kumar@temple.edu>

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## TempleU Evol GenomicsCompSci

Evolution/Genome Informatics Faculty Positions (Assistant/Associate Professors)

The Institute for Genomics and Evolutionary Medicine (iGEM) at Temple University invites applications for tenured and tenure-track faculty positions. We are interested in early and mid-career scientists who are developing theories, methods, algorithms, software, and resources for addressing significant problems in the domain of genome sequences and variation data.

As core faculty of iGEM (<http://igem.temple.edu>), successful candidates will be part of an interdisciplinary team of world-class faculty in biology, genomics and computer and information sciences. The successful faculty will have their tenure home in the Department of Computer and Information Sciences. Applicants for the assistant professor position should have the potential to develop a significant, extramurally funded research program Applicants for the senior position are expected to have an outstanding and continuing track record of research and funding.

Applicants should submit to [igem@temple.edu](mailto:igem@temple.edu) a single pdf containing a cover letter, a detailed curriculum vitae, a summary of current and future research interests, and a statement of teaching philosophy. Please include in the cover letter a link to a Google Scholar profile. Through their research and teaching statements applicants should inform the search committee about the transformative and cross-disciplinary aspects of their work. Review of applications will begin on March 21, 2015 and continue until the positions are filled.

Temple University is located in the heart of historic Philadelphia, and is the sixth largest provider of graduate school education in the USA. Situated between New York City and Washington DC, Philadelphia is home to a large biotech industry and has many outstanding academic, research, and cultural institutions. Temple University is an equal opportunity, equal access, affirma-

tive action employer committed to achieving a diverse community (AA, EOE, m/f/d/v).

Sudhir Kumar, Ph.D. Director, iGEM@Temple (<http://igem.temple.edu>) Institute for Genomics and Evolutionary Medicine Carnell Professor of Biology Temple University (SERC 602A) Philadelphia, PA 19122, USA [https://twitter.com/kumar\\_lab](https://twitter.com/kumar_lab) <http://www.kumarlab.net> s.kumar@temple.edu

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## TempleU PopulationGenetics

Postdoctoral and Assistant Research Professor positions in Computational Genetics/Genomics at Temple University

Multiyear NIH-funded support is available for either an early stage postdoctoral researcher, or an experienced postdoctoral researcher who would serve as Research Assistant Professor.

Research area: population genetics/genomics

The successful candidate will very likely have extensive experience in population genetic theory, particularly in the mathematical or statistical aspects of analyzing population genomics data.

The successful candidate will become a member of both the Center for Computational Genetics and Genomics (CCGG) and the Institute for Genomic and Evolutionary Medicine (iGEM). CCGG and iGEM are new centers of excellence in Temple University.

For the position of Research Assistant Professor, a key goal is developing research independence by writing and obtaining grant applications. The position also carries opportunities for teaching, both in the classroom and in the laboratory.

Please send a CV and a statement of research interests and career goals to:

Jody Hey email: [hey@temple.edu](mailto:hey@temple.edu)

Websites: <https://bio.cst.temple.edu/~hey> <https://bio.cst.temple.edu/~hey/CCGG/index.html> <http://igem.temple.edu/> [tuf29449@temple.edu](mailto:tuf29449@temple.edu)

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## UBath Tech EvolutionaryGenomicsMicrobes

We are excited to be recruiting a Research Technician to work on a project focused on the genetic basis and evolution of social and life-history traits in a microbe (a social amoeba). The project will combine high throughput measurements of traits with genome sequencing to understand the genetic basis to variation in natural populations. The technician will be required to work independently and will oversee several different technical components requiring different skill sets. The technician will support all aspects of the project, including culturing of strains, performing phenotyping assays, the preparation of genomic DNA samples and the processing of data sets.

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

The position is fixed-term of 24 months and available to start as early as May 2015, but later start dates may be possible, subject to negotiation and approval.

For further information and to apply please see: <https://www.bath.ac.uk/jobs/Vacancy.aspx?ref=SS3028> For an informal discussion about the role, please contact Prof Jason Wolf via email: [j.b.wolf@bath.ac.uk](mailto:j.b.wolf@bath.ac.uk) (telephone or Skype consultations can be arranged)

[jason@evolutionarygenetics.org](mailto:jason@evolutionarygenetics.org)

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## UCalifornia Merced SummerAssist ForestAdaptation

Lab/Field Assistant Job

I am a plant biologist at UC Merced looking for at least one full-time summer lab & field assistant. Research in our lab centers on forest ecology & genetics, particularly responses to climate change. The technician appointment would be for four months, with potential for renewal. Starting pay \$14.57/hour. Available start



dates: April 25-May 30, 2015.

Candidates must have a bachelors degree in a biology-related field, good organizational and time management skills, basic computer skills (excel, word processing, etc.), and a drivers license. Candidates must have either:

A) Experience with plant genetics, including sequencing, DNA extraction, PCR. Experience developing or working with SNPs would be desirable.

B) Forest ecology field experience, including measuring and identifying trees, collecting seed, etc.

or C) A mixture of these skills.

Additional skills that would be desirable (but not necessarily required) include experience with plant propagation, a working knowledge of statistics, and/or R programming. Please not if you have a drivers license and access to a vehicle.

Under-represented minorities are particularly encouraged to apply.

Duties may include:

- - Developing SNP markers for Ponderosa pine alongside collaborators at Davis
- - Locating and setting up field sites in the Sierra Nevada
- - Assisting with equipment ordering and testing of protocols in the lab
- - Literature searches to find data to parameterize forest models
- - Cleaning and maintaining laboratory equipment
- - Data entry and analysis

The laboratory assistant will also be expected to participate in lab meetings and update his/her skills by reading and participating classes/workshops as necessary.

To apply, upload your CV and a cover letter explaining your interest in the position to the UCM AP recruit system (<https://aprecruit.ucmerced.edu/apply>, position #5886) or follow this link: <https://jobs.ucmerced.edu/-n/staff/position.jsf?positionId=5886> . For full consideration, please apply before March 30.

For more information, please contact me at [emoran5@ucmerced.edu](mailto:emoran5@ucmerced.edu)

UC Merced is the newest school of the University of California system (<http://www.ucmerced.edu/>). The campus is small but diverse. Merced is a town of 80 thousand people located in the central valley, and cost of living is low. It is conveniently located 1 hour north of Fresno (the closest airport), 2 hours east of Berkeley and San Francisco, 2 hours south of Davis and Sacramento, and 2 hours west of Yosemite National Park.

Emily Moran, Assistant Professor, UC Merced

Emily Moran <[emoran5@ucmerced.edu](mailto:emoran5@ucmerced.edu)>

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## UConnecticut Bioinformatics

### Research Scientist Position in Genomics

A research scientist position in bioinformatics and computational biology is available in the Malone Laboratory of Gene Dosage and Evolution. The laboratory addresses questions of gene dosage, aneuploidy, sex chromosome evolution, and sex determination to ultimately understand the relationship between gene dose, genome balance, and phenotype.

The research scientist will take part in de novo assembly analyses of several frog species and analyze a variety of high-throughput sequencing datasets to address questions of dose, dosage compensation, and genome evolution. Proficiency with multiple scripting languages, high-throughput sequencing analysis, and tools for computational, comparative, and evolutionary genomic analysis are required.

The environment for genomic research at the University of Connecticut is vibrant, including the Institute of Systems Genomics, University of Connecticut Health Center, Jackson Laboratory for Genomic Medicine, and Center for Genome Innovation. The Malone laboratory interacts closely with these centers and resources, creating exciting new avenues for answering questions in genome biology. Candidates should expect to engage with the local genome analysis community.

Applicants should send a single PDF file that contains a cover letter describing your research interests and experience (maximum 2 pages), C.V., and contact information for three references to [john.malone@uconn.edu](mailto:john.malone@uconn.edu). Applications will be reviewed immediately until the position is filled.

Candidates interested in a postdoctoral position are also encouraged to apply and informal inquires from candidates with other backgrounds in genomics and evolutionary biology are welcome.

John H. Malone Assistant Professor of Genetics and Genomics Institute of Systems Genomics Department of Molecular and Cell Biology University of Connecticut <http://mcb.uconn.edu/john-malone/>  
[john.malone@uconn.edu](mailto:john.malone@uconn.edu)

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## UGoettingen 4 GeneticsBreeding

Dear colleagues,

please find enclosed an opening for four professorships in the newly created “Center for Integrated Breeding” at the Georg-August-University Goettingen. Further information can be found at <http://www.uni-goettingen.de/en/507592.html>, or you can contact me ([hsimian@gwdg.de](mailto:hsimian@gwdg.de)). Please feel free to bring this opening to the attention of potential applicants.

Thanks and best wishes

Henner Simianer

Dr. Henner Simianer Professor of Animal Breeding and Genetics Department of Animal Sciences Georg-August-University Goettingen Albrecht-Thaer-Weg 3, 37075 Goettingen Tel.: +49-551-395604, Fax: +49-551-395587 Email: [hsimian@gwdg.de](mailto:hsimian@gwdg.de) <http://www.uni-goettingen.de/tierzucht> The Faculty of Agricultural Sciences at the Georg-August University Göttingen seeks to fill four professorships within the framework of a new “Center for Integrated Breeding” at the earliest possible date.

The professorships are part of a “Center for Integrated Breeding” which is unique in Europe. This center is presently in the development stage und will bring together knowledge from plant- and animal-breeding with contributions from natural sciences as well as social sciences in order to establish an internationally leading role in this field. The establishment of the Center is being supported by leading German companies in the fields of animal and plant breeding. The successful candidates are expected to show a strong interdisciplinary approach and the willingness to cooperate with other faculties. There are excellent opportunities for research in cooperation with companies internationally active in the fields of animal and plant breeding.

In teaching, the professorships should contribute to the research orientated MSc-programme “Integrated Plant and Animal Breeding”, which is to be established, as well as to other programmes offered by the Faculty of Agricultural Sciences for BSc-, MSc- and PhD-students. Ability and willingness to teach in English are a prerequisite. The conditions for being appointed to a professorship are stated in §25 of the Niedersächsischen Hochschulgesetzes (NHG) vom 26.02.2007 (Nds. GVBl. S. 69). The University of Göttingen Public Law Foundation has

the right to appoint professors. Details will be gladly explained upon request. Applications from abroad are expressly welcome. Under certain circumstances, the positions may be filled on a part-time basis. The University of Göttingen strives to increase its proportion of female staff in fields where women are underrepresented and expressly encourages qualified women to apply. The university plans to make the professorships part of the Programme for Women Professors jointly organised by the German federal government and regional states. Disabled persons with equivalent qualification will be given preference.

Applications including a CV with a representation of the applicant’s academic education and career, publications and teaching record should be submitted electronically no later than April 19, 2015. Further information and the application portal: <http://www.uni-goettingen.de/en/507592.html> Full Professor “Functional Breeding” genetics and improvement of functional traits by breeding” The successful candidate will cover the field of development and implication of breeding methods for the purpose of improving functional traits in livestock with a focus on poultry. Research should contribute to combining the necessary genetic performance of livestock with the expression of functional traits such as fertility, health, behaviour and resource efficiency under the aspect of animal welfare. To this purpose, modern genome-based approaches including methods of quantitative genetics should be utilised. Facilities for experimental research with animals are available. Temporary professor (W2) with tenure track “Breeding Informatics”

The successful candidate will develop methods based on bioinformatics for the efficient use of data from genome sequencing, high-throughput phenotyping and high-throughput genotyping in animal and plant breeding. This entails the development of methods which combine bioinformatics approaches with concepts from quantitative genetics, statistical genetics and population genomics. The methods thus formulated should be tested with very large data sets (“Big Data”) stemming from practical breeding.

Full Professor (W3) “Plant Breeding Methodology” The successful candidate covers the discipline of Plant Breeding and all aspects of its role in crop production. A strong methodological focus on Quantitative Genetics / Population Genetics as well as Selection Theory is expected. At a later moment, the candidate will succeed Prof. Dr. Heiko Becker, Professor of Plant Breeding.

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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](http://mcmaster.ca/~brian/evoldir.html)

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## UGroningen MolResTech MarineAdaptation

Dear all,

We have a Molecular Research Technician position open in our lab. We are searching for a research laboratory technician for our general research program, which aims at population genetic and genomic analyses of pelagic marine vertebrates using “classic” and Next Generation molecular technologies. The ultimate goal of our research is to understand the mechanisms driving population structuring and adaptation in the marine environment. Many aspects of our research have conservation implications. The research laboratory technician will be responsible for the daily management of the laboratory facilities and perform a range of molecular analyses. The research laboratory technician will also be involved in teaching, training and the support of researchers and students.

This position is a 0.8 full time employment with a one year probation period and the perspective of long-term prolongation. The deadline is the 26th March 2015 (23h59 Dutch local time).

Details about the application are provided below and are available on the University website where you can also apply <http://www.rug.nl/about-us/work-with-us/job-opportunities/overview?details=00347-02S0004DIP>  
Best regards Michael C Fontaine

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**Organisation** Since its foundation in 1614, the University of Groningen has established an international reputation as a dynamic and innovative university offering high-quality teaching and research. Its 30,000 students are encouraged to develop their own individual talents through challenging study and career paths. The University of Groningen is an international centre of knowledge and ranks among the top research universities in Europe.

The Groningen Institute for Evolutionary Life Sciences in the Faculty of Mathematics and Natural Sciences of the University of Groningen invites applications for a position as molecular research technician placed with the research group Marine Evolution and Conservation (MarECON). MarECON's main research focus is on the evolution and conservation of pelagic marine verte-

brates. The group has excellent laboratory facilities for molecular analyses.

**Job description** We are searching for a research laboratory technician for our general research program, which aims at population genetic and genomic analyses of pelagic marine vertebrates using “classic” and Next Generation molecular technologies. The ultimate goal of our research is to understand the mechanisms driving population structuring and adaptation in the marine environment. Many aspects of our research have conservation implications. The research laboratory technician will be responsible for the daily management of the laboratory facilities and perform a range of molecular analyses. The research laboratory technician will also be involved in teaching, training and the support of researchers and students.

**Qualifications** We are looking for an enthusiastic, self-motivated and independent co-worker, who enjoys routine laboratory work, equipment and database maintenance as well as the adoption and implementation of new molecular methods (including NGS technologies).

**Required skills:** - a Master or professional (HBO) degree in biology or relevant related field (e.g., molecular biology) - at least one year working experience in a molecular biology laboratory - demonstrated understanding and experience in the application of molecular genetic laboratory procedures (e.g., DNA extraction, Sanger sequencing as well as microsatellite genotyping) - demonstrated understanding of Next Generation Sequencing technologies - demonstrated ability to execute working tasks efficiently and with rigor - demonstrated ability to independently acquire and implement novel molecular protocols and troubleshooting - proficiency in standard productivity software, such as Microsoft Office, basic genetic software (e.g., sequencing visualization and microsatellite genotyping) as well as database entry and management - good communication skills and a strong command of both written and spoken English.

**Additional desired skills:** - experience with next-generation molecular protocols including preparation of libraries for next generation sequencing - experience with student training and supervision in the lab - ability to manage a molecular laboratory - bioinformatic or computational biology experience - cloning, primer design and testing.

**Conditions of employment** The University of Groningen offers a salary dependent on qualifications and work experience starting at  $\hat{a}-2,067$  gross per month up to a maximum of  $\hat{a}-2,791$  (scale 7, step 10) gross / onderzoeksmedewerker'. The parttime (0.8 fte) appointment is initial.

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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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## UHawaii Hilo ResTech

Regular, Full-Time, RCUH Non-Civil Service position with the University of Hawaii at Hilo (UH Hilo), Tropical Conservation Biology and Environmental Sciences (TCBES), Centers for Research Excellence in Science and Technology (CREST) Program's Dynamic Interactions of Symbioses and Environment (DISE) sub-project, located in Hilo, Hawaii. Continuation of employment is dependent upon program/operational needs, satisfactory work performance, availability of funds, and compliance with applicable Federal/State laws.

**\*MONTHLY SALARY:**\* Commensurate with qualifications.

**\*DUTIES:**\* Prepares and analyzes genomic and transcriptomic data. Prepares and analyzes metabolomic and proteomics data. Prepares scientific manuscripts for publication. Advises faculty, graduate students, and undergraduate students in the analysis and management of genomic data on various local and University of Hawaii (UH) system data storage systems. Provides field and laboratory mentorship to TCBES Master's students and UH Hilo undergraduates. Collaborates with Principal Investigators (PIs) on technical writing to include annual and/or interim reports, peer-reviewed articles, and related works.

**\*PRIMARY QUALIFICATIONS: EDUCATION/TRAINING:**\* Master's Degree from an accredited college or university in Genetics, Bioinformatics, or related field. **\*EXPERIENCE:**\* Three to five (3-5) years of experience in conducting experiments in genomics, genetics, proteomics, and/or metabolomics. **\*ABIL/KNOW/SKILLS:**\* familiarity with software programs such as Trimmomatic, Trinity, Transdecoder, Trinotate, Remote Scanning Electron Microscopy (RSEM), JoinMap, and CLC Genomics Workbench, as well as genome, transcriptome, and protein databases. Ability to analyze genomic, transcriptomics, proteomics, and metabolomics data from Next-Gen sequencing technologies such as Ion-Torrent, 454 and Illumina. Excellent written and oral communications skills **\*POLICY AND/OR REGULATORY REQUIREMENTS:**\* As a condition of employment, employee will be subject to all applicable RCUH policies and procedures and,

as applicable, subject to University of Hawaii's and/or business entity's policies and procedures. Violation of RCUH's, UH's, or business entity's policies and/or procedures or applicable State or Federal laws and/or regulations may lead to disciplinary action (including, but not limited to possible termination of employment, personal fines, civil and/or criminal penalties, etc.).

**\*SECONDARY QUALIFICATIONS:**\* PhD from an accredited college or university in Genomics, Bioinformatics, or related field. Demonstrated experience supervising/mentoring research students. Experience working in multi-investigator teams. Experience in successfully submitting peer reviewed articles in genomics, proteomics, transcriptomics, and/or bioinformatics for publication.

**\*INQUIRIES:**\* Misaki Takabayashi 932-7595 (Hawaii).

**\*APPLICATION REQUIREMENTS:**\* Please go to [www.rcuh.com](http://www.rcuh.com), click on 'Employment'; select 'Apply' and navigate to 'See Job Announcements and/or Apply for a Job.' You must submit the following documents online to be considered for the position: 1) Cover Letter, 2) Resume, 3) Salary History, 4) Supervisory References, 5) Copy of Degree(s)/Transcript(s)/Certificate(s). All online applications must be submitted/received by the closing date (11:59 P.M. Hawaii Standard Time/RCUH receipt time) as stated on the job posting. If you do not have access to our system and the closing date is imminent, you may send additional documents to [rcuhr@rcuh.com](mailto:rcuhr@rcuh.com). If you have questions on the application process and/or need assistance, please call (808)956-8344.

EEO/AA Employer. Please apply before 04/04/2015

Dr. Donald Price Director TCBES Graduate Program Professor of Biology

Science and Technology Building 109 University of Hawaii at Hilo Hilo, HI 96720

808-932-7178 [donaldp@hawaii.edu](mailto:donaldp@hawaii.edu)

<http://tcbes.uhh.hawaii.edu/> <http://hilo.hawaii.edu/depts/biology/> <https://sites.google.com/a/hawaii.edu/price-lab-at-university-of-hawaii/> Donald Price <[donaldp@hawaii.edu](mailto:donaldp@hawaii.edu)>

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## UHelsinki Bioinformatics

The Department of Biosciences at the University of Helsinki's Faculty of Biological and Environmental Sciences invites applications for a

PROFESSOR / TENURE-TRACK ASSISTANT PROFESSOR in bioinformatics The position is shared between the Department of Biosciences, the Department of Computer Science and the Institute of Biotechnology.

The duties of the assistant professor/professor include the development of analysis methods for large sets of genomic data, and the analysis of the data. The new DNA and RNA based genome-wide sequencing analyses require expertise in bioinformatics to handle the data streams at the species, individual and cellular level so that research groups on the Viikki Campus can fully benefit from the extensive data generated by the new methods. Developing and teaching such expertise in bioinformatics is important for the whole Viikki Campus, particularly the Department of Biosciences and the Institute of Biotechnology. For the teaching in bioinformatics provided by the Department of Computer Science on the Kumpula Campus, the field of this position offers an important connection for the dialogue between theory and practice.

SEE THE ADVERTISEMENT:

<http://www.helsinki.fi/recruitment/index.html?id=3D101212> Arild Husby, Assistant Professor Department of Biosciences (Biocenter 3, office 5415), University of Helsinki PO box 65, FI-00014 Helsinki, Finland

web: <http://blogs.helsinki.fi/husby/> mail: arild.husby@helsinki.fi office phone: +358294157691

arild.husby@Helsinki.FI

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## UKansas Bioinformatics

### Genome Analysis and Bioinformatics Specialist

The University of Kansas is recruiting a research scientist with expertise in genomics and bioinformatics. The position is associated with the NIH-funded K-INBRE (Kansas IDeA Networks of Biomedical Research Excellence) Bioinformatics Core, directed by Stuart Macdonald.

We are seeking applications from dynamic, motivated individuals interested in providing computational biology and statistical expertise to help KU researchers develop and analyze genomics projects. The Bioinformatics Specialist will work closely with the KU Genome Sequencing Core facility to support investigators as they design genome biology experiments, particularly those that involve Illumina sequencing data. The user base

of the K-INBRE Bioinformatics Core is broad, and the successful candidate can expect to work on a diverse array of problems in a range of systems. The Bioinformatics Specialist would also be able to develop their own research program, mentored by, and collaborating with the many KU research faculty with strong interests in genome biology (for example, Justin Blumenstiel, John Kelly, Erik Lundquist, Stuart Macdonald).

Required qualifications: Masters in biology or computer science; Solid understanding of Linux/Unix, and demonstrated programming experience; A record of published, peer-reviewed research. Preferred qualifications include a PhD in biology or computer science, and experience with the analysis of next-generation sequencing data.

Queries about the position can be directed to Stuart Macdonald (sjmac@ku.edu), director of the facility. Further details, and instructions on how to apply for the position can be found at <https://employment.ku.edu/-staff/2962BR>. The position is open and review of applications will begin on April 3 and continue until the position is filled.

The K-INBRE Bioinformatics Core is closely associated with the Departments of Molecular Biosciences and Ecology and Evolutionary Biology, the Center for Computational Biology, and with the NIH COBRE-funded Center for Molecular Analysis of Disease Pathways. The University has a strong group of model organism (*Drosophila*, *C. elegans*) genetics and genomics researchers, and a number of quantitative and evolutionary genetics labs. The broad range of questions in evolutionary and computational biology addressed by KU labs provides an active, collaborative environment for research.

KU is an EO/AAE. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex (including pregnancy), age, national origin, disability, genetic information or protected Veteran status.

K-INBRE <http://www.k-inbre.org/> Stuart Macdonald <http://molecularbiosciences.ku.edu/stuart-j-macdonald>  
 Department of Molecular Biosciences <http://molecularbiosciences.ku.edu/> Department of Ecology & Evolutionary Biology <http://eeb.ku.edu/> Center for Molecular Analysis of Disease Pathways <http://cmadp.cobre.ku.edu/> KU Genome Sequencing Core <http://gsc.ku.edu/> ### Dr. Stuart J. Macdonald  
 Director, K-INBRE Bioinformatics Core Facility  
 Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas  
 Lawrence KS 66045 ### office: 785-864-5362 lab: 785-864-5777 fax: 785-864-5321 email: sjmac@ku.edu ###

sjmac@ku.edu

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## ULausanne parttime EvolutionaryMicrobiol

Microbiologist at the University of Lausanne (50% to 60% employment)

The Department of Fundamental Microbiology at the University of Lausanne in Switzerland is looking to hire a research associate to work on the evolution of social interactions between bacterial species. The goal of the project is to disentangle fitness effects over short and evolutionary time-scales between five species of bacteria that are used for biodegradation. The candidate will be employed part-time (50% to 60% ) for a period of 2 to 3 years.

The candidate should: - have obtained a Master's degree in biology (or equivalent) - possess skills in basic microbiology (required), molecular biology and microscopy - have an interest in researching microbial ecosystems - have good English language skills (written and oral) - be motivated, autonomous and organized - be open to developing and learning new skills and techniques

The candidate's main responsibilities will be to: - design and conduct basic microbiology experiments (bacterial cultures, quantification, etc.) - genetic modification of bacteria - design, conduct and follow long-term (months) evolutionary experiments - design and conduct experiments using microfluidic devices attached to a microscope - analyze data - train and supervise interns - manage laboratory and biological material

Employment will begin in July 2015 (flexible)

If interested, please send: - a motivation letter - an up-to-date CV - a copy of your latest graduation certificate - contact information for 2 references

to: Sara Mitri Department of Fundamental Microbiology (DMF) University of Lausanne, Switzerland E-mail: sara.mitri@unil.ch Tel: +41(0)21 692 56 12 <http://unil.ch/dmf/home/menuinst/research-units/mitri.html> Application deadline: April 30th, 2015.

Seeking to promote an equitable representation of men and women among its staff, the University encourages applications from women.

sara.mitri@unil.ch

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## UMiami MolResTech MarineMammals

Job Title: Sr. Research Associate 1 Pay Grade: 8 Pay Band Min / Max: \$42,697.00 - \$77,135.00 Position Number: 051168 Department / Hospital: COOP INST FOR MARINE AND ATMOS STUDIES

A web-based version of this job advertisement can be found at [http://um.hodesiq.com/job\\_detail.asp?JobID=4997310&user\\_id=&ViewAll](http://um.hodesiq.com/job_detail.asp?JobID=4997310&user_id=&ViewAll) The University of Miami is committed to educating and nurturing students, creating knowledge, and providing service to our community and beyond. We are leaders in the area of education, scholarship, intercollegiate athletics and service. Come join our team!

The Cooperative Institute for Marine and Atmospheric Studies (CIMAS) of the University of Miami invites applicants for a Sr. Research Associate I position in Marine Biology and Fisheries. We seek a research associate to join our group and work as a laboratory technician in the Marine Mammal Molecular Genetics laboratory. The incumbents primary focus will be collecting and analyzing DNA sequence and microsatellite data from a variety of marine mammal populations and species.

Candidates for this position should have (1) a Masters degree in Molecular Biology, Biology or related field (2) demonstrated experience with molecular biological techniques, particularly DNA extractions and DNA sequencing or microsatellite genotyping methodologies, (3) some experience with analyses of population structure and diversity from genetic data, and (4) the ability and desire to work as part of a collaborative team, (5) excellent problem solving and critical thinking skills, good organizational skills and the ability to plan daily duties.

The position will be located at the NOAA Fisheries Southeast Fisheries Science Center Protected Resources and Biodiversity Division located in Lafayette, LA. Start date is flexible, but ideally around 11 May 2015.

APPLY ONLINE FOR POSITION #051168 at: [www.miami.edu/careers](http://www.miami.edu/careers). Curriculum Vitae and the contact information for 3 people who can provide letters of recommendation are required.

The University of Miami offers competitive salaries and a comprehensive benefits package including medical and dental benefits, tuition remission, vacation, paid holidays and much more.

The University of Miami is an Equal Opportunity Employer - Females/Minorities/Protected Veterans/Individuals with Disabilities are encouraged to apply. Applicants and employees are protected from discrimination based on certain categories protected by Federal law.

Patricia Rosel - NOAA Federal  
<patricia.rosel@noaa.gov>

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### UOklahoma ResAssistProf Bioinformatics

Title of Position: Research Assistant Professor

University of Oklahomas Laboratories for Molecular Anthropology and Microbiome Research is seeking a Research Assistant Professor. Position requires PhD Degree in Biology with knowledge in bioinformatics and ancient biomolecules, NGS, and metagenomics. Duties include research, service to the community, and teaching university level courses in Anthropology and Biology.

Inquiries and applications (CV and 3 references) directed to Dr. Cecil M. Lewis Research Assistant Professor Search Molecular Anthropology Laboratories 101 David L. Boren Blvd. Norman, OK 73019.

“Lewis, Cecil M. Jr.” <cmlewis@ou.edu>

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### UPennsylvania Informatics

The Penn Institute for Biomedical Informatics at the Perelman School of Medicine at the University of Pennsylvania seeks candidates for several Full, Assistant, and/or Associate Professor positions in the tenure track. Rank will be commensurate with experience. Applicants must have an Ph.D. and/or M.D. degree and have demonstrated excellent qualifications in education and research.

The Penn Institute for Biomedical Informatics (IBI) at the Perelman School of Medicine of the University of Pennsylvania seeks candidates for several Assistant, Associate and/or Full Professor positions in the tenure track. The IBI is enabled by a recent multi-million dollar gift to expand faculty expertise, build computational

infrastructure, and strengthen educational opportunities across the spectrum of biomedical informatics. The IBI will integrate informatics disciplines including bioinformatics, translational bioinformatics, clinical informatics, clinical research informatics, consumer health informatics, and public health informatics.

Successful applicants will have strong training and skills to conduct biomedical informatics research. Applicants must have a Ph.D. and/or M.D. and have demonstrated expertise in research and education. The faculty appointment will be in an appropriate department in the Perelman School of Medicine. Applicants are expected to establish robust independent funding for their research program.

The University of Pennsylvania, founded by Benjamin Franklin, is a world-class research institution located near the center of Philadelphia. All of Penn’s twelve schools are located within walking distance of one another. The Perelman School of Medicine at the University of Pennsylvania is one of the top ranked medical schools in the nation for research and NIH funding.

Jason H. Moore, Ph.D., is Chair of the IBI Search Committee at the University of Pennsylvania Perelman School of Medicine.

We seek candidates who embrace and reflect diversity in the broadest sense.

The University of Pennsylvania is an EOE. Minorities/Women/Individuals with disabilities/Protected Veterans are encouraged to apply.

Apply for this position online at: [https://www.med.upenn.edu/apps/faculty\\_ad/index.php/-g/d3917](https://www.med.upenn.edu/apps/faculty_ad/index.php/-g/d3917)

Sarah Tishkoff, Ph.D. David and Lyn Silfen University Professor Departments of Genetics and Biology University of Pennsylvania Tel: 215-746-2670 tishkoff@mail.med.upenn.edu <http://www.med.upenn.edu/tishkoff/>

tishkoff@mail.med.upenn.edu

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### USussex ResearchTech 2 SocialBees

RESEARCH TECHNICIANS (2 POSTS) IN INSECT BEHAVIOUR (SHORT-TERM) Fixed term for 3-4 months, full time Salary range: starting at £20,198 and rising to £23,386 per annum. It is normal to appoint at the first point of the salary scale. Closing date

for applications: 13 April 2015 Expected start date : 1 May 2015

We seek two enthusiastic, self-motivated research technicians with an interest in insect behavioural ecology to assist with fieldwork and labwork for 3 or 4 months in the research group of Professor Jeremy Field at Sussex University (<http://www.sussex.ac.uk/lifesci/fieldlab/>). The work will involve helping a postdoctoral researcher to carry out fieldwork on small colonies of bees/wasps, as well as a range of labwork.

Successful applicants will preferably have a degree or equivalent in a relevant subject and an interest in animal behaviour/entomology. Demonstrated experience with the study of animal behaviour (especially social insects), and experience of fieldwork with insects would be useful. Some experience of biological fieldwork is essential.

Applicants should send a CV, a covering letter explaining their suitability for the post, a statement of the applicants availability for interview at Sussex University during 21-28 April 2015, and contact details (including email addresses) of 2-3 referees who would be available to provide references before interview. Please also provide clear statements concerning (a) the earliest date when the applicant would be available to start work after mid-April 2015, (b) whether the applicant has a full, clean driving licence; (c) that the applicant is not colour-blind (see Person Specification below). Applications that do not contain this information may not be considered.

Informal enquiries may be made to Professor Jeremy Field ([j.field@sussex.ac.uk](mailto:j.field@sussex.ac.uk)).

Please note that the full application, including CV, covering letter and completed standard application form should be sent to [lifescirecruitment@sussex.ac.uk](mailto:lifescirecruitment@sussex.ac.uk)

Closing date for applications: 13 April 2015

Interviews will be held between 21 and 28 April 2015 at Sussex University

For full details and how to apply see <http://www.sussex.ac.uk/aboutus/jobs/080> The University of Sussex is committed to equality of opportunity

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) <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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## UVermont LabTech Evolutionary Genomics

Lab technician in Evolutionary/Ecological Genomics

The Pespeni Lab in the Department of Biology at the University of Vermont is looking to hire an exceptionally motivated, organized, and skilled individual to work as a population genomics technician in our new research lab. We use genomics, developmental biology, and physiology to understand the underpinnings of resilience and vulnerability of marine species in the context of complex natural ecosystems, particularly changing climate conditions.

The technician will assist the PI in managing the lab and conducting research, with the opportunity for co-authorship on scientific publications. Specific duties will include ordering supplies and equipment, maintaining equipment, processing samples for genetic and physiology assays, microscopy, preparing RNA and DNA samples for sequencing, performing basic data analyses, training students, and maintaining an organized, safe and productive lab environment. The lab offers an exciting, integrative and supportive work environment, with opportunities to be involved in a wide range of research projects.

Minimum qualifications:

V A bachelors degree in a related field or an equivalent combination of education and relevant experience in population genetics, molecular biology, or molecular ecology

V Experience preparing reagents/buffers, gel electrophoresis, and PCR

V Exceptional organizational skills and strong ability to accomplish tasks independently

V Ability to master detailed laboratory procedures

V Excellent communication and computer skills

V The ability to lift at least thirty pounds

Preferred Qualifications

V Experience with aquaculture of marine organisms either as a hobbyist or professionally

V Familiarity with scientific computing languages such as R, Python, or Perl, and working on command line

V Strong knowledge in evolutionary biology and marine



biology

To apply, please visit the University of Vermont Jobs website <https://www.uvmjobs.com/> and search for Posting # S231PO. Please submit a resume, three (3) letters of reference, and a cover letter that highlights your previous experience in the laboratory. Review of applicants will begin immediately and continue until position is filled. The position will ideally begin in May.

This is a full-time position, initially appointed for a period of 12 months with benefits. The position can be extended for at least one year depending on performance.

More information about the Pespeni Lab can be found at <https://blog.uvm.edu/mpespeni/>. Please contact Melissa Pespeni ([mpespeni@uvm.edu](mailto:mpespeni@uvm.edu)) if you have any questions.

Melissa Pespeni, Ph.D. Assistant Professor University of Vermont Department of Biology Marsh Life Sciences, Rm 326A 109 Carrigan Drive Burlington, Vermont 05405

Lab website: \*<http://blog.uvm.edu/mpespeni/>\*  
Melissa Pespeni <[mpespeni@uvm.edu](mailto:mpespeni@uvm.edu)>

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## WillametteU VisitingProfessorship

The Department of Biology at Willamette University welcomes applications for a non-tenure-track, visiting assistant professor position to begin August 2015. The appointment will be for one year, with potential for renewal up to three years depending on successful teaching.

We are seeking a broadly trained biologist who is strongly committed to excellence in both teaching and research in a liberal arts college environment. The successful candidate 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) and an introductory course for biology majors in (Biology 125 Ecology, Evolution, and Diversity). The candidate will also be asked to teach intermediate and advanced courses in his or her area of expertise. These might include: General Ecology, Evolutionary Biology, Molecular Ecology, or Behavioral Ecology. Course sizes range from 12 to 48 students.

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. The Departmental culture encourages visiting faculty to seek extramural funding for research and pedagogical projects. Visiting faculty are also eligible to apply for department funding to support their teaching and scholarship.

About Biology at Willamette: Through a research-rich curriculum that affords high-impact student engagement, our students learn how to discover knowledge for themselves, becoming life-long learners and creators. 60% of our graduates enter careers in science and technology, including MD and PhD programs at the nation's leading research institutes. Our faculty aspire to be outstanding teacher-scholars, committed to excellence in teaching and research. Since 2005, the eight faculty members in Biology have received 41 research and education grants totaling \$3.7 million, including two NSF CAREER awards. These awards have provided research experiences for 103 undergraduates.

For more information about the Department of Biology, please visit <http://www.willamette.edu/cla/biology>. Applicants must have a Ph.D. in Ecology, Evolutionary Biology, or a related field; prior teaching experience is preferred but not required. A.B.D candidates will be considered, but the Ph.D. must be completed before beginning the appointment.

Prior teaching experience is preferred but not required.

To apply go to: <https://jobs.willamette.edu/postings/-1531> 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 teaching statement describing your teaching philosophy and practice, and identifying advanced courses that you would be interested in teaching.
4. A research statement describing your current and future research goals, and how you might involve undergraduates in your work.
5. A diversity statement describing your experience with diverse populations and importance of diversity in teaching and research communities.
6. Copies of your graduate transcripts.
7. Three reference letters that address both research and teaching potential.\*

\*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 letter of recommendation/reference on your behalf. Please note letters will only be accessible to the search committee.

Inquiries may be addressed to:

David Craig, Search Chair Biology Department

dpccraig@willamette.edu.

Open until finalists are selected. For full consideration, all application materials should be received by March 30, 2014.

If you need assistance applying for this position please contact Human Resources, human-resources@willamette.edu or 503.370.6210

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, with a GPA of 3.75 and average composite SAT scores of 1850. 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,

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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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## Other

Australia Cairns VolFieldAssistant FairyWrens . . . .	66	RohlfMedal 2015 CallNominations . . . . .	71
Cairns Australia VolFieldAssist FairyWrens . . . . .	67	SenseOfLife . . . . .	71
EvoDevoEcoNetwork Funding . . . . .	67	SocSystBiology GraduateStudentAward . . . . .	72
GainesvilleFL VolFieldAssist Anole . . . . .	68	Software DAMBE update . . . . .	72
Gene Flow Rates . . . . .	68	Transport blood samples . . . . .	73
LiveStreaming EvolMedMeeting . . . . .	68	Transport blood samples answers . . . . .	73
Namibia VolFieldAssist BaboonEvolution . . . . .	69	UMichigan BioStation SummerResearch . . . . .	74
NESCent 2015 VideoContest 2 . . . . .	70		
Omenn Prize winner announced . . . . .	70		

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### Australia Cairns VolFieldAssistant FairyWrens

Volunteer field assistants:

We are looking for field assistants to help expand and

monitor a colour-banded population of lovely fairy-wrens in Cairns (Queensland), Australia for a study on female ornamentation.

Time periods: June or September 2015 (3 to 6 months).

Duties include regular censusing of colour-banded birds, searching for and monitoring nests, mist-netting, recording song and measuring colouration, behavioural observations, video analysis, and data proofing. Working

days are long, with early starts six days a week. Enthusiasm, self-motivation and organisation, and a strong work ethic are a must.

Qualifications: experience monitoring colour-banded birds, nest-searching, and mist-netting. Good knowledge of English is a requirement. Must also be early riser, physically fit, able to work in extreme weather conditions, and enjoy basic shared living conditions. Having experience in behavioural observations and a driving licence is a plus but not a requirement.

Accommodation is provided, but assistants cover travel to the site and their own food costs. The project will reimburse up to AUD\$750/mo towards receipted food and travel expenses. For more information contact: Ana Leitao (avitorinoATstudent.unimelb.edu.au).

To apply, please email a letter outlining previous relevant field research experience, and a CV including names and contact information for 3 referees. Applications received until the 9th of April 2015 will receive full consideration. Later applications may be considered.

Ana V. Leitão PhD candidate School of BioSciences (Building 147) University of Melbourne, Parkville, VIC 3010 Australia

anamvleitao@gmail.com avi-  
torino@student.unimelb.edu.au

Australia: +61 450 643 982 Portugal: +351 964 479 857  
anamvleitao@gmail.com

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### Cairns Australia VolFieldAssist FairyWrens

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anamvleitao@gmail.com avi-  
torino@student.unimelb.edu.au

anamvleitao@gmail.com

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### EvoDevoEcoNetwork Funding

#### RESEARCH FUNDING OPPORTUNITY:

Dear Colleague,

This email is to remind you that the upcoming deadline for research exchange grants from the Evo-Devo-Eco Network (EDEN) is April 30, 2015. EDEN is funded by the National Science Foundation Research Coordination (<http://edenrcn.com/>).

One of EDENs major goals is to enable graduate students, postdoctoral fellows, and faculty to undertake research exchanges in the field of Evo-Devo-Eco, in order to develop or share techniques, protocols and tools for use with emerging model systems.

Please note that the updated eligibility for EDEN funding is as follows: Researchers based anywhere in the world can apply for funding to visit labs in the US.

Researchers based in the US are eligible for funding to visit labs anywhere in the world.

This spring EDEN will award multiple research exchanges to be held in 2015-2016. Each exchange will consist of an award of up to \$3,000 per researcher toward travel, lodging and subsistence costs. You can find out more about this program at <http://edenrcn.com/>-

[funding/index.html](#). If you know of outstanding lab personnel who would be interested, please forward this announcement to them.

You can read more about EDEN's activities and opportunities at <http://www.edenrcn.com>, where you will be able to obtain protocols for evo-devo-eco work developed with EDEN funding.

Please feel free to email [edenrcn@fas.harvard.edu](mailto:edenrcn@fas.harvard.edu) with questions about the program, and forward this email to colleagues who you think would be interested in EDEN.

Best wishes,

Cassandra Extavour

EDEN Grants <[edenrcn@fas.harvard.edu](mailto:edenrcn@fas.harvard.edu)>

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## GainesvilleFL VolFieldAssist Anole

\*Field Volunteer Needed for Anole Research in Gainesville, FL\*

I am looking for a field assistant to conduct behavioural research on \*Anolis sagrei\* in Gainesville, FL, from March 15 to May 15 (dates are somewhat flexible). The project is part of my dissertation research at Harvard University. Daily activities include searching for, capturing, marking, and observing lizards as well as collecting habitat data. We will work long hours on most days (beginning 7-8am). Applicants should be prepared for hot and humid work conditions. Applicants must be comfortable handling lizards, have a good work ethic, and should be adaptable to changing plans. This opportunity is unpaid, but all expenses (airfare, food, lodging, and other field-related expenses) will be covered.

If interested, please contact Ambika Kamath: [ambikamath@gmail.com](mailto:ambikamath@gmail.com), with a brief letter describing why you are interested in this position and any relevant research experience along with your CV and the names and contact information of a professional reference whom I may contact by email. I will review applications as they arrive until the positions are filled.

Ambika Kamath Ph.D. Candidate Losos Lab, Dept. of Organismic and Evolutionary Biology Harvard University [www.ambikamath.wordpress.com](http://www.ambikamath.wordpress.com) Ambika Kamath <[ambikamath@gmail.com](mailto:ambikamath@gmail.com)>

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## Gene Flow Rates

Dear Evoldir,

We are analyzing a dataset sampled from several geographic locations (let's say A,B,C,D,E,F). We would like to infer if there is evidence for a specific direction of gene flow and determine the gene flow rates... e.g. B→C→A→D→E→F and if possible to exclude some other scenarios e.g. that there is somewhere a source population (perhaps unsampled) that contributed genes to each of the (sampled) sub-populations. Using Approximate Bayesian Computation (ABC), we can either infer parameters from a specific scenario, or do a model selection... I'm wondering however, if there is any software or theory that will allow a general inference of the "migration history" or gene flow history.

Thanks a lot in advance Pavlos

P.S. answers will be submitted back to Evoldir

—  
Pavlos Pavlidis, PhD

Foundation for Research and Technology - Hellas Institute of Molecular Biology and Biotechnology Íkolaou Plastira 100, Vassilika Vouton GR - 711 10, Heraklion, Crete, Greece

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

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## LiveStreaming EvolMedMeeting

\*The final program for the inaugural meeting of the International Society for Evolution, Medicine, & Public Health is now available online. \* [http://issuu.com/evmedasu/docs/program\\_for\\_web?e=3D15964791/-11852215](http://issuu.com/evmedasu/docs/program_for_web?e=3D15964791/-11852215) All talks on Thursday March 19 will be live streamed at <http://www.ustream.tv/asutv> < [http://issuu.com/evmedasu/docs/program\\_for\\_web?e=3D15964791/11852215](http://issuu.com/evmedasu/docs/program_for_web?e=3D15964791/11852215) >The time zone is the same as California, so 3 hours earlier that EDT, and 7 hours earlier than London UK. \*Thursday\* \*At ASU Memorial Union\* \*Ventena Room\*6:30 7:00Continental Breakfast7:30 8:00Barbara Natterson- Horowitz, UCLA Zoobiquty and Evolutionary Medicine Introduction by

Charlie Nunn 8:15-8:30 8:45 Short break Chair: Gillian Bentley 9:00 Joe Alcock, University of New Mexico, "Identifying normal function in abnormal results: Reaction norms lead to a new normal for medical practice" 9:15 Gillian Pepper, Newcastle University, "Extrinsic mortality risk and socioeconomic differences in health behaviour: observational and experimental evidence" 9:30 Harvey Kliman, Yale University, "The pelvis skull conflict: why trophoblast inclusions are a marker of autism and may be the evolutionary basis of human intelligence." 9:45 Anne Stone, Arizona State University, "Mycobacterium tuberculosis: origins and evolutionary history of a major pathogen." 10:00 Martin Häusler, University of Zurich, "Are musculoskeletal disorders evolutionary trade-offs of bipedalism" 10:15 Break 10:30 Chair: Daniel Lieberman 10:45 Welcome remarks by Dean Garcia-Pichel and Manfred Laubichler (on behalf of Provost Page) 11:00 Marlene Zuk, University of Minnesota, "Evolution in sickness and in health" 11:15 Frank Ruhli, University of Zurich, "Evolutionary medicine as part of the medical curriculum in Switzerland and Australia: a qualitative and quantitative feedback" 11:30 Mark Schwartz, NYU School of Medicine, "Integrating evolutionary science into medical education" 11:45 Michael Muehlenbein, Indiana University, "Survey on evolution in health education" 12:00 Lunch at Memorial Union at ASU 12:15-12:30 12:45 13:00 Harvey Fineberg President, Gordon and Betty Moore Foundation Keynote: "Evolution in Medicine: Past, Present, and Future" 13:15 Introduction by: Randolph Nesse 13:30 13:45 Short break Chair: Robert Perlman 14:00 Michael Gurven, UC Santa Barbara, "Costs of reproduction in a high fertility and mortality population" 14:15 Grazyna Jasienska, Jagiellonian University, "Trade-offs between reproduction and aging: biomarkers, confounders and genetic factors" 14:30 Katie Hinde, Harvard University, "Insights into co-evolution of milk and microbes: subsistence strategy predicts glycan profile in breast milk among diverse human populations" 14:45 Daniel Lieberman, Harvard University, "An evolutionary medical perspective on shoes" 15:00 Allen Rodrigo, NESCent, "Neutral models of microbiome evolution" 15:15 Break 15:30 Chair: Ajit Varki 15:45 Sudhir Kumar, iGEM Temple, "Phylomedicine: Evolutionary Lessons and Solutions for Genomic Medicine" 16:00 David Haig, Harvard University, "Microchimerism and inclusive fitness" 16:15 Elizabeth Uhl, University of Georgia "Origin of canine distemper as a reverse zoonosis from human measles: insights from history, evolution and studies of codon usage bias" 16:30 Bernard Crespi, Simon Fraser University, "Imagination as a core diametric phenotype of autism spectrum and psychotic-affective spectrum conditions: evidence from schizophrenia genetic risk

scores" 16:45 Jacobus (Koos) Boomsma, University of Copenhagen, "Parent-of-origin gene-dosage effects in the womb may affect physical and mental health later in life" 17:00 Baba Brinkman-Rap Preview & RapUp 17:15 Flash talks Chair: Marlene Zuk 17:30-17:45 Poster session/ Appetizers 18:00 La Paz & Cochise rooms 18:15-18:30 18:45 19:00 19:15 Education and Outreach Committee Meeting 19:30 at Engrained Patio at the Memorial Union 19:45 20:00 20:15

Randolph M. Nesse, MD < <http://randolphnesse.com/> > The ASU Center for Evolution & Medicine < <https://sites.google.com/a/asu.edu/cemph/> > Full ISEMPH Conference Program available here < [http://issuu.com/evmedasu/docs/program\\_for\\_web?e=3D15964791/11852215](http://issuu.com/evmedasu/docs/program_for_web?e=3D15964791/11852215) >

rmnesse@gmail.com

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## Namibia VolFieldAssist BaboonEvolution

Hello,

We are recruiting field assistants for the 2015 field season on the Tsaobis Baboon Project. We have previously used this website to announce the position and would like to do it again since we found it very useful. The advert and the "graphical ad" are written (and attached) below. We would be so grateful if you could post this announcement on the EvolDir website.

Kind Regards,

Claudia Martina Luna

Large Animal Research Group Department of Zoology  
University of Cambridge Downing Street Cambridge  
CB2 3EJ E: cm798@cam.ac.uk

\*Tsaobis Baboon Project Volunteer Field Assistants\*

The Tsaobis Baboon Project is a long-term study of desert baboons in Namibia. Based at the Institute of Zoology (the research arm of the Zoological Society of London), and affiliated with the Gobabeb Research and Training Centre (Namibia), our aim is to carry out fundamental research in behavioural ecology and population ecology, and to inform conservation policy and practice for social species.

We are seeking to appoint four 3-month volunteer field-worker positions between 1 July and 30 September 2015. The fieldwork will primarily involve daily follows of ba-

boon troops on foot, collecting behavioural data from individually recognisable animals and their associated ecological conditions. Further information about the Tsaobis Baboon Project, the volunteer fieldworker positions, and the application procedure can be found on the Project's webpages:

\*[www.zsl.org/science/research/baboon](http://www.zsl.org/science/research/baboon) \*The deadline for applications is 9am Tuesday 24th March 2015\*

claudia.martinala@gmail.com

## NESCent 2015 VideoContest 2

NESCent/HHMI/SSE Evolution Film Festival/Video Contest

Scientists and science educators of all stripes - students, postdocs, faculty, and full- or part-time science communicators - are invited to enter the Fifth Annual Evolution Video Competition, sponsored by the National Evolutionary Synthesis Center (NESCent), Howard Hughes Medical Institute (HHMI) and the Society for the Study of Evolution (SSE). To enter, please submit a video that explains a fun fact, key concept, compelling question, or exciting area of evolution research in THREE MINUTES OR LESS.

Entries may be related or unrelated to your own research, and should be suitable for use in a classroom (K-12, undergraduate, graduate...your choice). Videos should be both informative and entertaining. (In other words, no taped lectures or narrated Powerpoint presentations!) Animations, music videos, and mini documentaries are all fair game.

The finalists will be screened at the 2015 Evolution meeting in Guarujá, Brazil. (You do not need to attend the conference in order to enter a video.)

In the past, our first-place and runner-up prizes were \$1,000 credit and \$500 credit, respectively, towards travel to a future conference. This year, the prizes will be the same amount, but in cold, hard, cash-money, baby! (Well...actually, in the form of a check, but you get the idea.) So make a video, and we'll make it rain!

The deadline to submit your video(s) is SUNDAY, MAY 31st, 2015 (11:00 PM, EST).

For more information (and to see entries from previous years) please visit [filmfestival.nescent.org](http://filmfestival.nescent.org) or contact Jory Weintraub ([jory@nescent.org](mailto:jory@nescent.org)).

Jory P. Weintraub, PhD Assistant Director, Education

& Outreach National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200, Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: [jory@nescent.org](mailto:jory@nescent.org) Skype: jory.weintraub

"Weintraub, Jory P" <[lviscrst@live.unc.edu](mailto:lviscrst@live.unc.edu)>

## Omenn Prize winner announced

The \$5000 Gilbert Omenn prize for the best paper in evolutionary medicine in 2014 goes to, "Escape from bacterial iron piracy through rapid evolution of transferrin" by Matthew Barber and Nels Elde from the University of Utah. The article appeared in *Science* 346:1362-6, 2014. First author Matthew Barber, a postdoctoral student, will receive the prize and present a talk on March 21 at the 2015 ISEMPH meeting in Tempe Arizona. <http://evmedmeeting.org> The prize is made possible by a generous donation from Gilbert Omenn and is awarded by the International Society for Evolution, Medicine, and Public Health for best article published each year on a topic related to evolution in the context of medicine and public health. Full details at <http://evmedreview.com/?p=2504> and at <http://evolutionarymedicine.org>

The Prize Committee "Sarah Tishkoff, Joe Alcock, Noah Rosenberg, and Alison Galvani" also selected three papers for honorable mention. They are listed below in alphabetical order.

Byars, Sean G., Stephen C. Stearns, and Jacobus J. Boomsma. "Opposite risk patterns for autism and schizophrenia are associated with normal variation in birth size: phenotypic support for hypothesized diametric gene-dosage effects." *Proceedings of the Royal Society B: Biological Sciences* 281.1794 (2014): 20140604. been difficult to unravel using standard approaches.

Pennings, Pleuni S., Sergey Kryazhimskiy, and John Wakeley. "Loss and recovery of genetic diversity in adapting populations of HIV." *PLoS genetics* 10.1 (2014): e1004000.

Warinner, Christina, et al. "Pathogens and host immunity in the ancient human oral cavity." *Nature genetics* 46.4 (2014): 336-344.

Please join the Society in congratulating the authors of the winning and runner up articles. Nominations for next year's prize will be received starting early in 2016. The Society also sponsors the \$5,000 George C. Williams Prize for the best paper published each year

in the Society's flagship journal, *Evolution, Medicine and Public Health*. All papers published in the journal in 2015 will have author's fees waived and will be automatically entered into the Prize competition.

Randolph M. Nesse President, The International Society for Evolution, Medicine, & Public Health

rmnesse@gmail.com

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## RohlfMedal 2015 CallNominations

### 2015 CALL FOR NOMINATIONS

The Rohlf Medal

The Rohlf Medal was established in 2006 by the family and friends of F. James Rohlf to mark his 70th birthday. He has been a longtime Stony Brook University faculty member and is currently Emeritus Distinguished Professor in the Department of Ecology and Evolution, and Research Professor in the Department of Anthropology.

Recipients of the Rohlf Medal will be recognized for excellence in their body of work on the development of new morphometric methods or for their applications in the biomedical sciences, including evolutionary biology, population biology, physical anthropology, and medicine. The term 'morphometrics' is intended to include high-dimensional pattern analyses of biological shape, especially those that analyze shape in a comprehensive way, or of covariation of shape with other variables. The award can recognize advances in the mathematical or statistical theory underlying morphometric methods, new software that implements or visualizes new methods, or specific new biological findings that rely crucially on contemporary morphometric methods and represent major advances.

Candidates for the Rohlf Medal may be self-nominated or nominated by others. They must possess a Ph.D. degree or the equivalent.

The winning candidate must agree to attend the award ceremony in person in order to accept the Rohlf Medal and then deliver the award lecture.

Nomination packages should include,

- (1) a description of the body of work (not to exceed two pages) on which the candidacy is based,
- (2) reprints of no more than three relevant papers and/or software products,
- (3) a curriculum vitae, and

(4) the names and addresses of three referees.

Nominating packages should be uploaded to the Rohlf Medal website ([http://life.bio.sunysb.edu/ee/-rohlf\\_medal/apply.html](http://life.bio.sunysb.edu/ee/-rohlf_medal/apply.html)) and received by 5 pm, EST, 15 July 2015 to be assured of full consideration.

The successful candidate will receive the Rohlf Medal and a cash prize at Stony Brook University, planned for October 26th, 2015. She or he will deliver a lecture that is appropriate for a broad audience, ranging from the exact sciences to the humanities, concerning the morphometric methodology, software, or findings for which the Rohlf Medal was awarded

Paul O'Higgins Professor of Anatomy Centre for Anatomical & Human Sciences Department of Archaeology and Hull York Medical School University of York Heslington York YO10 5DD U.K.

T: +44 (0) 1904 328872 E: [paul.ohiggins@hyms.ac.uk](mailto:paul.ohiggins@hyms.ac.uk) W: <http://research.hyms.ac.uk/researchcentres/cahs> Paul O'Higgins <[Paul.O'Higgins@hyms.ac.uk](mailto:Paul.O'Higgins@hyms.ac.uk)>

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## SenseOfLife

Zimmer and Emlen's *Evolution: Making Sense of Life*, Second Edition

I'm pleased to announce that in August we'll be publishing the new edition of Carl Zimmer and Douglas Emlen's *Evolution: Making Sense of Life*. The second edition is thoroughly revised with new research and arresting illustrations and includes, free of charge, a study guide by Alison Perkins that helps students solidify their understanding of the key concepts of evolution.

The book has been highly praised. Neil Shubin (U. Chicago) says that "Zimmer and Emlen have produced a book that not only conveys the explanatory power of evolution, but is also permeated with the joy of doing science." Matthew Miller (UC Riverside) says "Zimmer is the master of taking current primary literature and making it come alive." Lena Strewe (Rutgers University) says "I think evolution has never before been presented with such clarity and in this engaging way to college students...."

If you teach an evolution course for biology majors, we'd be delighted to send you an exam copy. If you'd like to consider the book for the fall 2015 semester, please let us know so we can send you pre-publication materials. The book will be ready in plenty of time for fall classes.

Sincerely,

Ben Roberts

Ben Roberts <info@roberts-publishers.com>

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## SocSystBiology GraduateStudentAward

### SSB Graduate Student Research Award

The Society of Systematic Biologists (SSB) announces the 2015 annual Graduate Student Research Award competition. PROPOSAL SUBMISSION DEADLINE IS APRIL 24, 2015.

The purpose of these awards is to assist students in the initiation (FIRST TWO YEARS ONLY) of their systematics projects and in the collection of preliminary data to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but MUST be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: <http://systbio.org/?q=node/6>). Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply. Only students in their first two years of a degree program are eligible. Awards range between \$1200 - \$2000 and approximately 10-15 awards will be made.

How to Apply: applicants must submit

1. a curriculum vitae (maximum one page);
2. brief research proposal including objectives, methods, significance, and schedule (maximum of three single-spaced pages including literature cited and any figures and tables);
3. budget and budget justification (maximum one page);
4. and arrange for two reference letters; one letter must be from the student's current graduate advisor.

All application materials must be in electronic format. Applicants and those writing reference letters are required to use pdf format to minimize difficulties in file transfer. Applicants should send all materials (except reference letters) in a SINGLE pdf file. Letters of reference should be sent separately by the referees in pdf format or in the text of an e-mail; please include the FULL NAME OF APPLICANT in reference letters.

Please email all application materials and queries to Sean Brady, Chair of the SSB Awards Committee at

bradys@si.edu. IN THE SUBJECT LINE OF THE EMAIL, PLEASE INDICATE "Student Research" FOLLOWED BY FIRST INITIAL AND LAST NAME.

To be considered for this year's award, ALL application materials, INCLUDING letters of recommendation, must be received electronically no later than April 24, 2015.

Please see the SSB website (<http://systbio.org/?q=node/22>) for additional submission instructions. Questions via email may be addressed to Sean Brady (bradys@si.edu).

Sean Brady Awards Director Society of Systematic Biologists bradys@si.edu 202-633-0997

"Brady, Sean" <BRADYS@si.edu>

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## Software DAMBE update

Dear All,

I have uploaded a new version of DAMBE with three additional functions:

1. Phylogenetics with pairwise alignment: Pairwise alignment by dynamic programming is guaranteed to generate the optimal alignment (or at least one of them), but getting good multiple alignment is difficult with highly diverged sequences. One way to avoid this problem is to use pairwise alignment only to reconstruct phylogenetic trees. The greatest advantage of distance-based methods is in their capability to build trees based on pairwise alignment only, although this advantage is rarely realized because all major software packages for phylogenetic analysis do not implement this method. To access this function, read in a file with unaligned sequences, and click 'Phylogenetics|Phylogenetics with pairwise alignment'. The function incorporates pairwise alignment of nucleotide, amino acid or codon sequences with frequently used evolutionary distances (independently and simultaneously estimated distances based on F84 and TN93) and tree-building algorithms (UPGMA, neighbor-joining, FastME, etc.). This function should give you surprisingly good trees with highly diverged sequences (amino acid sequences are recommended for extremely diverged sequences). Keep in mind that, while distance-based methods are fast, pairwise alignment is slow.

2. I have added multiple correspondence analysis (MCA) for aligned short sequence motifs. These functions are



useful to identify site associations and can be accessed by clicking 'Bioinformatics|motif MCA'. You may also use 'Bioinformatics|Motif PCA' (for principle component analysis).

3. I have added more codon tables from more than 100 species to facilitate the use of the new Index of Translation Elongation which extended CAI to accommodate background mutation bias (Xia X. 2015. A major controversy in codon-anticodon adaptation resolved by a new codon usage index. *Genetics* 199:573-579)

For those not familiar with DAMBE, it is a comprehensive software package for data analysis in molecular biology and evolution, available free for Windows/Linux/Mac at: <http://dambe.bio.uottawa.ca/dambe.asp> Best Xuhua <http://dambe.bio.uottawa.ca> [http://www.biology.uottawa.ca/bio/professor\\_details.html?en/31](http://www.biology.uottawa.ca/bio/professor_details.html?en/31) Xuhua Xia Professor Biology Department University of Ottawa Rm 278 Gendron 30 Marie Curie, Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886

Xuhua Xia <Xuhua.Xia@uottawa.ca>

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## Transport blood samples

Dear all,

I would very much appreciate some pointers for how to transport blood samples stored in ethanol internationally (from UK to New Zealand). I had been intending to bring a chilly bin full of samples on dry ice\* / ice packs on a flight from the UK to New Zealand with me, however I have recently become aware that many (all?) airlines classify ethanol as a dangerous good\*\* and restrict the total volume that can be checked in. According to FAA guidelines (which I'm not sure apply globally, but Air New Zealand's guidelines seem very similar) I think you are not allowed more than 1L of total ethanol.

>From what I have read, the alternative is to send as a dangerous good with one of the international carriers e.g. Fedex, however this is likely to be prohibitively expensive. An online quote suggests the chilly bin we have in mind would cost around NZD \$2,500 to transport, and this is before I've even mentioned the 'hazardous' contents.

Any help would be very much appreciated!

With many thanks, Anna Santure University of Auck-

land, New Zealand

\*also a dangerous good... \*\*apparently litres of duty free gin, vodka, wine and rum are not dangerous goods though!

asanture@gmail.com

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## Transport blood samples answers

Dear all, I would like to thank all of you in the evoldir community for your very helpful replies to my question on sending blood samples in ethanol internationally. We are still deciding exactly what to do, but I had some very good suggestions to send the blood+ethanol by courier (or even normal post) without the dry ice / ice packs, which would mean the packaging would be much smaller and lighter and hence cheaper. Provided IATA guidelines are followed\*, some people had good experience taking samples as checked luggage, however it was pointed out to me that in the end the pilot has a final decision of whether to accept the luggage, even if all of the paperwork is in order (which could end up with quite a stressful experience at the airport!). Others had suggestions for alternative storage solutions including lysis buffer and RNAlater. And I had many people emphasising the importance of checking the regulations and ensuring that all the paperwork at both ends of the journey is prepared thoroughly. I have compiled all the replies below, following a copy of my initial message. Thank you again for your excellent ideas! Very best wishes, Anna asanture@gmail.com

\*from my understanding, in my case where we have eppendorfs of ~1mL of blood, these should be put in a hard container (i.e. an eppendorf box), sealed in a plastic bag, an absorbant material wrapped around and then sealed inside another plastic bag, and then up to 10 of these boxes (i.e. <1L total ethanol) can be packaged together to form one package for either posting via airmail or checking in as checked luggage. Airline's own guidelines may differ.

\*Original email: \* I would very much appreciate some pointers for how to transport blood samples stored in ethanol internationally (from UK to New Zealand). I had been intending to bring a chilly bin full of samples on dry ice\* / ice packs on a flight from the UK to New Zealand with me, however I have recently become aware that many (all?) airlines classify ethanol as a dangerous good\*\* and restrict the total volume that can be checked in. According to FAA guidelines (which I'm not sure

apply globally, but Air New Zealand's guidelines seem very similar) I think you are not allowed more than 1L of total ethanol.

>From what I have read, the alternative is to send as a dangerous good with one of the international carriers e.g. Fedex, however this is likely to be prohibitively expensive. An online quote suggests the chilly bin we have in mind would cost around NZD \$2,500 to transport, and this is before I've even mentioned the 'hazardous' contents.

Any help would be very much appreciated!

With many thanks, Anna Santure University of Auckland, New Zealand

\*also a dangerous good... \*\*apparently litres of duty free gin, vodka, wine and rum are not dangerous goods though!

\*Responses - thank you all again!\* # I can only tell you something you probably won't like so much: my experience is to best leave it to a carrier, which is indeed expensive. I use World Courier a lot, much more reliable than FedEx or DHL etc. they are known to lose a lot of their packages, I would not risk that. Dry ice/ ice packs are usually not permitted on flights and I can only say the very best about World Courier, they are fast and professional, which you can see in their prices :( contact their office and ask about prices, but you can expect about double than FedEx. I guess it really depends on how valuable those samples are, but they know how to handle transport and customs.

# I've flown with ethanol samples several times before. The easiest thing to do is to pour off as much of the ethanol as possible before transporting them and then top them up once you arrive at your destination. Of course, this is a lot easier if the sample is tissue - I'm not quite sure how it would work with blood. Perhaps you could spin them down and pour the top ethanol layer off and then just transport them as blood samples'?

# About your question, depending on how serious the checks you think will be and how important/unique are the samples, you could decide to just put them in your checked luggage (maybe paying also for an extra luggage) and cross your fingers. In case the material you're transporting needs some sort of permit to be exported from the UK or imported in NZ, make sure you have one so that in case of problems you can always show them the documents. Otherwise, you can always have some sort of official letter. I doubt they'll be willing to stick their face in blood samples to check if they're in ethanol. At that point they'll be more concerned if you're bring-

ing some sort of bio-hazard rather than the ethanol. So the idea is: you put them in your luggage and then you have some official document stating that those samples are safe and you're allowed to transport them. I know this is not exactly sticking to the rules but I know some people who have done this in inter-continental flights.

— / —

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

## UMichigan BioStation SummerResearch

The University of Michigan Biological Station (UMBS) is pleased to offer the Project CLEAR Fund Fellowship for summer 2015. We are North America's largest inland field station and are situated in the heart of the Great Lakes.

<http://lsa.umich.edu/umbs/students/-studentresearchopportunities/-studentresearchfellowships>

ELIGIBILITY: Graduate or undergraduate students who will conduct independent research on freshwater ecosystems (e.g. water quality improvement, ecosystem protection or stewardship, or freshwater sustainability); involve/engage local communities in their research/research findings; and enroll concurrently in 1 summer session field class at UMBS. (<http://lsa.umich.edu/umbs/students/courses>)

SUPPORT: This fellowship provides room, board, research fees and supplies at UMBS. The Tip of the Mitt Watershed Council is participating with UMBS to help fellows find and engage appropriate communities.

A note about course enrollment: This fellowship does not cover tuition for the field class. However, we have separate financial aid for students taking classes for which you should apply.

TO APPLY: Send resume and letter of interest to UMBS Associate Director Karie Slavik, [slavik@umich.edu](mailto:slavik@umich.edu).

DEADLINE: Friday, April 3, 2015.

[farmeral@umich.edu](mailto:farmeral@umich.edu)

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## PostDocs

AMNH NewYork BioinformaticsComputationalBiology 75	UEastAnglia Bioinformatics ..... 95
ClemsonU ComputationalGenomics ..... 76	UFlorida AppliedEvolutionaryPhysiology ..... 96
DesMoinesU Paleobiology ..... 77	UHaifa PhD PDF Phylogenetics ..... 97
HarvardU BioMath InfectiousDisease HIV ..... 78	UJyvaskyla HumanSocialBehavior ..... 97
IBG2 Germany CropEvolutionDomestication ..... 78	ULausanne Bioinformatics ..... 98
IISER-TVM Kerala India EvolutionaryEcol ..... 79	UManchester TraitVariationGenetics ..... 99
ImperialCollegeLondon SpeciationPopulationGenomics 79	UMissouri DinosaurCranialBiomechanics ..... 100
KielU MicrobialEvolutionaryGenomics ..... 80	UMontana EvolutionaryGenomics SexualSelection 100
Lausanne GenomicsSocialPolymorphism ..... 81	UNamur Belgium Bioinformatics ..... 101
Lyon Epigenetics GenomeStability ..... 81	UNewEngland Australia PlantSpeciationGenomics 102
MonashU EvolutionaryGenetics ..... 82	UNewHampshire BeeSociogenomics ..... 103
MonashU TelomereEvolution ..... 82	UNotreDame MalariaComputBiol ..... 103
MountSinai StatisticalGenomics ..... 83	UOregon BioinformaticsHostMicrobe ..... 104
NorthCarolinaStateU MosquitoPopGenetics ..... 83	UOregon MicrobialEcology Bioinformatics ..... 105
OklahomaStateU ComputationalQuantitativeGenomics 84	UOregon MicrobialEcologyEvolution ..... 105
OmahaZoo MadagascarBiodiversityGenomics ..... 85	UOslo 3yr AvianHybridization ..... 106
Oslo FungalMolecularEvol ..... 86	UOtago EvolutionaryGeneticsZosterops ..... 106
PennsylvaniaStateU CoralEvolution ..... 86	UOtago NZ GenomicsComplexCognition ..... 107
PurdueU SalmonidEvolution ..... 86	UOulu PopulationStatisticalGenomics ..... 108
QUT Brisbane Australia MammalEvolution DNA mor- phologyFossils ..... 87	UPernambuco Brazil EvolutionaryBiol ..... 108
Rostock Germany Bioinformatics ..... 88	UPittsburgh Plant-PollinatorInteractions ..... 109
SangerInst ParasiteGenomics ..... 88	USDA ARS Gainesville PopulationGenomics ..... 109
Senckenberg Frankfurt CommunityEvolution ..... 89	USheffield PlantPopGenomics ..... 110
SLU Sweden PlantPathogenEvolution ..... 90	UToledo FishGenomics ..... 110
SwanseaU SalmonEpigenetics ..... 90	UUtah Evolutionary GeneticsGenomics Development 111
Toronto PopulationGenomics ..... 91	UUtah HerbivoreMicrobiomeBiodiversity ..... 111
UAberdeen AvianMatingSystems ..... 91	UUtah PlantAnimalMolEvol ..... 112
UARizona 2 GenomicsInvasivePlantAdaptation .... 92	UVermont LoyolaU ChagasGenomics ..... 112
UBath EvolutionaryGenomics SocialMicrobes ..... 93	UVirginia EvolutionaryGenomics ..... 113
UCDavis DevelopmentalEvolutionaryGenomics .... 93	UWashington PlantFrugivoreCoevolution ..... 114
UChicago EvolutionaryGenomics ..... 94	UWisconsin Madison PlantQuantGenet ..... 114
UCollege London TetrapodEvolution ..... 94	Vienna 6 EvolutionaryBiology ..... 115
	Wageningen MicrobialSyntheticBiol ..... 116

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### AMNH NewYork Bioinformatic- sComputationalBiology

American Museum of Natural History Postdoctoral Fellowships in Bioinformatics and Computational Biology

The American Museum of Natural History seeks highly qualified applicants for its Gerstner Postdoctoral Fellows program in Bioinformatics and Computational Biology. Successful applicants must be able to work effectively in applying innovative techniques to pursue independent and collaborative bioinformatics and computational research in integrative studies of genomics or spatial bioinformatics or biodiversity informatics, alongside faculty and other researchers interested in phylogenetics, phy-

logeography, evolutionary studies, and phenomics (the use of high-throughput computational methods to analyze morphological, physiological, and other phenotypic form and function). Fellows also will participate in the design, development and implementation of new algorithms, bioinformatics tools and infrastructure and computational methods to facilitate genomic assemblies and analyses, as well as developing methods to catalyze ongoing synthesis of phylogenetic information and address 'big data' issues from a computational perspective.

A portion of each Fellows' efforts also will include: 1) teaching, training and workshops, 2) research collaboration with and assistance to faculty, postdoctoral fellows, students, and other Museum colleagues in accessing including data storage, retrieval, and assembly; and 3) maintaining software and related resources.

The initial appointment will be for one year, potentially renewable for one to two additional years based on performance.

**Requirements:** Applicants must have a PhD in Biological Sciences, Bioinformatics, Computational Biology, Computer Science, Molecular Biology, Genomics, or a related discipline, with experience in computational biology, bioinformatics, creating databases and computational pipelines, and analysis of large biological data sets. Proficiency in programming and scripting required (ideally Python, Perl, and R), and familiarity with other languages, such as mysql, C++/C, or Java, is desirable. For bioinformatics and computational biology tool development, candidates should have documented skills in various areas of expertise, such as next-generation sequence processing (quality screening and error correction), de novo and reference guided assembly for non-model eukaryotic whole genomes and transcriptomes, read mapping, gene annotation and discovery, and/or processing phenomic, transcriptomic, and phylogenomic datasets. Experience in a bioinformatics setting and in operating and maintaining high performance linux/unix servers preferred. Candidates should have extensive research experience with a solid publication record, ideally with some experience in phylogenetic methods, and excellent interpersonal, writing and problem-solving skills.

**Application:** Applicants should submit the following materials electronically, preferably as PDF files, via a single email message to Gerstnerbioinfopostdoc@amnh.org (Subject line: 2015 Gerstner Bioinformatics-Computation Postdoc: your name): 1) a cover letter in which you indicate your interest, experience, and qualifications for the position; 2) a short (2-4 page) prospectus of the type of research project(s) and bioinformatics-computational biology tools you propose to develop during the postdoctoral appointment, 3) a

curriculum vitae, with names of at least 2 references; and 4) PDF files of up to five recent publications, or other documentation of relevant accomplishments in bioinformatics/computational biology. Applicants also must arrange for 2 academic reference letters to be sent by the due date to Gerstnerbioinfopostdoc@amnh.org (Subject line: 2015 Gerstner Bioinformatics-Computation Postdoc Reference Letter: applicant name). DUE DATE: April 27, 2015.

The American Museum of Natural History is an Equal Opportunity/ Affirmative Action Employer. The Museum encourages Women, Minorities, Persons with Disabilities, Vietnam Era and Disabled Veterans to apply. The Museum does not discriminate due to age, sex, religion, race, color, national origin, disability, marital status, veteran status, sexual orientation, or any other factor prohibited by law.

Anna Manuel <amanuel@amnh.org>

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## ClemsonU ComputationalGenomics

Computational Genomics Postdoctoral Research Associate Position Clemson University

The Lawton-Rauh Lab is recruiting a computational genomics postdoctoral research associate to join the RosBREED team on the newly-funded RosBREED2 project ([www.rosbreed.org](http://www.rosbreed.org); USDA-Specialty Crops Research Initiative, 5 years). The RosBREED team is an extensive collaboration amongst computational scientists, breeders, geneticists, physiologists, pathologists, and socio-economists. A major goal of this project is to translate genome evolution and diversity/divergence amongst cultivars and wild relatives into modern DNA-based diagnostic tools to help deliver new cultivars with combined superior horticultural quality and disease resistance.

This computational genomics scientist will be based at Clemson University to work with Amy Lawton-Rauh as postdoctoral advisor. Resources will include the Institute for Translational Genomics (Stephen Kresovich), the CU-Genomics and Computational Biology Lab (Chris Sasaki), and research computing training opportunities (<http://citi.clemson.edu/ciprac/>). This position is targeted to begin late spring/early summer 2015 and is currently funded for two years.

**Activities:** The major research focus for this postdoc will be on comparative genomics analysis of domestication-

related genome regions plus locus-specific and genome-wide haploblock discovery and diagnostic tool implementation and optimization. This post has several specific, cutting-edge objectives for basic research-enabled tool development to successfully achieve goals of this grant coupled with excellent opportunities for other related exploratory projects. Scientific publications, extension articles, participation in conferences and project meetings, and networking across breeding programs and allied science programs both U.S-wide and internationally are expected.

Job functions: \* Work with the CU-GCBL web portal computational genomics group to collate and curate relevant genome sequence data from multiple platforms  
\* Employ and optimize comparative analytical methods to discover haplotype blocks (haploblocks) in cultivars, diverse germplasm, and wild relatives  
\* Actively participate in networking and project team activities (including extensively with the international RosBREED group)  
\* Communicate results in multiple formats (journals, conferences, project reports, plus miscellaneous relevant media)

Qualifications: Applicants must have a Ph.D. in Genetics, Bioinformatics, Genomics, Computational Biology, Biological Sciences, Crop Sciences, or a closely related field. The successful candidate will be a highly motivated team player with excellent communication skills and computational genomics experience. Preference will be given to candidates with evidence of successful management and documentation of large datasets and a strong publication record. Experiences with complex genomes, diverse sequencing platforms, workflow implementation and optimization, creative problem-solving, and a commitment to translation of genome dynamics models to practical applications are highly desired. Familiarity with the following is advantageous but not required: statistical genetics, population and quantitative genetics, and domestication processes.

Pay & work schedule: Standard hours: 37.5. Salary will be commensurate with credentials and experience. This position is funded for two years.

Applying: If you are interested in this position, please send inquiries to Amy Lawton-Rauh (amylr@clemson.edu). To apply, email the following: a cover letter, current CV, and the contact information (phone number and email address) of three referees.

Consideration of applications will begin immediately and will continue until the position is filled. To ensure full consideration, please submit materials by April 3, 2015. Applications will be reviewed as received and qualified applicants will be invited to interview on or after April 3, 2015 or until the position is filled.

JOB LOCATION: Biosystems Research Complex (BRC) - Clemson Main Campus

The Jeanne Clery Disclosure Act requires institutions of higher education to disclose campus security information including crime statistics for the campus and surrounding areas. As a current or prospective Clemson University employee, you have a right to obtain a copy of this information for this institution. For more information regarding our Employment, Campus Safety and Benefits, please visit the Human Resources-Prospective Employees web page below: <http://www.clemson.edu/-cao/humanresources/prospective/> Clemson University is an Affirmative Action/Equal Opportunity employer

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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>

## DesMoinesU Paleobiology

Paleobiology postdoc position to start early Summer 2015. Des Moines University, Des Moines, IA

Description: Applications are now being accepted for a postdoctoral scholar for an NSF-funded project on Natural Trap Cave to start in early Summer 2015. This 2-year postdoctoral position will be based in Des Moines, IA at Des Moines University with PI Julie Meachen. The postdoc will be working with the field site of Natural Trap Cave, Wyoming. Duties will include being the field manager for 3 weeks each year at the field site, this includes organizing and appointing duties in the camp, and overseeing the crew during paleontological field work. The postdoc will also travel to Lawrence Livermore Laboratories in the Bay Area of California to analyze AMS radiocarbon samples (this will be about 1 month per year on-site in Livermore), a living stipend will be offered to defray these costs. When not at the Wyoming camp or in California, the postdoc will be based at Des Moines University and will work with the PI on morphology-based projects related to Natural Trap Cave. There will also be time for the postdoc to work on independent research projects and with students. If desired, the candidate may also obtain some human gross anatomy laboratory experience.

Qualifications include a Ph.D. in a paleo-related field (Biology, Geology, or Anthropology), with a degree in

hand no later than July 1, 2015. Field experience is required, and the candidate should have the ability to do rigorous fieldwork (rappelling and ascending 85 feet). Experience with AMS radiocarbon dating is a plus, but not a requirement. Experience using R programming language is also viewed positively. The candidate must be willing to travel for 2 months a year and be able to work independently.

Des Moines University ([www.dmu.edu](http://www.dmu.edu)) is a private, non-profit, osteopathic medical college. Des Moines University is the second oldest osteopathic medical school and the fifteenth largest medical school in the United States. It offers Doctorate degrees in Osteopathy, Physical Therapy, and Podiatry and Master's degrees in Biomedical Sciences, Health Care Administration, Physician's Assistant Studies, and Anatomy. It is located in the heart of Des Moines, IA, an affordable city, which offers the amenities of a bigger city with the convenience of a small town. It was voted Forbes Magazine "Best City for Young Professionals" in 2014. More about Des Moines can be found here: <http://www.dmgov.org/Pages/default.aspx>. To Apply: Please send an email including a CV and research statement to Julie Meachen at [julie.meachen@dmu.edu](mailto:julie.meachen@dmu.edu). Please direct questions about the position to the same email. Initial screening of applicants will begin immediately and will continue until the position is filled.

Julie Meachen, Ph.D. Assistant Professor Anatomy Department Des Moines University 3200 Grand Ave. Des Moines, IA 50312 Office: 515-271-1568 Fax: 515-271-4252

"Meachen, Julie" <[Julie.Meachen@dmu.edu](mailto:Julie.Meachen@dmu.edu)>

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### HarvardU BioMath InfectiousDisease HIV

Postdoctoral Fellow position, Mathematical Modeling of Infectious Disease, Harvard University, Boston, MA, USA

The Program for Evolutionary Dynamics at Harvard University welcomes applications for a postdoctoral fellow to work in the field of infectious disease modeling with Dr. Alison Hill and Professor Martin Nowak. We are seeking a motivated and creative PhD-level scientist with experience applying mathematics to biological systems. The successful candidate would be invited to work on established projects, as well as be encouraged to pursue independent research of mutual interest.

A major focus of the group is on an NIH-funded effort to develop mathematical models to predict the outcomes of new, potentially-curative treatment strategies for HIV infection. We also use viral dynamic models to understand outcomes of antiretroviral therapy, the risks of drug resistance, the influence of patient adherence, and the potential impact of new drug delivery mechanisms. We regularly work with data from experimental collaborators testing new therapies in vitro, in animal models, and in patients. More generally, we are interested in factors influencing the evolution of infectious diseases and the emergence of drug resistance, both at the individual and population levels. Our work is conducted in close collaboration with experimental and clinical researchers.

More information about the position can be found at : <https://academicpositions.harvard.edu/postings/-6053> Inquiries can be directed to Alison Hill ([alhill@fas.harvard.edu](mailto:alhill@fas.harvard.edu))

[alhill@fas.harvard.edu](mailto:alhill@fas.harvard.edu)

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### IBG2 Germany CropEvolutionDomestication

/A one-year Research Fellowship on 'Crop Evolution and Domestication' for a Postdoctoral Researcher and sponsored by the Università Politecnica delle Marche, will be published soon (<http://www.univpm.it>). This will be spent at the Forschungszentrum Juelich GmbH, Institute of Bio and Geo Sciences, IBG2 Plant Sciences (<http://www.fz-juelich.de/>), in Germany. For more information please contact the Project Leader: Prof. Roberto Papa ([r.papa@univpm.it](mailto:r.papa@univpm.it)).

Prof. Roberto Papa Università Politecnica delle Marche D3A-Dipartimento di Scienze Agrarie, Alimentari e Ambientali, Via Breccie Bianche, 60131 ANCONA ITALY phone +39-0712204984/280 mobile +39-3393921616 email: [r.papa@univpm.it](mailto:r.papa@univpm.it) <http://publicationslist.org/r.papa> [www.univpm.it/~roberto.papa](http://www.univpm.it/~roberto.papa) <http://orcid.org/0000-0001-9598-3131> Roberto Papa <[r.papa@univpm.it](mailto:r.papa@univpm.it)>

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## IISER-TVM Kerala India EvolutionaryEcol

POSTDOCTORAL POSITION AT IISER-THIRUVANANTHAPURAM, KERALA, INDIA.

A postdoctoral position in Evolutionary Ecology is available at IISER Thiruvananthapuram, Kerala, India, in the Vanasiri Evolutionary Ecology Group of Ullasa Kodandaramaiah ([www.vanasiri.in](http://www.vanasiri.in))

**DEADLINE:** Screening of applications will start April 30th, but will continue until a suitable candidate is found.

**SALARY:** Rs. 43,200 - 48,000 per month (including Housing Rent Allowance; commensurate with experience)

**RESEARCH SUBJECT(S):** Our research group works on various questions within evolutionary ecology including prey-predator interactions, insect-hostplant co-evolution, parasite-host co-evolution, biogeography, phylogeography, population genetics, etc. More information at [www.vanasiri.in/research](http://www.vanasiri.in/research). Currently used model systems include different insects (primarily butterflies), plants and reptiles.

Collaborations with candidates who can design projects that complement ongoing work in the group are welcome. I also welcome collaborations with candidates through projects on new kinds of questions, and/or new model organisms, which will enrich research in our group. The permanent campus of IISER Thiruvananthapuram is an outstanding location (see [www.vanasiri.in/facilities](http://www.vanasiri.in/facilities)) for ecological and evolutionary studies.

You are encouraged to contact me informally ([ullasa@iisertvm.ac.in](mailto:ullasa@iisertvm.ac.in)) to discuss your ideas and their feasibility before sending in your formal application.

**SELECTION:** Selection will be based on the scientific credentials of the candidate (needless to mention, a PhD is a must), quality of the research proposal and feasibility of carrying out the research proposal. The formal advertisement, including details about how to apply is here [http://iisertvm.ac.in/openings/read\\_opening/115](http://iisertvm.ac.in/openings/read_opening/115)

**DURATION:** The initial contract will be for 1 year, but can be extended to 2 years based on performance. The selected candidate is expected to join as soon as possible.

LIFE IN KERALA AND THIRUVANANTHAPURAM

(TRIVANDRUM): The coastal city of Thiruvananthapuram is the capital of Kerala, and has a rich cultural heritage. It is within a stone's throw away from world-famous beaches such as Kovalam and Varkala, and lovely backwater tourism areas such as Poovar. Several hill stations (e.g Ponmudi) and wildlife sanctuaries are close by. Being a major medical tourism destination, the city has excellent medical care facilities.

It is a relatively small city, and the cost of living tends to be considerably lower than in bigger Indian cities. A 2-bedroom apartment can be had for Rs 8,000 - 10,000 per month. There are plenty of options for dining out - a meal at a decent local restaurant can start from Rs 50, but a good meal with a drink even in a five-star hotel usually costs less than Rs 1000. Costs for groceries and other daily needs can be looked up here ([www.kada.in](http://www.kada.in)). Taxis can be hired from Rs 10 per km (with a minimum fare of Rs 50), while the cost of driving your own small car (not for the faint-hearted!) is about Rs 5 per kilometer (petrol: Rs 67/litre, diesel: Rs 55/litre).

Ullasa Kodandaramaiah [ullasa@iisertvm.ac.in](mailto:ullasa@iisertvm.ac.in)

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## ImperialCollegeLondon SpeciationPopulationGenomics

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Postdoctoral Research Associate in Evolutionary Genomics

Department of Life Sciences, Imperial College London, United Kingdom.

Salary: £33,410 - £42,380 per annum (maximum starting salary £35,190 per annum)

Closing date: 24 April 2015 (midnight BST)

This is an exciting opportunity for a Research Associate with interests in speciation and evolution. The successful candidate will carry out cutting edge research on the genetic mechanisms of ecological speciation in a well-known group of anciently asexual animals, the bdelloid rotifers. You will sequence whole genomes for related bdelloid species living in different habitats and use population genomic analyses to test alternative mechanisms behind their divergence. The work will involve bioinformatics, statistical methods in population genomics and

computer models. You will work closely with a Research Technician who will conduct molecular labwork.

The position is funded for up to 3 years by the Natural Environment Research Council and will be based at the Silwood Park Campus. The successful candidates will work closely with Professor Tim Barraclough and his research group.

You must have a PhD or equivalent qualification in evolution, ecology, genetics or a closely related discipline, and one or more first author (or joint first author) publications. The successful candidate will have expertise in population genomics and/or statistics and modelling with a strong interest in evolutionary biology. Experience of bioinformatics including scripting and/or programming is essential. While not essential, experience of handling and archiving large datasets and experience of genome assembly and/or population genomics analysis, would be an advantage.

You must have experience of working in a team, be able to develop and apply new concepts and have a creative approach to problem-solving. You must also have excellent verbal and written communication skills and be able to write clearly and succinctly for publication.

Further details of the research group can be obtained from the research group website: <http://www3.imperial.ac.uk/people/t.barraclough>. For more information or with queries, contact Tim Barraclough at [t.barraclough@imperial.ac.uk](mailto:t.barraclough@imperial.ac.uk).

Our preferred method of application is online via our website <http://www.imperial.ac.uk/employment> (please select "Job Search" then enter the job title or vacancy reference number including spaces - NS 2015 053 JT into "Keywords"). Please complete and upload an application form as directed.

Alternatively, if you are unable to apply online, please contact Mrs Christine Short on 020 7594 2276 or email [c.j.short@imperial.ac.uk](mailto:c.j.short@imperial.ac.uk) to request an application form.

Closing date: 24 April 2015 (midnight BST)

Committed to equality and valuing diversity. We are also an Athena SWAN Silver Award winner, a Stonewall Diversity Champion, a Two Ticks Employer and are working in partnership with GIRES to promote respect for trans people.

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Prof. Timothy G. Barraclough, Professor of Evolutionary Biology

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Department of Life Sciences, Imperial College London, Silwood Park Campus, Ascot, Berkshire, SL5 7PY, UK  
E-mail: [t.barraclough@imperial.ac.uk](mailto:t.barraclough@imperial.ac.uk) Telephone: +44

(0)207 594 2247 Fax: +44 (0)207 594 2339 Web-page: [www.imperial.ac.uk/people/t.barraclough](http://www.imperial.ac.uk/people/t.barraclough) –Apple-Mail=\_7AE1A3EE-185A-4316-A805-BAEC39417C6B  
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## KielU MicrobialEvolutionaryGenomics

The Genomic Microbiology Group at the Institute of Microbiology in Christian-Albrechts University of Kiel, Germany, invites applications for:

Postdoc Position in Microbial Evolutionary Genomics

The Genomic Microbiology Group research interests are focused on microbial genome evolution with an emphasis on the study of DNA acquisition dynamics in natural environments. In our research we use both computational and experimental approaches (see <http://www.mikrobio.uni-kiel.de/de/ag-dagan>). The working language of the group is English.

The position offers the opportunity to develop an independent research profile within the group research focus. In addition, the successful applicant is expected to consult MSc and PhD biology students in the analysis of genomic data and participate in teaching of genomics and programming (PERL/Python).

Candidate qualifications: (1) Doctoral or PhD degree in Molecular Evolution, Bioinformatics or related fields; Post-Doctoral work is an advantage. (2) Knowledge and experience in the analysis of genomic data. Any of following expertise is an advantage: phylogenomics, genomics, transcriptomics, programming, biostatistics. (3) Good oral and written communication skills (English is required, German a plus). (4) Skills and motivation to communicate and interact with other scientists.

Applicants should upload curriculum vitae with a list of publications, a motivation statement and contact addresses of two referees to <https://bewperle.uni-kiel.de/-ifam/>. For enquiries regarding the position please contact Prof. Tal Dagan, email: [tdagan@ifam.uni-kiel.de](mailto:tdagan@ifam.uni-kiel.de)

The position is initially offered for two years at the German TV-L E13 pay scale and may be extended up to four years.

Application deadline: 15.04.2015 or until the position is filled. Interviews will take place during April-May 2015. The planned starting date for the position is July 2015.

Prof. Dr. Tal Dagan



Genomic Microbiology Group Institute of Microbiology  
Christian-Albrechts-University Kiel ZMB, Am Botanischen  
Garten 11 24118 Kiel, Germany

Tel: +49 431 880 5712 Fax: +49 431 880 5747 e-mail:  
tdagan@ifam.uni-kiel.de web: <http://www.mikrobio.uni-kiel.de/de/ag-dagan> tdagan@ifam.uni-kiel.de

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## Lausanne GenomicsSocialPolymorphism

POSTDOCTORAL POSITION, ECOLOGICAL GENOMICS OF SOCIAL POLYMORPHISM, 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.

We have identified a social chromosome associated with variation in colony queen number in the Alpine silver ant *Formica selysi* (Purcell et al. *Cur. Biol.* 2014). We plan to study the origin and maintenance of this polymorphism by combining 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 and genomics. Experience in one or more of the following areas would be an asset: population genomics, comparative genomics, genotyping-by-sequencing, transcriptomics, evolutionary ecology, experimental behavioural ecology.

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.

Michel Chapuisat

Department of Ecology and Evolution Biophore,  
Quartier Sorge University of Lausanne CH-1015 Lau-

sanne Switzerland

Office: 3123, Biophore Phone: +4121 692 41 78 Web-  
site: <http://www.unil.ch/dee/page7642.html> Michel  
Chapuisat <Michel.Chapuisat@unil.ch>

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## Lyon Epigenetics GenomeStability

\*Post Doctoral position in epigenetics and genome stability, Lyon\*

We are welcoming applications from enthusiastic and independent post-doctoral candidates to participate in our FRM grant-funded project related to epigenetics and genome stability. The fellowship is for 2 years and should start before June 2015. Applications are accepted until the end of March.

\*Background\*

Genomic stability can be disturbed by the activity of repeated sequences such as transposable elements (TEs). Epigenetic mechanisms allow the silencing of these sequences. As a consequence, the presence of TEs in a genome may affect the chromatin structure of the regions in which they are inserted. Environmental factors have also been described as affecting genome stability, namely by affecting the rate of transposition, and could be associated with environment related diseases such as cancer. \*\*

\*Project\*

The purpose of the project is to establish the link between TEs, environment and epigenetics. *Drosophila* is one of the best-fitted model for this project since we have an easy access to *Drosophila* natural variability, the species genome is small and harbors low amounts of TEs, and it is easily manipulated in the lab. The project consists in the analysis of *Drosophila* responses to stress by analyzing chromatin structure, piRNA abundances and mRNA levels, with an emphasis on TEs.

\*Candidates\*

The applicants are expected to have a strong background in epigenetics with a confirmed interest in genomics and evolutionary biology. Skills in data analysis and/or bioinformatics are necessary, but the candidate will benefit from the LBBE bioinformatics and statistical environment. The ideal candidate should be highly motivated, curious and enthusiastic to work in a collaborative team. Proven ability to identify research objectives and meet agreed deadlines, self-motivation and flexibility are es-

sential. Excellent written and oral skills in English are required.

**\*Environment\***

The host laboratory (LBBE, <http://lbbe.univ-lyon1.fr/>) is a stimulating, cosmopolitan and pleasant place to work, where one can meet biologists, computer scientists, mathematicians and statisticians working on problems that range from ecology to medicine, through genomics and evolution. Lyon is the second largest city in France, is famous for its food, is a UNESCO World Heritage site and enjoys a very convenient central location in Europe.

Please send one PDF file to

Cristina Vieira [cristina.vieira@univ-lyon1.fr](mailto:cristina.vieira@univ-lyon1.fr)  
<<mailto:cristina.vieira@univ-lyon1.fr>>

including:

- a cover letter
- a concise summary of previous research activities (2 pages max) - a curriculum vitae including publication list - contact details for 2-3 referees
- Cristina Vieira Institut Universitaire de France Laboratoire de Biométrie et Biologie Evolutive UMR CNRS 5558 Université Lyon 1 43 bd du 11 novembre 1918 69622 Villeurbanne cedex Tel. 04 72 43 29 15 <http://lbbe.univ-lyon1.fr/-Equipe-Elements-transposables-.html> Cristina Vieira <[cristina.vieira@univ-lyon1.fr](mailto:cristina.vieira@univ-lyon1.fr)>

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## MonashU EvolutionaryGenetics

Postdoctoral opportunities are available to work with Tim Connallon, in Monash University's School of Biological Sciences (Melbourne, Australia). I have broad research interests in evolutionary genetics, including the following areas:

- The role of genetic constraints in adaptation - The evolution of sexual dimorphism - Sex chromosome evolution
- Population genetic signals of adaptation - Adaptation with gene flow - Theoretical population genetics

Current research in my group combines theory development, analyses of publicly available datasets, and quantitative genetics experiments using *Drosophila*.

I am interested in theoretical and empirical projects that fit within the general areas mentioned above. There is considerable flexibility regarding the specific projects that may be undertaken, and these will ideally be designed in collaboration with the successful candidate.

The successful candidate should have a PhD in biology or a related discipline, a solid track record of independent scholarship, including high-quality publications, and good written and verbal communication skills. Strong quantitative or computational abilities are a plus. Two years of support is guaranteed, provided satisfactory progress is met, and there are good opportunities for extended support beyond the first two years. The position is at the postdoctoral academic level A, with starting salary of ~\$75K per year AUD.

The School of Biological Sciences at Monash houses a diverse and interactive group of academics, and the school provides a stimulating and supportive environment for carrying out research in ecology, evolution and genetics. Opportunities are excellent for scientific collaboration, for mentorship, and for developing an independent research program. For more information about the school, see: <http://www.monash.edu/-science/schools/biological-sciences> Interested candidates should please send a letter of research interests and a CV to [tim.connallon@monash.edu](mailto:tim.connallon@monash.edu). Informal queries are encouraged at this time. Instructions for formal application through the Monash University system will follow in a subsequent post.

[tim.connallon@monash.edu](mailto:tim.connallon@monash.edu)

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## MonashU TelomereEvolution

Post-doctoral RESEARCH FELLOW: Quantitative molecular ecologist Monash University (Melbourne, Australia) to study ecology of telomere dynamics in fairy-wrens Application deadline: 28 March 2015 Start date: between April and Sep 2015

Anne Peters at Monash University, Melbourne, Australia, in collaboration with Simon Verhulst, Groningen University, The Netherlands, is seeking an experienced Quantitative Molecular Ecologist to explore the ecology of molecular senescence (telomere attrition). Telomeres shorten as organisms age and short telomeres are associated with greater predisposition to diseases, accelerated organismal senescence and shorter lifespan. Telomere shortening rate is known to vary with external influences and individual quality. This project will use longitudinal sampling of telomere length in individual fairy-wrens, of known age and pedigree. The telomere information will be combined with state of the art statistical methods to study telomere dynamics in relation to life-history and ecology, to disentangle effects of senescence and selective

disappearance, and to assess environmental and genetic effects on telomere attrition rate.

As the successful candidate, you will join Anne Peters group studying behavioural and evolutionary ecology of fairy-wrens, based at Monash University (Melbourne, Australia). You will be expected to optimise and implement existing qPCR protocols for use in fairy-wrens and apply these to blood/DNA samples (2000 longitudinal samples). You will further be expected to maintain consistently high research output in the form of quality publications, supervise and train students, develop and submit grant proposals to external funding agencies, contribute more generally to research activities of the group, and participate in appropriate career development activities. The position (Level A, starting salary ~\$75 p.a. with annual increments) is for three years subject to satisfactory annual progress.

Requirements: - A PhD in molecular ecology, with extensive experience in qPCR, preferably of telomeres - A publication track record in high-quality journals that clearly reflects the ability to conduct and publish research in the field of molecular ecology - Demonstrated evidence of a strong interest in applying state-of-the-art molecular methods to current evolutionary and ecological questions with meticulous attention to detail and high quality lab work - Strong quantitative skills in the R-environment are highly advantageous, especially animal modelling framework - Ability to work independently in a collaborative research team - Experience in or enthusiasm for supervision and training of students - Experience in developing and submitting grant proposals - Ability to communicate effectively with other scientists at the interface of lab and field ecology - Strong command of English

For further details about the host and institution see: <https://sites.google.com/site/petersresearchgroup/> <http://monash.edu/science/about/schools/biological-sciences/> and <http://www.rug.nl/staff/s.verhulst/> Send a letter that addresses these requirements and includes a brief statement about why you are interested in this post-doc plus a full academic CV that includes including the names and contact details (email, phone) of 2-3 references, to Anne Peters (anne.peters@monash.edu) by the closing date of 28 March 2015.

Anne Peters <anne.peters@monash.edu>

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## MountSinai StatisticalGenomics

Stahl Lab | Post-doctoral scientist in statistical/human genomics

Two positions are available, one with a primary focus on data analysis, and one with a primary focus on genetic modeling and inference methods. Both using GWAS and/or sequence data; range of applications in discovery, integration, prediction; any disease area. Focus on medical genetics, evolutionary impacts and implications are of course relevant. Secondary evolutionary/population genetic focused projects are welcome/available.

Please see the Stahl Lab Positions web page <http://research.mssm.edu/stahl/positions.html> for more information and how to apply.

The Stahl Lab is part of the Center for Statistical Genetics (Dir. Shaun Purcell), in the Division of Psychiatric Genomics (Chief Pamela Sklar).

Thank you

Eli A. Stahl, PhD Assistant Professor Center for Statistical Genetics, Division of Psychiatric Genomics Institute for Genomics and Multiscale Biology, Department of Genetics and Genomic Sciences Icahn School of Medicine at Mount Sinai New York, NY

eli.stahl@mssm.edu

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## NorthCarolinaStateU MosquitoPopGenetics

Postdoc: Modeling Population Genetics for Suppression of Mosquito-Vectored Diseases

PROJECT DESCRIPTION: Dengue is a mosquito-vector disease that affects over 100 million people each year. With funding from the NIH, FNIH, and W. M. Keck Foundation, we have developed a set of mathematical models ranging from simple to complex, aimed at assisting the design and deployment of novel approaches for suppressing transmission of dengue by its major mosquito vector, *Aedes aegypti*. We are especially interested in evaluating the potential utility and risks associated with using genetically engineered,

selfish genetic elements to drive genes into mosquito populations that render them incapable of transmitting dengue fever or decrease mosquito density. Our new work also extends to models relevant to suppressing malaria.

New developments in molecular genetics promise to increase the efficiency of building gene drive systems with novel properties. The postdoc in this position will build a set of simple to complex models to examine the expected dynamics of these gene drive systems in mosquitoes and other taxa.

The most detailed model that we have developed simulates the population dynamics and population genetics of *Ae. aegypti* in a city on the Amazon river, Iquitos, for which there are rich data sets on both mosquito dynamics and dengue epidemiology. An accompanying epidemiological model is currently under development. The goals of two other postdocs in our group are to expand the mosquito model and the human epidemiology model to encompass the entire city of about 400,000 people. The postdoc in this new position will also collaborate with the other postdocs to use these detailed models to test gene drive systems.

In addition to working on model development and analysis, the person in this position will collaborate in an interdisciplinary research group composed of mosquito ecologists, disease epidemiologists, molecular biologists, biomathematicians, ethicists, and scientists from disease-endemic countries. The person in this position will have the opportunity to visit Iquitos to better understand one of the systems being modeled. Desirable skills include the ability to program in C++ or knowledge of a related programming language, and training in evaluation of mechanistic models.

To apply: email a cover letter and CV to [Fred\\_Gould@ncsu.edu](mailto:Fred_Gould@ncsu.edu)

For more details on the project see the following publications:

Esvelt, K. M., A. L. Smidler, F. Catteruccia, G. M. Church. 2014. Concerning RNA-guided gene drives for the alteration of wild populations. *eLife*. 10.7554/eLife.03401.

Oye, K. A. et al. 2014. Regulating gene drives. *Science*. 345:626-628 Published online 17 July 2014

Huang, Y., Lloyd, A.L., Legros, M., Gould, F. 2010. Gene-drive into insect populations with age and spatial structure: a theoretical assessment. *Evol. Appl.* ISSN 1752-4571.

Gould, F., Huang, Y., Legros, M., Lloyd, A. L. 2008. A killer-rescue system for self-limiting gene drive of

anti-pathogen constructs. *Proc. Royal. Soc. Lond. B.* 275:2823-2829.

Magori, K., M. Legros, M. Puente, D. A. Focks, T. W. Scott, A. Lloyd, F, Gould. 2009. Skeeter Buster: a stochastic, spatially-explicit modeling tool for studying *Aedes aegypti* population replacement and population suppression strategies. *PLoS Negl Trop Dis* 3(9): e508. doi:10.1371/journal.pntd.0000508

Okamoto KW, Robert MA, Gould F, Lloyd AL (2014) Feasible Introgression of an Anti-pathogen Transgene into an Urban Mosquito Population without Using Gene-Drive. *PLoS Negl Trop Dis* 8(7): e2827. doi:10.1371/journal.pntd.0002827

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## OklahomaStateU ComputationalQuantitativeGenomics

Postdoc Position in Computational and Quantitative Genomics at the Oklahoma State University

The Crop Genomics Group at the Oklahoma State University is seeking enthusiastic applicants to lead a systems biology effort related to climate challenge and food security. The research interests of the group focus on integrating genomics, transcriptional variation and semantic comparison to characterize genetic interaction, network responsible for the important agronomical trait variation. Crop Genomics Group at OSU works very closely with Genomics Core Facility, transcriptome and metabolomics research groups as well as the wheat improvement team in the Oklahoma Agricultural Experimental Station.

The successful candidate will have:

- \* A PhD in Quantitative and Statistical Genetics, Computational Biology, Information Science, or related field
- \* An innovative, creative individual with strong interest in data modeling, systems biology and genomics technologies
- \* Experience with handling 'omic' data, hierarchical Bayesian statistics and/or informatics pipeline development, programming and bioinformatics skills are required
- \* Good communication and interpersonal skills, and enjoy collaborative research environment

The initial appointment will be 12 months, with the possibility of extension depending on performance and funds availability

Candidates should email the following information to Dr. Charles Chen ([charles.chen@okstate.edu](mailto:charles.chen@okstate.edu))

\* A cover letter addressing research interest, experience and skills that fulfill the requirements \* A full C.V. \* Most recent or most significant publication \* Contact information for 3 potential referees

Charles Chen Assistant Professor Department of Biochemistry and Molecular Biology Oklahoma State University 246 Noble Research Center Stillwater, OK 74074  
charles.chen@okstate.edu

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## OmahaZoo MadagascarBiodiversityGenomics

Postdoctoral Fellow - Madagascar Biodiversity Genomics

Applications are invited for a Postdoctoral Fellow - Madagascar Biodiversity Genomics within the Conservation Genetics Department at Omaha's Henry Doorly Zoo & Aquarium (<http://www.omahazoo.com/careers/>). Based in Omaha, Nebraska, the post doctoral researcher must have an interest and expertise in the generation and analysis of next-generation sequencing data of lemurs, tortoises, and other taxa from Madagascar.

Duties: The successful applicant will construct genomic library for high throughput sequencing as well as assemble and analyze sequence data and manage next-generation sequence workflows. This individual will be responsible for development, implementation, and support of software applications related to variant detection and interpretation from high-throughput experiments involving multiple species of lemurs, tortoises, and taxa from Madagascar. Interested candidates should be highly motivated, organized, independent, and have extensive experience with molecular genomics and bioinformatics. Travel to Madagascar to support the field programs of OHDZA-CG is required for a minimum of five week intervals twice a year.

Basic Qualifications:

Applicants should hold a PhD in bioinformatics, computer science, molecular genomics or related field and have more than one year of experience in high-throughput genome sequence analysis. Applicants should be experienced at software related to next generation sequencing data and be able to manipulate genomic data for phylogenetics and phylogeography. Our groups focus is large-scale sequencing for phylogenetics, phylogeography and evolutionary studies of lemurs, tortoises and other taxa from Madagascar. Thus, previous expe-

rience in genome assemblies, annotation and analysis of next generation sequencing (NGS) are preferable. The ideal candidate will be independent, highly motivated, productive, and able to work effectively in a team with members from a variety of diverse backgrounds with outstanding written and verbal communication skills. The successful applicant must be interested in interdisciplinary science and field research and have a solid publication record that illustrates ability to conduct novel, independent research.

Preferred Qualifications

Candidates should have 3+ years of experience in molecular biology, genetics, or bioinformatics. The position requires proficiency in programming (Perl, C++) and Linux operating systems. Applicants are also expected to be familiar with bioinformatics tools and genomics databases and have extensive and creditable laboratory experience with constructing genomic libraries.

Must be legally entitled to work in the USA. Visa sponsorship is not available.

Appointment: The selected candidate will be based primarily at OHDZA-CG, but the individual will be required to travel and conduct field work with the projects under the management of the Madagascar Biodiversity Partnership, ONG ([www.madagascarpartnership.org](http://www.madagascarpartnership.org)). The initial appointment is for duration of two-years, but may be renewable for an additional two years based on performance.

Application: Applicants should send curriculum vitae, a statement of research interests and career goals, and the names and addresses of three academic references to:

Dr. Edward E. Louis Director of Conservation Genetics Center for Conservation and Research Omahas Henry Doorly Zoo and Aquarium 3701 South 10th Street, Omaha, NE 68107 Email: [genetics@omahazoo.com](mailto:genetics@omahazoo.com)

Candidates must also submit a copy of your application materials through the Omahas Henry Doorly Zoo and Aquarium career site at: <http://www.omahazoo.com/careers/> Review of applications will begin immediately and will continue until the position is filled.

Genetics Department <[genetics@omahazoo.com](mailto:genetics@omahazoo.com)>

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## Oslo FungalMolecularEvol

Three year position as Postdoctoral Research Fellow in fungal molecular ecology available at the University of Oslo, Norway:

Soil fungi play important functional roles in forest ecosystems; while saprotrophic taxa are essential for organic matter decomposition; mycorrhizal root-associated fungi mediate the link between living plants and the below-ground community. Recent studies indicate that plant-fungi interactions through mycorrhiza affect the efficiency of decomposition by fungi, and works as a main driver for soil carbon sequestration in forest ecosystems. The goal of this project (MycSoil), which is funded by the Norwegian Research Council, is to make fundamental progress in the understanding of the community ecology and functions of fungi in boreal forest soils, how they are organized spatiotemporally and how they influence on carbon sequestration processes. We will take advantage of linking the project to two long-term surveys of boreal forests. State-of-the-art DNA metabarcoding and metatranscriptomics approaches will be used to analyze spatiotemporal variation in the soil fungal communities.

For more information see <http://uio.easycruit.com/-vacancy/1352849/96323?iso=no> or contact Håvard Kauserud at [haavarka@ibv.uio.no](mailto:haavarka@ibv.uio.no)

[havard.kauserud@ibv.uio.no](mailto:havard.kauserud@ibv.uio.no)

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## PennsylvaniaStateU CoralEvolution

The Baums lab in the Department of Biology at Penn State (<http://bio.psu.edu/directory/ibb3>) is looking for an experienced researcher to conduct NSF-funded experiments on acclimatization of shallow-water corals to increased temperature as a result of the 2014 bleaching event in the Florida Keys. Responsibilities include organizing and conducting a microcosm experiment over three months in the Florida Keys (July - Sep 2015) with little supervision, requiring the researcher to live in the Florida Keys during this time. Experience with aquarium experiments on corals and AAUS SCUBA

certification is required. The successful candidate will be proficient in using molecular tools such as gene expression analysis, RADtag sequencing and bacterial 16s tag sequencing as well as analysis of next generation sequencing data. An advanced degree in marine biology or molecular ecology or related fields is needed. This position will be filled at the research assistant or research associate level, depending upon education and experience. Candidate must be able to begin work on 1 June 2015. Position initially funded for 6 months with possibility of continuation. Applications must be submitted electronically at <https://psu.jobs/job/56345> and include a cover letter detailing research interests and experience, a current CV and names and contact information for three references. Review of applications will begin immediately and continue until position is filled.

CAMPUS SECURITY CRIME STATISTICS: For more about safety at Penn State, and to review the Annual Security Report which contains information about crime statistics and other safety and security matters, please go to <http://www.police.psu.edu/clery/>, which will also provide you with detail on how to request a hard copy of the Annual Security Report.

Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to minorities, women, veterans, disabled individuals, and other protected groups.

Job URL: <https://psu.jobs/job/56345> [ibb3@psu.edu](mailto:ibb3@psu.edu)

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## PurdueU SalmonidEvolution

A postdoctoral position is available in the laboratory of Mark Christie at Purdue University (<https://markchristie.wordpress.com/>) to examine the rapid evolution of steelhead trout (*Oncorhynchus mykiss*) to the Great Lakes. Steelhead were introduced to the Great Lakes around 1890 and have self-sustaining populations where the fish continue to swim up rivers to spawn, but now forage and grow in the Great Lakes rather than the ocean environment. Whole genome resequencing will play a central role in this project, thus the ideal candidate will have a strong background in relevant laboratory work and bioinformatics. Proficiency with Unix/Linux (bash shell) command line and one or more scripting languages (Perl/Python etc.) will be highly regarded. Familiarity with R and analytical methods in population genetics will also be viewed favorably. The

candidate is expected to be highly motivated and able to work both collaboratively and independently. The position is to be filled as soon as possible with August being the latest possible start date.

Applicants must have a PhD. Exceptional candidates that will complete their PhD within the next few months will also be considered. Applicants should submit 1. a cover letter that describes your research interests and goals, 2. a full CV (including publications), and 3. the names and contact information for three individuals that are willing to serve as references. Please submit all application materials as a single PDF file to markchristie@purdue.edu. Funding is available for two years contingent upon a successful one-year review. Review of applications will begin April 1st and continue until the position is filled.

Purdue has substantial bioinformatics resources and state-of-the-art computational facilities ideal for working with high-throughput sequencing data. West Lafayette is a typical college town located about 1 hour away from Indianapolis and two hours from Chicago. Farmers markets, local parks, and performing arts (<https://www.purdue.edu/convocations/>) all make for enjoyable living conditions. Purdue University is an EEO/AA employer.

markchristie@purdue.edu

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## QUT Brisbane Australia MammalEvolution DNA morphologyFossils

**POSTDOCTORAL RESEARCH FELLOW: Mammal Evolution, DNA, morphology, and fossils**

The vertebrate evolution group at Queensland University of Technology (Brisbane, Australia) is seeking a Postdoctoral Fellow to conduct research into mammalian evolution at the interface of evolutionary inference, genomics and palaeontology. The position is funded through an Australian Research Council Discovery Grant to Matt Phillips and Peter Prentis.

\* Full-time, 2 years with extension possible. \* Starting May-July 2015 and open to Australian and International applicants. \* Annual salary AUD \$60,670 to \$82,324 plus 17% superannuation. \* Applications close 29 March

The vertebrate evolution group at QUT is within the School of Earth, Environmental and Biological Sciences

(in the Science and Engineering Faculty).

The Fellow will lead the development of novel methods for integrating molecular and fossil data to answer major questions in mammalian evolution. Such as the timing of major diversifications and the roles of competition and environmental change in mammalian diversification and extinction. In turn, the Fellow will co-supervise PhD projects that seek to uncover mechanisms that underpin biodiversity variation across marsupial and placental mammal faunas. The position will also support the group's broader research interests in vertebrate evolution and offers opportunities to collaborate internationally. A full duty statement is provided at: <http://www.mphillipsbiol.com/contacts-vacancies.html>

The position is at QUT's Gardens Point Campus, which is located in the centre of Brisbane, nestled between the Brisbane River and the Botanic Gardens.

The successful applicant will have excellent bioinformatic or phylogenetic skills. Molecular lab skills will be highly regarded, although are less important if the application is otherwise strong.

Essential selection criteria:

1. Completion of a PhD qualification in either evolution, genetics, bioinformatics or an equivalent combination of qualifications and experience in a similar molecular/quantitative field.
2. Demonstrated molecular laboratory skills, including PCR and ideally, high-throughput sequencing.
3. A proven research track record in bioinformatics related to either genomics, phylogenetic inference or morphometrics.
4. Well-developed interpersonal skills with a demonstrated ability to work collaboratively as part of a team.
5. Proven ability to work effectively with minimal supervision to initiate, execute and report research within prescribed timelines.
6. Well-developed written and oral communication skills with a demonstrated track record in publishing in high quality journals and presenting at conferences.
7. Ability to actively participate in and contribute to establishing and maintaining an effective safe and healthy workplace.

Desirable selection criteria:

1. Demonstrated experience with coding languages, ideally related to developing bioinformatic or evolutionary inference tools.
2. Publication record in vertebrate (especially mammal) evolution, ecology, morphology or palaeontology.

To apply, follow the link from:

<http://www.mphillipsbiol.com/contacts-vacancies.html>

You will need to supply your CV, referee details, and an address to the selection criteria.

Informal enquiries to Matt Phillips  
 m9.phillips@qut.edu.au +61 7 3138 4805 <http://www.mphillipsbiol.com/>  
 For human resources details associated with application, contact Anya Levina (HR Advisor) a.levina@qut.edu.au +61 7 3138 4134

Matthew Phillips <m9.phillips@qut.edu.au>

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## Rostock Germany Bioinformatics

Postdoctoral Scientific Researcher with a focus on (evolutionary) bioinformatics in Rostock (Baltic Coast), Germany

The Institute for Biostatistics and Informatics in Medicine and Ageing Research at the Rostock University Medical Center (Germany) seeks, pending budgetary approval, and starting in Mai/June to be continued for up to 5 years, candidates for the position of a

Full-time Postdoctoral Scientific Researcher, with a focus on bioinformatics, in an EU-funded project.

Your tasks:

- Database development for data on health and ageing.
- Multi-Species Omics data analyses (gene, protein and metabolite abundance).
- Evolutionary comparative analysis of worm, mouse and human data.
- Machine learning and network-biology based analyses and data integration.
- Writing of scientific reports and papers.
- Website development and maintenance.

Advantages for you:

- A stimulating environment where your contribution can have a real impact.
- Researching the mechanisms behind healthy aging is fascinating, and gaining importance in the light of demographic development.
- A dedicated and experienced team, fun to work with.

What you need to bring to the table:

- Doctorate related to bioinformatics, or a research field in the medical/life/natural sciences.
- Programming/scripting skills, e.g. in R.
- Strong communication skills (oral presentations and in writing).

-(Desirable:) Project management experience.

If this describes you and your intentions then please send your application until March 30 to [bioinfo-jobs@med.uni-rostock.de](mailto:bioinfo-jobs@med.uni-rostock.de) in a single PDF document, consisting of:

- CV.
- Brief statement of research interests and qualifications.
- contact information for 2-4 scientists who may write a letter of recommendation.

For further information you may contact:

Prof. Dr. Fuellen, [bioinfo-jobs@med.uni-rostock.de](mailto:bioinfo-jobs@med.uni-rostock.de), Director of the Institute for Biostatistics and Informatics in Medicine and Ageing Research.

For most of the year, Rostock (at the Baltic Coast) is a number one vacation area in Germany, with a very pleasant climate and nice beaches nearby.

The University strives for a high proportion of women in research and teaching. Applications from qualified female scientists are therefore particularly welcome. Disabled persons will be given preference in filling vacancies within the existing legal provisions if equally qualified. Reimbursement of travelling costs for interviews is not possible according to the rules of the state of Mecklenburg-Vorpommern.

Georg Fuellen

[bioinfo-jobs <bioinfo-jobs@med.uni-rostock.de>](mailto:bioinfo-jobs@med.uni-rostock.de)

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## SangerInst ParasiteGenomics

Postdoctoral Fellow - Parasite Genomics

Salary range: £30202 to £37860 per annum plus excellent benefits.

We are seeking to recruit an enthusiastic and ambitious Postdoctoral Fellow to play a leading role in a large, collaborative project using genomic approaches to understand the genetics of anthelmintic drug resistance in *Haemonchus contortus* and *Teladorsagia circumcincta*, the most important gastrointestinal nematode parasites of small ruminants. The post is funded by BBSRC, and will be for 3 years in the first instance, with the possibility of extension for an additional 2 years. Key aspects of the role are the analysis and interpretation of whole genome resequencing data from a genetic cross, of populations of worms from UK farms, and of individual worms from the same populations. The role will also



include working with colleagues to produce a reference genome for *T. circumcincta*.

The project aims to leverage the understanding of anthelmintic resistance we gain to develop practical guidance for on-farm management, and so will involve collaboration with vets, parasitologists, modelers and economists (<https://bugconsortium.wordpress.com>). Strong candidates will need excellent communication and organizational skills, as explaining the results of genomic analyses to these professionals in an accurate but accessible way will be critical. The post will be based with the parasite genomics group, a diverse and collaborative research environment, and the institute has unparalleled resources and expertise available to support genomic research.

This post is fixed-term for 3 years in the first instance, possible extension to 5 years. Closing date for applications is: 29th March 2015. Please see <http://tinyurl.com/q3v8wzw> for further details and to apply

James Cotton Senior Scientist Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge. CB10 1SA UK

james.cotton@sanger.ac.uk 01223 494864

The Wellcome Trust Sanger Institute is operated by Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is 215 Euston Road, London, NW1 2BE.

jc17@sanger.ac.uk

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## Senckenberg Frankfurt Community Evolution

Postdoc “Molecular community ecology and evolution”

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A postdoctoral research position in molecular community ecology and evolution is available in the lab of Prof. Imke Schmitt at the Senckenberg Biodiversity and Climate Research Centre and Goethe University Frankfurt. You will have the opportunity to participate in ongoing projects and develop your own research profile. Attractive computing infrastructure (high-RAM computers, clouds and clusters) and high-end experimental facilities are available.

\*Your tasks: \*

ecological and evolutionary processes in complex communities using high-throughput sequencing (metabarcoding, metagenomics, or metatranscriptomics)

structural and functional change in communities of microorganisms in response to environmental change\*\*

\*\*

\*Your profile: \*

.D. in evolutionary or computational biology, ecology or a related field

in metabarcoding of environmental samples, metagenomics, metatranscriptomics, regardless of the organism group (experiences with fungi/prokaryotes/small eukaryotes are a plus)

in bioinformatics of next generation sequencing data and in subsequent ecological analyses

background in ecological theory

record of prior publication in metabarcoding/metagenomics/metatranscriptomics

skills in R, python, bash, perl are welcome

written and oral English language skills

Salary and benefits are according to a public service position in Germany (TV-H E 13). The contract should start on \*June, 1<sup>st</sup> 2015 \*and will be restricted to three years. The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please send your application before \*April, 1<sup>st</sup> 2015\* preferably by e-mail (attachment in a single pdf document), mentioning the reference of this position \*(Ref. 8.5-1)\* and including a cover letter detailing research interests and experience, a C.V., a copy of your PhD certificate, and a list of three professional references. Please be sure to highlight skills and experience related to genome assembly, statistics, bioinformatics, or programming and send your application to the address below

Dr. Tobias Schneck

c/o Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt

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

For scientific enquiries please contact Prof. Dr. Imke Schmitt, imke.schmitt@senckenberg.de.

Am Forschungsinstitut Senckenberg (FIS) ist in der Abteilung Limnologie und Naturschutzforschung ab dem 01

Imke Schmitt <imke.schmitt@senckenberg.de>

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### SLU Sweden PlantPathogenEvolution

One year postdoc stipend on Solanum - Phytophthora interaction

We are seeking a postdoc for one year that will be based at the Department of Plant Protection Biology, unit of Resistance Biology at Swedish University of Agricultural Sciences (SLU) in Alnarp, Sweden (hosted by Åsa Lankinen, Laura Grenville-Briggs and Erik Andreasson). The postdoc will work on plant pathogen interactions between wild and cultivated Solanum and the oomycete *Phytophthora infestans*.

Late blight in potato, caused by infection with the oomycete *Phytophthora infestans*, leads to large economic losses. Introduction of new resistant potato varieties is countered by rapid evolution of new pathogenicity factors in *P. infestans*. However, increased insights into plant-pathogen interactions in natural systems can aid the development of sustainable crop management practices. The postdoc will work within a project that studies interactions between *P. infestans* and its hosts - potato and three wild Solanum species found in Sweden - and combines ecology and evolutionary biology with genetics and molecular mechanisms to answer questions related to pathogen virulence and plant defence to late blight disease. The work will involve both screening of resistance and tolerance to *P. infestans* in the lab and field work to explore potential overwintering of *P. infestans* in wild Solanum populations.

Requirements: A PhD degree in biology or biology-related fields, not older than 3 years (as the main aim is training of the candidate, and living costs will be covered by a stipend, 20,000 SEK, approx. 2,200 euro, per month). Candidates should be fluent in spoken and written English. Previous experiences from work on plant-pathogen interactions in the lab or field, ecology and evolutionary biology are merits. The candidate must also be capable of independent planning, execution and evaluation of experiments, and be able to function

well in a group. Applicants that hold a driving license will be evaluated favourably.

Starting date: By agreement during late spring/early summer 2015, preferably in May or as soon as possible.

Please send your cv, a motivation for why you are well suited for this work and contact details of at least two references to Åsa Lankinen, asa.lankinen@slu.se, no later than 7th of April.

Stefan Andersson <stefan.andersson@biol.lu.se>

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### SwanseaU SalmonEpigenetics

Post-doctoral position in epigenetic management of stress and disease resistance in Atlantic salmon @ Swansea University

Institutions: Swansea University, Cardiff University, University of Aberdeen, University of East Anglia

Collaborators: Landcatch, Marine Harvest

To meet global food demands, aquaculture is expected to intensify fish production, but stress during intensification can also compromise animal health, particularly during early life when the teleost immune system is being formed. Many farmed fish are already highly inbred and further intensification will likely make them more susceptible to infectious diseases and pathogens more detrimental. Stress during intensification could change the expression of genes via epigenetic programming, but knowledge of fish epigenomes is very limited. We are looking for 1 Postdoctoral Research Fellow to work on an exciting project that will use a multidisciplinary, cutting-edge approach to investigate how stress experienced during early life can change the epigenome and subsequently affect the ability of fish to respond to pathogens.

The project will involve a BACI design to manipulate stress in Atlantic salmon during embryogenesis and assess its effects on subsequent gut health and fitness by carrying out a gut bacterial community profiling using metagenomics. As a fitness indicator it will also examine fluctuating asymmetry and challenge fry with *Saprolegnia parasitica*, a pervasive fish pathogen, and monitor fry survival in relation to expression of immune-related genes through RNAseq, and patterns of DNA methylation. Following fish from fertilization to first feeding, will allow for the first time to relate the effects of early stress to (1) health, (2) an indicator of fitness

and (3) resistance to parasites, and examine these in relation to variation in the genome and the epigenome.

A Research Fellow position is available at Swansea University for 22 months starting June 2015, starting salary approx. £31,000. Travelling to partner Universities (Cardiff and Aberdeen mainly) will be required to complete parts of the work.

Applicants are expected to match the following criteria: - Have a PhD in a relevant field (e.g. Biology, Ecology, Genetics). - Have published, confirmed accepted or in press, at least 3-4 papers in ISI accredited peer-reviewed journals by the starting date of the position. (Applicants with longer periods of postdoctoral experience will be expected to have proportionally higher numbers).

Desirable criteria are: experience working on fish, genetics/genomics background, experience programming in R/Python.

Informal enquiries can be directed to: Carlos García de Leaniz (c.garciadeleaniz@swansea.ac.uk) or Sonia Consuegra (s.consuegra@swansea.ac.uk)

“CONSUEGRA S.” <s.consuegra@swansea.ac.uk>

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## Toronto Population Genomics

Postdoctoral Positions in Population and Medical Genomics

Postdoctoral positions are available in the population and medical genomics laboratories of Philip Awadalla in Toronto at U. of Toronto and Ontario Institute for Cancer Research. Researchers will be involved in analysis, development of methods and next-gen sequencing experiments. The successful candidate will be nearing the completion/having a PhD or equivalent postdoctoral training in genomics or population/ statistical genetics. Postdoctoral research scientists can work on projects of their choosing related to the labs current projects.

Some recent publications from the lab are listed below: <http://www.nature.com/ng/journal/vaop/ncurrent/full/ng.3216.html> <http://www.sciencemag.org/content/344/6182/413> <http://genome.cshlp.org/content/23/3/419>

Possible projects include: 1) Capturing germ-line, somatic, tissue specific and cell-specific mutation and recombination events. Fitness consequences of mutations from genome-wide collections of empirical population and comparative data. 2) Next-generation ap-

proaches (whole genome, exome, RNA-seq, methylation and ChIP-seq data) for genomic epidemiology studies of large population cohorts. Our lab is directing the longitudinal collection of genomic material for the CARTAGENE population program ([www.cartagene.qc.ca](http://www.cartagene.qc.ca)), investigating the genetics of endophenotypes from among over 40,000 French-Canadian participants, and the Canadian Partnership for Tomorrow Project, which has enlisted 300,000 participants across Canada. 3) Developing methods for large scale cohort data integration of phenotypes and genotypes through a new Genome Canada Innovation Centre for bioinformatics and genomics. 4) Identify genetic and molecular control points associated with simple and complex disorders oncological/hematological phenotypes or diseases including immunodeficiencies, child-hood cancer, and sickle cell anemia.

Our lab also works in close collaboration with a number of research laboratories throughout Montreal, and internationally, including new programs in cancer with the Ontario Institute of Cancer Research (U. of Toronto), projects on neurological disorders with the Montreal Neurologic Institute, and malaria with programs in west and central Africa. Projects are well supported by institutional resources for next generation sequencing and bioinformatics. Interested individuals should please write to Philip Awadalla ([philip.awadalla@oicr.on.ca](mailto:philip.awadalla@oicr.on.ca) or [philip.awadalla@mcgill.ca](mailto:philip.awadalla@mcgill.ca)).

Sincerely, Philip Awadalla, PhD

[Philip.Awadalla@oicr.on.ca](mailto:Philip.Awadalla@oicr.on.ca)

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## UAberdeen Avian Mating Systems

We seek a Research Fellow in Evolutionary Ecology to join the research group of Professor Jane Reid at the University of Aberdeen, United Kingdom.

The post is central to a European Research Council-funded project that aims to firstly, build new theory explaining the evolution and persistence of mating systems and reproductive strategies, and secondly, test this theory using more than 20 years of complete life-history and pedigree data from free-living song sparrows (*Melospiza melodia*).

The successful applicant will undertake extensive statistical analyses of the long-term song sparrow dataset in order to elucidate patterns of variation in extra-pair reproduction in relation to temporal and spatial varia-

tion in population social structure and relatedness. The post-holder will work in close collaboration with Professor Reid, other members of the ERC project team and key international collaborators to undertake appropriate analyses and thereby test key components of evolutionary theory. The post-holder will also have substantial flexibility to develop their own ideas and approaches to the overall problem, potentially including opportunities for fieldwork as well as data analysis.

The post provides an exciting opportunity for a highly motivated researcher with expertise in statistical analysis, mating system variation, evolutionary ecology and/or behavioural ecology, and interest in confronting evolutionary theory with data from wild populations. It provides an opportunity to work within a dynamic and successful international research team, with ample opportunities for further international collaboration, high-profile publication and career development (see <http://www.abdn.ac.uk/biologicalsci/staff/details/-jane.reid>).

The post is funded by the European Research Council and will be offered for a period of 2 years.

Full details are available at <http://www.abdn.ac.uk/-jobs/>, click on 'External applicants' and search under School of Biological Sciences. Closing date is April 1st 2015.

The University of Aberdeen is a charity registered in Scotland, No SC013683. Tha Oilthigh Obar Dheathain na charthannas cl?raichte ann an Alba, ?ir. SC013683.

"Reid, Dr Jane M." <jane.reid@abdn.ac.uk>

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## UArizona 2 Genomics Invasive Plant Adaptation

NOTE: Updated job description and start dates below.

Two postdoctoral research positions funded by the United States Department of Agriculture are available to work with Dr. Katrina Dlugosch (<http://-dlugoschlab.arizona.edu/>) and Dr. David Baltrus (<http://cals.arizona.edu/research/baltruslab>) at the University of Arizona on the ecological genomics of adaptation of resource allocation and microbial interactions in the invasive plant yellow starthistle (*Centaurea solstitialis*). We are investigating the evolution of resource allocation and species interactions during range expansion and the impact of evolution on the spread of invading populations, and we are seeking postdoctoral researchers

with interests and experience in these areas.

One successful candidate will be responsible for next-generation genomic sequence generation and bioinformatic analyses, particularly by 1) analyzing metagenomic surveys of plant-associated microbial communities and 2) quantifying rates of gene flow across the genome in invading plant populations using a high-throughput RADseq next-generation approach. Additional opportunities will be available for the pursuit of related projects of interest to the candidate. Preferred start date in late 2015. To apply, submit a statement of interest and curriculum vitae to job #57623 at <https://www.uacareertrack.com>. A second successful candidate will be responsible for 1) mapping QTL associated with the genetic basis of variation in resistance to bacterial pathogens using large-scale greenhouse experiments and genome-wide RADseq markers, and 2) quantifying population-level impacts of infection using phenotypic data collection in combination with existing demographic models in collaboration with Dr. Sarah Swope (Mills College). Additional opportunities will be available for the pursuit of related projects of interest to the candidate. Preferred start date in late 2015 or early 2016. To apply, submit a statement of interest and curriculum vitae to job #57624 at <https://-www.uacareertrack.com>. Positions are for one year, with reappointment for up to two additional years subject to satisfactory performance. Positions are open until filled.

Minimum qualifications \*PhD in Biology or a related field \*Authorship of peer-reviewed publications of research in a field related to the position \*Strong communication skills \*Ability to work independently and in a team

Preferred Qualifications (Applicants without these skills will be considered): \*Experience producing and analyzing molecular genetic data, particularly next-generation genomic data \*Experience culturing bacterial colonies \*Experience rearing plants under standard greenhouse conditions \*Experience collecting and documenting field specimens

Inquiries about the positions may be directed to Dr. Katrina Dlugosch ( [kdlugosch@email.arizona.edu](mailto:kdlugosch@email.arizona.edu)).

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Katrina M. Dlugosch, PhD [katrina.dlugosch@gmail.com](mailto:katrina.dlugosch@gmail.com)  
Katrina Dlugosch <[katrina.dlugosch@gmail.com](mailto:katrina.dlugosch@gmail.com)>

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**UBath EvolutionaryGenomics  
SocialMicrobes**

We are excited to be recruiting a Postdoctoral Research Associate (PDRA) to work on a project focused on understanding the evolutionary processes shaping natural variation in a social amoeba. The project combines large scale genome sequencing with high throughput phenotyping to dissect the molecular basis of natural variation in social and non-social traits, with a goal of identifying the patterns of selection shaping underlying sequence variation. The PDRA will contribute primarily to genome reconstruction, association analyses (including both GWAS and candidate gene based approaches) and application of molecular evolution models to sequence data, but will also contribute to the generation of data in the initial phase of the project. The project also offers the successful candidate flexibility to pursue other questions using the data, including those related to social evolution, the genotype-phenotype relationship, biogeography, and speciation.

The successful candidate will have a background in evolutionary or statistical genetics (including bioinformatics). Skills related to the handling of large scale sequence data are essential as is the ability to work both independently and collaboratively as part of a research team. Candidates should have a demonstrated ability to publish high impact science as well as good interpersonal and communication skills. Some skills in molecular quantitative genetics and the analysis of molecular evolution are preferred but not required.

The successful candidate will be based in Prof Jason Wolf's Lab at the University of Bath, working in close collaboration with Prof Laurence Hurst. The candidate will also work with collaborators at the University of Manchester and the Federal University of São Carlos (Brazil).

The position is fixed-term of 36 months at pounds 31,342 and is set to start in May 2015, with later start dates subject to approval by the funding agency.

Informal enquiries may be directed to Prof Jason Wolf via email: [j.b.wolf@bath.ac.uk](mailto:j.b.wolf@bath.ac.uk) (telephone or Skype consultations can be arranged)

For further information and to apply please see [www.bath.ac.uk/jobs/Vacancy.aspx?ref=SS3006](http://www.bath.ac.uk/jobs/Vacancy.aspx?ref=SS3006) Jason Wolf <[jason@evolutionarygenetics.org](mailto:jason@evolutionarygenetics.org)>

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**UCDavis DevelopmentalEvolution-  
aryGenomics**

A postdoctoral position is available at the University of California - Davis to study the molecular mechanisms, phylogenetic patterns, and functional consequences of transcriptome evolution in *Drosophila*. The project is based on the integration of RNA-seq, ChIP-seq, transgenic manipulation of gene expression and DNA-protein binding, and quantitative phylogenetic analysis to understand the roles of gene cooption, gene duplication, and de novo gene origin in the evolution of tissue-specific regulatory circuits. This work involves a collaboration between the labs of Artyom Kopp (developmental genetics and evo-devo), David Begun (evolutionary and population genomics), and Brian Moore (phylogenetic and comparative analysis). Additional aspects of this project may range from cell type specification to the evolution of enhancer sequences. Postdocs will be encouraged to develop independent research reflecting their own interests, within the broad field of developmental and evolutionary genomics.

Candidates should have demonstrated expertise in experimental molecular genetics and genomics, with an emphasis on RNA-seq and ChIP-seq analysis, genome annotation, and comparative genomics. Some experience in developmental biology and transgenic methods is also desirable. Initial appointment is for one year, extendable by mutual agreement. Our labs and the entire department provide a very supportive atmosphere. The broader research environment at UC - Davis offers postdoctoral fellows chances for collaboration with leading experts in fields ranging from cell and developmental biology to evolutionary genomics and phylogenetics. Northern California, where Davis is located, provides outstanding recreational opportunities. Interested applicants should contact Artyom Kopp ([akopp@ucdavis.edu](mailto:akopp@ucdavis.edu)) with a CV, a brief statement of research interests and experience, and the names of three references.

[akopp@ucdavis.edu](mailto:akopp@ucdavis.edu)

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## UChicago Evolutionary Genomics

Background: A March of Dimes/Burroughs Wellcome Trust funded post-doctoral position is available in the Lynch Lab, in the Department of Human Genetics at The University of Chicago, for a highly motivated scientist to study the mechanisms that underlie the evolutionary origin of progesterone responsiveness and decidualization in endometrial stromal cells. The project will use comparative transcriptomics to identify genes that evolved endometrial expression during the origins of pregnancy, and siRNA-screens to characterize the functions of recruited genes. The project is expected to contribute to a basic understanding of the mechanisms that underlie decidualization and the evolution of pregnancy.

Skills: Candidate must have a Ph.D. in molecular or cell biology, genetics, or a related discipline, be self-motivated, have excellent communication and organizational skills. A strong background with basic methods in molecular biology (for example: PCR, cloning, sequencing, Western blotting, protein-protein interaction assays such as co-IP) and demonstrated expertise in cell culture and gene expression manipulation (for example: siRNA mediated gene knockdown and overexpression) are required. Previous experience or strong interests in gene expression analyses, bioinformatics, and genome editing are desirable.

Application information: To apply, please email a cover letter describing previous research experience, current research interests, and career goals, a current CV, and the names and contact information for three professional references to Dr. Vincent Lynch at [lynchlabpositions@gmail.com](mailto:lynchlabpositions@gmail.com).

Consideration of applications will begin immediately and continue until the position is filled.

Lab website: <http://lynchlab.uchicago.edu> Location: Chicago, IL USA

“Vincent J. Lynch, Ph.D.” <[vjlynch@uchicago.edu](mailto:vjlynch@uchicago.edu)>

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## UCollege London Tetrapod Evolution

Morphological evolution and modularity of tetrapods

The Goswami Lab in the Department of Genetics, Evolution & Environment at University College London is now accepting applications for a postdoctoral research position in evolutionary morphology and diversification of tetrapods. The successful applicant will be employed for three years to work as part of a team on a European Research Council-funded project conducting a large-scale quantitative analysis of evolutionary rates, morphological disparity, and phenotypic integration across tetrapods. The postdoctoral researcher will focus on a subclade of sauropsids (‘reptiles’) and will be responsible for building a comprehensive dataset of 3-D images spanning their living and extinct diversity and extracting surface morphometric data from images. With these data, they will conduct extensive analyses to reconstruct the patterns and processes underlying ecomorphological evolution and identify the major intrinsic and extrinsic factors shaping clade diversity. Further duties will involve supervision of short-term undergraduate and Master’s student projects, assistance in field expeditions, and uploading new data to online resources for free dissemination.

The postdoctoral researcher may take up their position from June 2015, although there is flexibility in start time. Applications for this position will be accepted via the UCL online application system until April 7, 2015. Informal enquiries and requests for further details can be directed to Anjali Goswami ([a.goswami@ucl.ac.uk](mailto:a.goswami@ucl.ac.uk)).

Project Background:

Morphological variation is the foundation of evolutionary theory, but the basic influences on morphological variation are still poorly understood. Developmental interactions are often discussed as a major control on variation, but direct analysis of this hypothesis has been hindered by the lack of quantitative comparative data. Similarly, robust analyses analysing both extrinsic and intrinsic influences on morphological evolution are often limited by data availability.

Using advanced biological imaging techniques (CT- and laser scanning) combined with surface-based

3-D morphometrics, this project will build on existing work in mammals by providing the first broad comparative data on modularity and disparity of skulls, jaws and

limbs for living and fossil tetrapods. Each team member in this project will focus on building and analysing an extensive 3-D morphometric dataset for a large clade on non-mammalian tetrapods, such as amphibians and sauropsids, which have incredible diversity in reproductive strategies, ecology and morphology. This project will require extensive international travel for data collection, as well as running analyses and implementing new code in R. In addition to working with new data, the postdoctoral researcher will integrate data provided by project collaborators in order to maximize taxonomic representation. In combination with existing data from an ontogenetic sequence of *Xenopus*, and juvenile and adult neontological and paleontological specimens of mammals, this project will produce a robust analysis of the relationships among modularity, morphological disparity, evolutionary rates across tetrapods and how each of these responds to major life history and ecological transitions as well as large-scale biotic and environmental events.

In addition to training in biological imaging and quantitative analyses, there will be opportunities for international palaeontological fieldwork during the course of this project.

Closing date: April 7, 2015

Details and link to the UCL application site available at [www.goswamilab.com](http://www.goswamilab.com) UCL Department / Division  
Division of Biosciences

Specific unit / Sub department

Genetics, Evolution & Environment

Grade

7

Hours

Full Time

Salary (inclusive of London allowance)

33,353 to 35,196 per annum

Key Requirements

Applicants must have a PhD (awarded or about to be awarded) in relevant discipline. Experience of vertebrate morphology and experience of morphometrics and comparative methods. Applicants must also have a proven track record of high quality research in vertebrate evolution, comparative macroevolutionary analyses or a related field.

Appointment at Grade 7 is dependent upon having been awarded a PhD. Or if about to submit a PhD, the appointment will be at Grade 6B (29,193 - 30,783 salary, inclusive of London Allowance) with payment at Grade

7 being backdated to the date of final submission of the PhD thesis.

For further information about the post please contact Dr Anjali Goswami on [a.goswami@ucl.ac.uk](mailto:a.goswami@ucl.ac.uk)

For further information on the application process please contact Biosciences Staffing on [biosciences.staffing@ucl.ac.uk](mailto:biosciences.staffing@ucl.ac.uk)

Dr. Anjali Goswami Reader in Palaeobiology Department of Genetics, Evolution, and Environment and Department of Earth Sciences University College London Darwin Building 218A Gower Street London WC1E 6BT +44 (0)20 7679 2190

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## UEastAnglia Bioinformatics

POSTDOCTORAL BIOINFORMATICIAN, UNIVERSITY OF EAST ANGLIA, UK

A postdoctoral bioinformatician position (Senior Research Associate, ref. RA1169) is available for work on the genetic basis of worker behaviour and caste determination in bees at the School of Biological Sciences, University of East Anglia, UK.

The postdoctoral bioinformatician will work on two projects, funded by NERC and BBSRC, in a team supervised by Professors Andrew Bourke and Tamas Dalmay. A common aim of the projects is to use RNA-Seq to profile gene expression differences in adult and larval bumble bees (*Bombus* spp.). The wider aim is to elucidate the molecular-genetic basis of worker reproduction and caste determination in eusocial insects. The postholder will conduct bioinformatic analyses of transcriptomic and related data generated by the team. The salary will be £31,342 to £37,394 per annum.

Applicants should have a PhD in a relevant area, and be able to fulfil the essential criteria on the person specification. This full time post is available from 1 April 2015 for a fixed term period of 29 months, but must end by 31 August 2017. Informal enquiries to: Andrew Bourke ([a.bourke@uea.ac.uk](mailto:a.bourke@uea.ac.uk)).

Closing date: 12 noon on 18 March 2015.

Further particulars and an application form are available at: [www.uea.ac.uk/hr/vacancies/](http://www.uea.ac.uk/hr/vacancies/) or Tel. +44 (0)1603 593493.

“Tracey Chapman (BIO)”  
<Tracey.Chapman@uea.ac.uk>

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## UFlorida Applied Evolutionary Physiology

A postdoctoral position in applied ecological and evolutionary stress physiology is available in Dan Hahn’s lab at the University of Florida.

Our work takes a vertically integrated approach to understanding both the plastic mechanisms that organisms use to rapidly respond to environmental perturbation, and the consequences of this rapid physiological plasticity for organismal performance from evolutionary and applied perspectives.

The initial appointment will be for 2 years starting as early as summer 2015, with extension for additional years based on performance. The postdoctoral associate is expected to spend 2/3-3/4 of their time on a project centered around understanding how exposure to hypoxic and/or hypercapnic atmospheres can alter the physiology of insects to promote cross-resistance to other stressors (i.e., hormesis). The remaining 1/3-1/4 of time will be available for other creative activities related to the postdoctoral associates interests, particularly if they pertain to other projects in our lab group (see Additional Projects Section below).

**The Main Project:** Exposure to low-oxygen environments can be damaging in the long term, but many insects are highly resistant to short-term exposures to hypoxia and hypercapnia. In fact, short term exposures to modified atmospheres can promote cross-tolerance to other stressors, including oxidative stressors. Here we will investigate how exposure to modified atmospheres can affect insect physiology to impart resistance to irradiation stress (from gamma sources or x-rays). Specifically, the postdoc will: 1) study the effects of modified atmospheres on irradiation tolerance on several insect pests, 2) investigate the fundamental physiological mechanisms that are associated with enhanced resistance to irradiation stress, and 3) use this knowledge in a physiologically guided approach to developing biomarkers for irradiation stress and resistance. Applications for this work include expanding the use of low-dose irradiation

as an alternative to chemical pesticides to prevent the movement of insect pests in fresh fruits and vegetables. This work is a recent area of inquiry in our lab that has implications for both our basic understanding of ecological and evolutionary physiology and applications to agriculture and international trade. Although we have not published much in this area yet, two related papers from our lab on irradiation biology in the context of sexual selection and biological control by the sterile insect technique and one general review of irradiation as a phytosanitary treatment are listed below.

Lopez-Martinez, G., and D.A. Hahn. 2012 Short-term anoxic conditioning hormesis boosts antioxidant defenses, lowers oxidative damage following irradiation, and enhances male sexual performance in the Caribbean fruit fly, *Anastrepha suspensa*. *Journal of Experimental Biology*, 215:2150-2161.

Lopez-Martinez, G. and D.A. Hahn. 2014. Early-life hormetic treatments decrease irradiation-induced oxidative damage, increase longevity, and enhance sexual performance during old age in the Caribbean fruit fly. *PLoS One* 9(1): e88128. doi:10.1371/journal.pone.0088128

Hallman, G.J., N.M. Brilz, L.J. Zettler, and I.C. Winborne. 2010. Factors affecting ionizing radiation phytosanitary treatments, and implications for research and generic treatments. *Journal of Economic Entomology*. 103:1950-1963.

The postdoctoral fellow must be interested in working at the boundary between basic and applied sciences and must be interested in working in a multidisciplinary and collaborative atmosphere. Knowledge of physiology, respirometry, biochemistry, multivariate data analysis, and high-throughput screening, or strong interest in learning these techniques is needed. International applicants are encouraged to apply, but a strong command of spoken English is a must for this position in addition to demonstrating the ability to effectively write peer-reviewed manuscripts in English.

**The Setting:** The University of Florida is located in Gainesville and offers a rich scientific community for evolution, ecology, physiology/cell biology, and genomics that spans many departments including Entomology and Nematology (the academic home for this appointment), Biology, Wildlife, Forestry, the Genomics Institute, the US Department of Agriculture, and the College of Medicine. Our lab currently includes 3 postdoctoral associates, 3 PhD students, and 9 undergraduates with which you would interact daily. There will be substantial opportunities for interdisciplinary training across units at our institution and within our network of collaborators, as well as additional training opportunities in teaching/instruction and scientific outreach to the



public. Our group has an excellent record of career development with former postdocs and students placed in tenure-track academic positions, biotech industry positions, and government science. We strongly recognize the value

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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>

## UHaifa PhD PDF Phylogenetics

A Postdoctoral and Ph.D. positions in Computational Genomics and Phylogenetics are available at the Institute of Evolution at the University of Haifa. The research projects will be done in collaboration with the Phylogenetics and Computational Genomics lab of Prof. Sagi Snir. The positions are targeted to two projects:

1. Tree reconstruction in light of conflicting signals. Real life data provide high degree of incongruent data that needs to be reconciled into a single tree. This is normally done by means of supertree methods. We have developed several approaches to this that rely on non trivial algorithmic and computational/mathematical tools. We decompose the inputs into the most basic informational unit and summarise them across all the data. This data aggregation provides us with information that is invisible at the single tree level or at the level of the entire data collection. Using this novel techniques we are able to distinguish between e.g. toxic and non-toxic genes. We investigate both theoretical and practical questions associated with these approaches.

2. Detection and analysis of horizontal gene transfer (HGT) in prokaryotes. HGT is a major factor in prokaryotic evolution and plays a significant role in developing antibiotic resistance. Current methods rely on a very strong and clear HGT signal that is frequently absent, e.g. HGT between strains of a species. We have developed several novel methods to detect HGT where existing methods fail. The methods use evolutionary signals, unique to HGT, that are detected by rigorous statistical approaches.

The successful candidates must have familiarity with computational/mathematical biology. Essential requirements include proficiency in computer-programming skills, such as C/C++/Java and scripting languages

(e.g. Perl, Python), demonstrated ability in applying the devised algorithms. Duties of the role will include algorithm development, implementation and testing by simulation and application on real biological data.

The Institute of Evolution is world leading in broad aspects of evolution, both theoretical and practical. The team of Prof. Snir is characterized by works with both algorithmic and evolutionary appeal with ample collaboration with other leading labs around the world.

Applicants should send a CV, a statement of research interests and the names and contact information for 3 references. Review of the applications will start immediately until positions are filled. The initial contract is for the postdoc is one year with possibility of extension. For Ph.D. students, the contract is for three years with possible additional year extension.

Please send applications by email to:

Prof. Sagi Snir, Department of Evolutionary and Environmental Biology and The Institute of Evolution, University of Haifa Mount Carmel, Haifa 31905 ISRAEL  
Tel: (972) 4 828-8774 Email: [ssagi@research.haifa.ac.il](mailto:ssagi@research.haifa.ac.il)  
[sagi.snir@gmail.com](mailto:sagi.snir@gmail.com)

## UJyvaskyla HumanSocialBehavior

PostDoc: Human Social Behavior University of Jyväskylä, Finland

**JOB DESCRIPTION:** The postdoctoral researcher will work in the project “Evolution of Conflict and Cooperation in Human Groups”, funded by the Academy of Finland and led by Dr. Mikael Puurtinen. In this project, we study factors influencing levels of cooperation and competition in human groups, and are especially interested in the interplay of within-group cooperation and between-group competition. The main focus of the postdoctoral researcher will be on the design and execution of decision-making experiments to investigate e.g. the role communication, social sanctions, and group identifiers have in mediating the nature of within- and between-group interactions. However, there is considerable scope for the postdoctoral researcher to develop his/her own research ideas. The project involves development of theory to complement the empirical studies, and theoretically oriented researchers are also encouraged to apply.

For published work on the topic by the research

group see: Between-group competition and human cooperation < <http://rspsb.royalsocietypublishing.org/content/276/1655/355> >. Proc R Soc B 2009. Costly punishment prevails in intergroup conflict < <http://rspsb.royalsocietypublishing.org/content/early/2011/03/30/rspsb.2011.0252> >. Proc R Soc B 2011. The joint emergence of group competition and within-group cooperation < <http://www.sciencedirect.com/science/article/pii/S1090513814001408> >. Evolution and Human Behavior 2015.

**DURATION:** The position will be filled for a maximum of two years. The starting date for the position is flexible, between May 1st 2015 and January 1st 2016.

**SALARY:** euro 37,560 - 43,800 per annum, depending on qualifications. Healthcare included.

**QUALIFICATIONS:** PhD in Biology, Psychology, Economics, or a related field. The applicant must possess a thorough understanding of evolutionary concepts. Excellent written and good oral English skills are required. The applicant is expected to have good skills in experimental design and in statistical analysis of experimental data. Experience in programming and/or mathematical modelling is considered an asset.

**THE PLACE & THE PEOPLE:** The position is at the Department of Ecology and Evolutionary Biology at the University of Jyväskylä, Finland. To quote a recent international evaluation: "This is a very happy, collaborative and successful department with highly motivated and enthusiastic members of uniform high quality." The postdoc will join a group led by Dr. Mikael Puurtinen < <http://users.jyu.fi/~hemipu/> > (Academy Research Fellow 2013-2017), which at the moment consists of the PI, one Post-Doc, two PhD students and one MSc student. The applicant will also become a member of the Centre of Excellence in Biological Interactions (<https://www.jyu.fi/bioenv/en/divisions/coe-interactions>), which offers excellent networking possibilities among top scientists.

**APPLICATION:** In the application, include a brief letter of motivation, CV, and contact details of two senior academics available for reference. View the full job announcement and submit the application < [https://www.saimanet.com/certiahome/open\\_job\\_view.html?did=5600&jc=12&id=0000905&lang=fi](https://www.saimanet.com/certiahome/open_job_view.html?did=5600&jc=12&id=0000905&lang=fi) > by April 15, 2015. (link address: [https://www.saimanet.com/certiahome/open\\_job\\_view.html?did=5600&jc=12&id=0000905&lang=fi](https://www.saimanet.com/certiahome/open_job_view.html?did=5600&jc=12&id=0000905&lang=fi))

**INFORMAL QUERIES** are welcome, send email to mikael.puurtinen@jyu.fi.

Dr. Mikael Puurtinen Department of Biological and En-

vironmental Science Centre of Excellence in Biological Interactions University of Jyväskylä, Finland tel. +358 50 3758975

"Puurtinen, Mikael" <mikael.puurtinen@jyu.fi>

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## U Lausanne Bioinformatics

Postdoc in bioinformatics

A postdoc position is available on a project to study the evolutionary dynamics of genomes and transcriptomes. The postdoc will work in collaboration on two projects:

(1) Evo-devo genomics, in the Robinson-Rechavi lab: evolutionary study of the duplication history of chordate genomes, including de novo assembly of a Mediterranean amphioxus genome from PacBio long reads, and comparative transcriptomics analysis from RNA-seq; (2) Evolution of sex chromosomes, in the Pannell and Perrin labs: assembly and polymorphism analysis of sex chromosomes from plants and amphibians.

The postdoc would be expected to take a leading position on the bioinformatics of the genomics of non-model organisms, and to participate actively in evolutionary analyses and interpretation. The postdoc will work closely with other bioinformaticians and evolutionary genomicists on both projects. In the medium term, the postdoc will be expected to develop his or her own subproject and publications.

The position will be in co-supervision between Profs Marc Robinson-Rechavi, John Pannell and Nicolas Perrin, all three in the Department of Ecology and Evolution. Prof Robinson-Rechavi is also a group leader at the Swiss Institute of Bioinformatics, and the postdoc will also be a full member of the SIB. The starting contract will be for 1 year, starting as soon as possible, renewable for up to five years; the postdoc will participate in some undergraduate and/or masters teaching, in English or in French.

The ideal candidate would have a doctorate degree in bioinformatics, genomics, or a related field; a good command of Unix and another programming language; hands-on experience with genomic data; and an interest in pursuing research on non model organisms. Experience with the R language and cluster computing would be beneficial.

Full applications, which should include a cover letter, a CV, and the contact information of 3 referees, should

be sent to marc.robinson-rechavi@unil.ch as a single PDF document. Informal enquiries should be directed to marc.robinson-rechavi@unil.ch; john.pannell@unil.ch; and/or nicolas.perrin@unil.ch.

Deadline for applications: all applications received by April 12, 2015, will be given full consideration, but the position will remain open until the right candidate has been appointed.

For background on the labs in which you would be working, please see: Robinson-Rechavi lab: <http://bioinfo.unil.ch/> Pannell lab: <http://www.unil.ch/dee/home/menuinst/research/group-pannell.html> Perrin lab: <http://www.unil.ch/dee/home/menuinst/research/group-perrin.html>

Pannell John Richard <John.Pannell@unil.ch>

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## UManchester Trait Variation Genetics

We are recruiting a postdoctoral research associate to work on the genetics of natural trait variation in a social microbe. This is a 36 month position based in Prof Chris Thompson's Lab at the University of Manchester. The postdoc will work as part of a collaborative team that includes researchers at the University of Bath and the Federal University in Sao Carlos (Brazil). Further details about the project and the position are included below:

Explaining why so much natural genetic variation exists in fitness related traits is a fundamental problem in evolutionary genetics. Many competing explanations have been proposed, but cleanly distinguishing between them experimentally has been challenging. For example, we find surprisingly high genetic variation in key fitness related social behaviour traits across a huge diversity of taxa, despite a general expectation that variation will be removed by selection. To understand the processes shaping such variation we will employ a novel combination of approaches to dissect the genetics and evolution of social and non-social traits using the social amoeba *D. discoideum* (Dd). The Dd system provides a uniquely powerful model to dissect the processes shaping genetic diversity in a natural microbial population, while providing critical insights into how the genomes of more complex species are shaped by evolution.

Specifically, we will employ a powerful integration of computational, genomic and experimental approaches:

- . high throughput phenotyping will be used to quantify phenotypic variation in a range of social and non social traits.

- . whole genome sequencing will be used to identify genes that show sequence variation associated with natural diversity in social and non-social traits,

- . you will experimentally validate the causal role of natural genetic variants using cutting edge molecular and gene replacement techniques,

- . you will test whether the same genes affect both social and non-social traits, suggesting that they are constrained and their joint evolution is shaped by pleiotropy,

- . using this data we will develop models to determine the evolutionary processes that have shaped variation in this system.

Together, these objectives will lead to fundamental advances in our understanding of the types of variation underlying phenotypic diversity in natural populations and the evolutionary processes shaping that variation.

The Thompson lab at the University of Manchester has extensive experience in whole genome, molecular genetics and experimental evolution approaches in *Dictyostelium*. For further information, see <http://thethompsonlab.wordpress.com>).

Professor Chris Thompson Email: Christopher.thompson@manchester.ac.uk Telephone: 0161 275 1588

For further details and how to apply see:

<https://www.jobs.manchester.ac.uk/-displayjob.aspx?jobid11> Note that this position is funded under the same project as previous advertised positions at the University of Bath based in the lab of Jason Wolf. For more information about these other positions, please see:

Postdoc (36 months) using computational and empirical approaches to understand natural variation in social and non-social traits: <https://www.bath.ac.uk/jobs/Vacancy.aspx?idX06> Technician (at least 24 months), who will contribute to all aspects of the project: <https://www.bath.ac.uk/jobs/-Vacancy.aspx?idX54> (NOTE THAT THIS POSITION LISTS A MAY START DATE, BUT LATER START DATES ARE POSSIBLE)

jason@evolutionarygenetics.org

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## UMissouri DinosaurCranialBiomechanics

Casey Holliday (hollidayca@missouri.edu) and I (middletonk@missouri.edu) have an opening for a three-year, NSF-funded postdoc to study cranial biomechanics and evolution in dinosaurs in collaboration with Larry Witmer (Ohio University) and Julian Davis (University of Southern Indiana). Details and application information are below. Feel free to pass along to interested researchers and direct any questions to Casey or me.

—  
Kevin Middleton, Ph.D. Department of Pathology & Anatomical Sciences University of Missouri School of Medicine <http://web.missouri.edu/~middletonk> —

### Position Details:

Project title: Evolution of Dinosaur Jaw Musculature and the Origins of Avian Cranial Kinesis. Postdoctoral Fellow, University of Missouri, Columbia, MO.

The Department of Pathology and Anatomical Sciences at the University of Missouri School of Medicine invites applications for a postdoctoral research associate. The position is for one year and is renewable up to 3 years. The successful applicant will work under the supervision of Drs. Casey M. Holliday and Kevin M. Middleton on a National Science Foundation-funded program in 3D Cranial Biomechanics and Morphometrics. The position is 80% Research and 20% Outreach (allocation is negotiable) and offers a competitive salary plus benefits. Review of applications will begin March 1, 2015 and remain open until filled with an anticipated start date of August 1, 2015.

### Responsibilities:

- 1) The candidate will work directly with PIs Holliday, Middleton, Davis, and Witmer to develop and conduct analyses of cranial biomechanics and morphometrics of fossil and extant dinosaur species.
- 2) The candidate will help develop 3D anatomical and biomechanical visualizations and mobilize these data to appropriate online databases and outreach locations.
- 3) The candidate will present findings in collaboration with project leaders and associated students. The candidate will develop and participate in the Inside Dinosaurs education and outreach program at University of Missouri. Funds for research expenses and travel are

available.

### Qualifications:

By the start date, all elements of the PhD, including the dissertation, must be completed and the degree conferred in biological, earth sciences, engineering or similar field, with an emphasis on vertebrate biomechanics and paleobiology.

Additional qualifications include demonstrated experience in one or more of the following: 3D computational biology, Morphometric analysis, and/or 3D anatomical visualization such as experience working with CT image data and with 3D model rendering software (Amira, Maya), MATLAB, and R; demonstrated experience managing personnel and leading research projects; and demonstrated ability to publish in English-language peer-reviewed journals.

Preference will be given to individuals with interests in morphology-based research and whose interests complement those of current faculty in the Integrative Anatomy group (<http://anatomy.missouri.edu>) will be given priority. The Integrative Anatomy Group provides a collegial environment with substantial opportunities for intellectual creativity and diverse research.

### Application Materials:

To apply please submit (1) cover letter including contact information for three references; (2) curriculum vitae; and (3) a research statement including previous experience and future plans

University of Missouri web site is [hrs.missouri.edu/find-a-job/academic/](http://hrs.missouri.edu/find-a-job/academic/). At the top of the webpage, select prospective employees and search for pathology to reach the link for the position. The Job ID number is 15786.

[middletonk@health.missouri.edu](mailto:middletonk@health.missouri.edu)

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## UMontana EvolutionaryGenomics SexualSelection

Postdoc:EvolutionaryGenomicsSexualSelection.University\_of\_Montana  
Post-doctoral RESEARCH FELLOW: EvolutionaryGenomicsSexualSelection The University of Montana, to study the genetic basis for rapid weapon evolution in rhinoceros beetles

Application deadline: 31 March 2015 Start date: between May and June 2015

Doug Emlen at the University of Montana, Missoula,

in collaboration with Laura Corley Lavine, Washington State University, is seeking an Evolutionary Biologist with programming/bioinformatics/genomics experience to explore the evolution of extreme weapons in rhinoceros beetles. This project focuses on populations of rhinoceros beetle that differ dramatically in the relative size of a weapon, a pitchfork horn projecting from the heads of males. The successful candidate will join our international collaborative team to help sample animals from populations across Asia, prepare and sequence whole genomic DNA from these samples using RAD-seq, and use divergence mapping approaches to screen for evidence of recent selection. In addition, the candidate will use RAD-seq to conduct a QTL analysis on F2 animals produced from a cross between a long- and a short-horned population. Proposed genetic studies build on a decade of prior research by the PIs and their collaborators on the developmental mechanisms regulating horn growth in this species, which have identified a rich suite of candidate developmental genes and pathways.

The successful candidate will join a vibrant and productive department with a thriving evolutionary genetics group (<http://cas.umt.edu/dbs/default.php>), and will be expected to maintain consistently high research output in the form of quality publications, supervise and train students, contribute generally to research activities of the group, and participate in appropriate career development activities. The position is for two years subject to satisfactory annual progress.

Requirements: - A PhD in evolutionary genetics, population genetics, or genomics, with extensive experience in next-generation sequencing, preferably RAD-seq - A publication track record in high-quality journals that clearly reflects the ability to conduct and publish research in the field of evolutionary genetics - Demonstrated evidence of a strong interest in applying state-of-the-art molecular methods to current evolutionary questions with meticulous attention to detail and high quality lab work - Strong quantitative/programming skills are highly advantageous - Ability to work independently in a collaborative research team - Experience in or enthusiasm for supervision and training of students - Ability to communicate effectively with other scientists at the interface of lab and field ecology

Send a letter that addresses these requirements and includes a brief statement about why you are interested in this post-doc plus a full academic CV that includes the names and contact details (email, phone) of 3 references, to Doug Emlen ([doug.emlen@mso.umt.edu](mailto:doug.emlen@mso.umt.edu)). Review of applications will begin on 31 March 2015, and will continue until the position is filled.

Doug Emlen <[doug.emlen@mso.umt.edu](mailto:doug.emlen@mso.umt.edu)>

"Emlen, Doug" <[doug.emlen@mso.umt.edu](mailto:doug.emlen@mso.umt.edu)>

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## UNamur Belgium Bioinformatics

\*Postdoctoral bioinformatician in Evolutionary genomics, UNamur, BE\*

A 3-year postdoctoral bioinformatician position is available to work on the genome evolution of bdelloid rotifers within the group of Prof. Karine Van Doninck (Laboratory of Evolutionary Genetics and Ecology) at the University of Namur (Belgium). The postdoctoral researcher will work on two projects, funded by ARC and FNRS-MIS, with as main objective to investigate the origin and causes of the genomic peculiarities found in the bdelloid rotifer *A. vaga*.

Using next-generation sequencing (NGS) we previously characterized the degenerate tetraploid genome structure of the bdelloid rotifer *A. vaga* with massive genomic rearrangements involving most of the longest scaffolds. As a consequence, no homologous pair of chromosomes could be identified within this genome providing the first genomic hallmark of ameiotic evolution within this bdelloid rotifer clade. Another peculiarity observed in the genome of *A. vaga* is the high percentage of genes (8%) of non-metazoan origin and probably acquired through horizontal gene transfer (HGT) (see Flot et al. Nature 2013). These features could be conferred by their long-term ameiotic evolution. Nonetheless, the unusual lifestyle of many bdelloid rotifers, involving repeated cycles of desiccation and the associated DNA DSBs (see Hespels et al. JEB 2014), may also contribute to genome structure evolution. In order to determine the origin and causes of these genomic peculiarities we are starting a comparative analysis of genomes of different bdelloid species that diverged a long time ago, including lineages that have lost the ability to withstand desiccation, and of an *A. vaga* clone submitted to several rounds of desiccation. The postdoc will conduct bioinformatic analyses of genomic (and transcriptomic) data generated by the team. The current team of researchers working on bdelloid rotifers within the 2 projects include 3 Principal Investigators (Prof. K. Van Doninck and Dr. F. Chainiaux from UNamur and Prof. B. Hallet from UCL), 2 postdoctoral researchers, 3 PhD students, 2 Master students and 2 technicians.

\*Contacts:\*

Prof. Karine Van Doninck,  
karine.vandoninck@unamur.be

University of Namur, Laboratory of Evolutionary Genetics and Ecology

<http://www.lege-unamur.be> \*Application://\*

Applicants should have a PhD in a relevant area. Priority will be given to candidates with a proven track record (with several publications as a first author) who will express their motivation to the project.

The position is for 3 years starting latest on the 1<sup>st</sup> of July 2015. \*The closing date for applications is 5<sup>th</sup> of May, 2015. \*Interested applicants should send a cover letter (briefly describing research experience, interests, and career goal), curriculum vitae (with list of publications), and the names of three references (including address, phone number and Email) to Karine VAN DONINCK (karine.vandoninck@unamur.be)\*\*

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Karine VAN DONINCK Full Professor Department of Biology

T. +32 (0)81 724 407 F. +32 (0)81 724 362  
karine.vandoninck@unamur.be <http://perso.fundp.ac.be/~kvandoni/> Université de Namur ASBL Rue de Bruxelles 61 - 5000 Namur Belgique

Let's respect the environment together. Only print this message if necessary!

Karine Van Doninck <karine.vandoninck@fundp.ac.be>

## UNewEngland Australia PlantSpeciationGenomics

We've extended our postdoc position to the 30th of March (see below). The HR server has been preventing submissions for several days and I haven't had a clear answer on when they'll have it fixed, so please let me know if you've been affected or if you have any other questions about the position. Rose rose.andrew@une.edu.au

Postdoctoral Research Fellow (Plant Speciation Genomics)

We are seeking a highly motivated postdoctoral researcher to fill an ARC Discovery-funded postdoctoral position. The project will involve whole-genome shotgun sequencing of many individuals across 10 woodland Eu-

calyptus species. This widespread genus of Australian trees includes several hybridising species that co-occur in woodlands across large portions of Eastern Australia, offering an unusual degree of replication for studying comparative landscape genomics and the role of inter-specific gene flow in local adaptation. A second aim of the project is landscape genomic association studies on thousands of trees to identify environmentally adaptive loci. A third aim will be to validate adaptive loci segregating in hybrid progeny by growing seedlings in climate chambers phenotyping stress response with plant phenomics.

To be considered for this position applicants must have a PhD in Evolutionary Genetics, Genomics or a related area, with an excellent research record relative to opportunity, including articles in high quality, peer-reviewed journals. In addition the successful applicant will have research experience in population genomics, admixture analysis and/or landscape genomics.

This is a full-time fixed-term position available for 2 years, with the possibility of further appointment, subject to the availability of funding. The successful candidate will be expected to participate actively in the School and to interact with undergraduate and postgraduate students in the research group. The research fellow will join Dr Rose Andrew's research group at UNE, which conducts genome-enabled research on adaptation and speciation in a range of organisms (e.g. orchids, sunflowers, feral cats). This project is a collaboration with Professor Justin Borevitz at the Australian National University, who specialises in plant genomics for climate adaptation and high-throughput phenotyping.

Informal enquiries may be directed to Dr Rose Andrew, phone: +61 2 6773 3160 or email rose.andrew@une.edu.au. To find out more about the school visit: <https://www.une.edu.au/about-une/-academic-schools/school-of-environmental-and-rural-science> About UNE and Armidale: The University of New England, as Australia's oldest regional university, has a long history of excellence in research across many major fields of study, including Ecology and Botany. The School of Environmental and Rural Science is home to the N.C.W. Beadle Herbarium and has strengths in animal and plant genetics, and evolutionary biology. Armidale a vibrant university city recognized as a centre of culture, is well served with art, music, theatre, sport and public and private education. To explore our region visit: [www.armidaleregion.com.au/](http://www.armidaleregion.com.au/) and/or [www.experiencethehighs.com.au/](http://www.experiencethehighs.com.au/) \* 2 years fixed-term, full-time, with possible extension subject to funding availability \* \$75,717 Salary to \$81,196 Salary per annum (Level A) \* Plus up to 17% employer superannuation contribution. Optional salary packaging

is available.

\*\*\*\*\*New Closing Date: 9am on the 30th March (AEDT)\*\*\*\*\* Reference No: 215020 Applicants must provide a response to each of the selection criteria contained in the position statement at [www.une.edu.au/-jobs-at-une](http://www.une.edu.au/-jobs-at-une), where applications are also to be lodged. Equity principles underpin all UNE policies and procedures.

Dr Rose Andrew Lecturer in Molecular Ecology School of Environmental and Rural Science University of New England Armidale, NSW, 2351 AUSTRALIA Ph: +61 2 6773 3160 [rose.andrew@une.edu.au](mailto:rose.andrew@une.edu.au) <http://www.une.edu.au/-staff-profiles/randre20> <https://sites.google.com/site/roseandrewresearch/> [randre20@une.edu.au](mailto:randre20@une.edu.au)

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## UNewHampshire BeeSociogenomics

The laboratory of Dr. Sandra Rehan is seeking a Postdoctoral Scholar. This 36-month position is in collaboration with the lab of Dr. Amy Toth at Iowa State University ([amytoth@iastate.edu](mailto:amytoth@iastate.edu); [http://www.public.iastate.edu/~amytoth/Toth\\_lab/Home.html](http://www.public.iastate.edu/~amytoth/Toth_lab/Home.html)), a PhD position is available at Iowa State University, and funded by the NSF-IOS Animal Behavior Program. The Postdoctoral Scholar position at the University of New Hampshire involves comparative genomics and transcriptomics to understand the molecular basis of sociality in bees. We are seeking expertise in bioinformatics, especially comparative genomics and molecular evolution of social insects. Possibilities for both fieldwork and molecular biology exist. Candidates should demonstrate a track record of publication; have strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team. For further information, please feel free to contact Dr. Rehan ([sandra.rehan@unh.edu](mailto:sandra.rehan@unh.edu); [www.unhbeelab.com](http://www.unhbeelab.com)). Interested applicants should email a curriculum vitae, a 1-2 page statement of research interests that explicitly describes professional qualifications for this position, and contact information for three referees. Review of applications will begin April 1st 2015, and continue until a suitable candidate is found.

Sandra Rehan, Assistant Professor Department of Biological Sciences University of New Hampshire 191 Rudman Hall, 46 College Road Durham, NH, USA 03824 mobile phone: (267) 650-2528 office phone: (603) 862-5310 office fax: (603) 862-3784 email: [sandra.rehan@unh.edu](mailto:sandra.rehan@unh.edu)

website: [www.unhbeelab.com](http://www.unhbeelab.com) [sandra.rehan@gmail.com](mailto:sandra.rehan@gmail.com)

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## UNotreDame MalariaComputBiol

Computational Biology of Pathogen Drug Resistance Evolution

The Ferdig lab (<http://www3.nd.edu/~ferdilab/>), in The Eck Institute for Global Health and the Department of Biological Sciences at the University of Notre Dame, is seeking a computational biologist with interest in network-based inference and large-scale data integration. The fellow will work both independently and as part of a collaborative team using whole-genome approaches to study drug targets and drug resistance evolution in the malaria parasite, *Plasmodium falciparum*.

A range of available projects includes: (1) Characterization and mining of transcript and regulatory networks of drug resistant parasites; (2) Systems genetics, using segregating parasite populations and mutant parasite libraries along with genome-scale data to connect genotypes to phenotypes; and (3) Integration of newly generated and existing public data to find drug targets, map chemical/cellular space not currently exploited by drugs and to predict effective drug combinations.

To align with these projects, the candidate should have a strong working knowledge of cellular mechanisms and biological pathways along with interest/expertise in one or more of the following:

- Regulation of gene expression; network analytical methods and data mining; accessing and integrating data resources; evolutionary genomics - Mining of biological information, including transcript data from both microarrays and RNAseq; machine learning; skills in scripting languages such as Python, Perl, Matlab, or R.

The position is designed to ensure a strong training trajectory for a computational scientist aspiring to an independent research career. This includes a rich opportunity to interface with other quantitative/computational/evolutionary biologists across campus, including the Interdisciplinary Center for Network Science Applications (iCeNSA, <http://www.icensa.com/>), along with collaborators at other institutions. Salary will be at standard levels per NIH and institutional guidelines.

Submit a current C.V. and names of 3 references to Dr. Michael Ferdig, Professor, Department of Biological Sciences, University of Notre Dame, IN 46556-0369,

ferdig.1@nd.edu (574) 631-9973.

The Eck Institute for Global Health (EIGH, <https://globalhealth.nd.edu/>) is a university-wide institution that recognizes health as a fundamental human right and endeavors to promote research, training, and service to advance health standards for all people, especially people in low- and middle-income countries who are disproportionately impacted by preventable diseases.

The University of Notre Dame is an Affirmative Action/Equal Opportunity Employer. Women and minority candidates are encouraged to apply.

mferdig@nd.edu

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## UOregon BioinformaticsHostMicrobe

University of Oregon Posting 15063 Position Announcement

Post-doctoral Research Scholar: Bioinformatics of Host-Microbe Systems Microbial Ecology and Theory of Animals Center for Systems Biology

We are seeking a postdoctoral research scholar with significant expertise in bioinformatics and research interests at the intersection of mathematics, biology and computer science to join the Microbial Ecology Theory in Animals (META) Center at the University of Oregon ([meta.uoregon.edu](http://meta.uoregon.edu)). The META Center is an NIH-funded Center of Excellence in Systems Biology, focused on the development and application of biological theory, integrated with empirical studies, to better understand host-microbe systems. Every multicellular organism is associated with a diverse array of microbes, and although it has become evident that these microbes contribute significantly to their hosts  $V$  and that hosts influence their microbiota - the biological mechanisms underlying these interactions are still unclear. The META Center aims to generate fundamental new knowledge regarding these interactions by integrating concepts from genomics, developmental biology, ecology and evolution, and by developing new approaches for imaging, mathematical modeling, systems and functional biology, and analysis of next generation sequence data.

The ideal candidates will have a demonstrated record of past scholarly success and experience in developing and applying computational methods in the analysis of complex data sets, especially those that address problems that are computationally challenging and data intensive.

Preference will be given to candidates who can work independently as well as a member of a research team. Optimal candidates will be willing to work in a highly interactive group of researchers spanning a wide range of disciplines, and be eager to challenge themselves by working in novel areas bridging mathematics, biology and computer science. A strong interest in addressing fundamental questions about host-microbe systems using insights from ecological and evolutionary theory is especially desirable. This position also provides an opportunity to develop innovative curriculum for undergraduate and graduate level courses in bioinformatics. The successful candidate will support and enhance a diverse learning and working environment.

Applicants must have a Ph.D. from a relevant discipline, such as physics, mathematics, statistics, computer science, ecology, evolution, systems biology, microbiology, genomics or a related field. The positions are initially for a 1 year term with the possibility for renewal contingent upon satisfactory performance. The start date is flexible, but preference will be given to applicants who can begin before June, 2015. Please email questions regarding these positions, the META Center, or its scientific mission to any of the META Center scientists listed below:

Karen Guillemin ([kguillem@uoregon.edu](mailto:kguillem@uoregon.edu)) William Cresko ([wresko@uoregon.edu](mailto:wresko@uoregon.edu)) John Conery ([conery@uoregon.edu](mailto:conery@uoregon.edu))

To apply, please include as a single attachment: (1) a brief cover letter explaining your background and career interests (2) CV (including publications), (3) names and contact information for three references.

Submit materials to [ie2jobs@uoregon.edu](mailto:ie2jobs@uoregon.edu). Subject: META Posting 15063 To ensure consideration, please submit applications by April 2, 2015. This position will remain open until filled.

Women and members of groups underrepresented in science are encouraged to apply. We invite applications from qualified candidates who share our commitment to diversity. The University of Oregon is an EO/AA/Veterans/Disability institution committed to cultural diversity.

<http://jobs.uoregon.edu/unclassified.php?id=5039> – INSTITUTE OF ECOLOGY AND EVOLUTION 5289 University of Oregon, Eugene OR 97403-5289 F (541) 346-2364 <http://IE2.uoregon.edu> EO/AA/ADA institution committed to cultural diversity. The University encourages all qualified individuals to apply, and does not discriminate on the basis of any protected status, including veteran and disability status.

[ie2jobs@uoregon.edu](mailto:ie2jobs@uoregon.edu)



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## UOregon MicrobialEcology Bioinformatics

Postdoctoral Research Scholar in Bioinformatics/Microbial Ecology Institute of Ecology and Evolution Posting: 15074

Jessica Green (<http://biology.uoregon.edu/people/-green/>) is currently seeking a bioinformatics postdoctoral research scholar to explore fundamental questions in microbial ecology and evolution. Applicants must have a Ph.D. with extensive training using bioinformatics to understand the ecology and/or evolution of complex biological systems, and strong writing skills. The ideal candidate will have experience with statistical analysis, next-gen sequence data analysis, software development, and/or experience with combining and analyzing complex datasets from multiple sources and technologies. The successful candidate will have the ability to work effectively with faculty, staff and students from a variety of diverse backgrounds.

The successful candidate will have the opportunity to creatively and independently engage in research at the Biology and Built Environment (BioBE) Center (<http://biobe.uoregon.edu/>), funded by the Alfred P. Sloan Foundation. The BioBE Center is training a new generation of innovators to study the built environment microbiome - the diversity of microorganisms interacting with each other and with the indoor environment. The vision of this national research center is to understand buildings as complex ecosystems and to explore how architectural design mediates urban microbial ecology and evolution. For a description of partner projects see <http://www.microbe.net/>. The position is available for 1 year with the possibility for renewal depending on performance. The start date is flexible. Please email questions regarding the position to Jessica Green ([jl-green@uoregon.edu](mailto:jl-green@uoregon.edu)).

To apply

A complete application will consist of the following materials in a single attachment:

- (1) a brief cover letter explaining your background and career interests
- (2) CV (including publications),
- (3) names and contact information for three references.

Submit materials to [ie2jobs@uoregon.edu](mailto:ie2jobs@uoregon.edu). Subject:

BioBE Posting 15074

To ensure consideration, please submit applications by April 2, 2015. This position will remain open until filled.

The University of Oregon is an equal opportunity, affirmative action institution committed to cultural diversity and compliance with the ADA. The University encourages all qualified individuals to apply, and does not discriminate on the basis of any protected status, including veteran and disability status.

– INSTITUTE OF ECOLOGY AND EVOLUTION 5289 University of Oregon, Eugene OR 97403-5289 F (541) 346-2364 <http://IE2.uoregon.edu> EO/AA/ADA institution committed to cultural diversity. The University encourages all qualified individuals to apply, and does not discriminate on the basis of any protected status, including veteran and disability status.

[ie2jobs@uoregon.edu](mailto:ie2jobs@uoregon.edu)

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## UOregon MicrobialEcologyEvolution

Postdoctoral Research Scholar - Microbial Ecology and Evolution Posting 15060 Institute of Ecology and Evolution Brendan Bohannan at the University of Oregon (<http://pages.uoregon.edu/bohannanlab/>) is currently seeking a postdoctoral research scholar to explore fundamental questions in microbial ecology and evolution. Applicants must have a Ph.D. in a biological, computational, or mathematical field and strong writing skills. Experience developing and applying theory and and/or modeling to microbial systems is highly desirable.

The successful candidate will support and enhance the university's and the institute's commitment to diversity and be a key member of the META Center for Systems Biology (<http://meta.uoregon.edu>). The Microbial Ecology and Theory of Animals (META) Center for Systems Biology is devoted to understanding how host-microbe systems function and how this knowledge can be used to advance human health. The successful candidate will interact closely with other META Center members, as well as take a leadership role in the Bohannan Research Group. We are especially interested in candidates who have a strong desire to ask fundamental ecological and evolutionary questions of host-associated microbial communities. Women and minorities encouraged to apply. We invite applications from qualified candidates who share our commitment to diversity. The position is available for 1 year with the possibility of renewal con-

ditional on performance and funding. The start date is flexible. Please email questions regarding the position to Brendan Bohannon (bohannon@uoregon.edu). To apply A complete application will consist of the following materials in a single attachment: (1) a brief cover letter explaining your background and career interests (2) CV (including publications) (3) names and contact information for three references Submit materials to ie2jobs@uoregon.edu. Subject: Posting 15060 To ensure consideration, please submit applications by April 2, 2015. This position will remain open until filled. Position subject to criminal background check. EO/AA/Veterans/Disability institution committed to cultural diversity.

<http://jobs.uoregon.edu/unclassified.php?id=5037> – INSTITUTE OF ECOLOGY AND EVOLUTION 5289 University of Oregon, Eugene OR 97403-5289 F (541) 346-2364 <http://IE2.uoregon.edu> EO/AA/ADA institution committed to cultural diversity. The University encourages all qualified individuals to apply, and does not discriminate on the basis of any protected status, including veteran and disability status.

ie2jobs@uoregon.edu

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### UOslo 3yr AvianHybridization

3-year research position in Evolutionary Genetics at Centre for Ecological and Evolutionary Synthesis (CEES), University of Oslo (UiO)

The project is part of a larger research program entitled “On the role of hybridisation in evolution-the case of Eurasian Passer Sparrows ” funded by the Norwegian Research Council.

Hybridization can have different evolutionary outcomes, ranging from speciation reversals to hybrid speciation. The Italian sparrow (*Passer italiae*) is the first documented case of hybrid speciation in birds (Hermansen et al. 2011). This bird originated from past events of hybridization between two divergent parental species, the house sparrow (*P. domesticus*) and the Spanish sparrow (*P. hispaniolensis*) some thousands of years ago. Today, the hybrid taxon is sympatric or parapatric with both parent species in certain regions, enabling investigations of current gene flow and the nature of reproductive barriers. Moreover, the parent species live sympatrically in large regions around the Mediterranean Sea, enabling comparisons of the reproductive barriers that isolate the parent species with those that isolate the hybrid species

from either parent.

The project integrates evolutionary genetic, genomic, quantitative genetic and ecological approaches to investigate the consequences of hybridization in the interplay with recombination and selection. Phenotypes of interest include beak morphology, plumage coloration, vocalization, migration behaviour and intrinsic reproductive barriers (genetic incompatibilities). Of genomic resources we have de novo assembled the house sparrow genome, which will be used as a reference for resequencing and genotyping efforts in this project. We aim at increasing our understanding of the modularity of the genome and of the processes of adaptation and speciation. The successful candidate will be allowed to choose aspects of the larger program as best fits her/his skills and research interests. She/he will also be encouraged to develop additional, complementary avenues of research.

The candidate must have a PhD or other corresponding education in a relevant field, such as evolutionary biology, genomics, genetics and/or bioinformatics. Documented skills in population genetic/genomic and/or quantitative genetic analysis will be emphasized.

The research will be conducted in close collaboration with Prof. SÅtre and his group at CEES. The research team will also include other scientists from Norway, Sweden and Finland. The working language will be English. Fieldwork may be conducted at a variety of locations, including Italy and other Mediterranean countries.

The application must include: Application letter, CV, copies of educational certificates, transcript of records, A complete list of publications and up to 5 academic works, Names and contact details of 2-3 references.

Apply online within 24th March via Easyrecruit: <http://uio.easycruit.com/vacancy/1351119/-96871?iso=no> Contact: Glenn-Peter SÅtre, e-mail: g.p.satire@ibv.uio.no

Anna Runemark <anna.runemark@ibv.uio.no>

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### UOtago EvolutionaryGeneticsZosterops

Postdoctoral Fellow - Zoology (1500512)

DEPARTMENT OF ZOOLOGY UNIVERSITY OF OTAGO DUNEDIN NEW ZEALAND

Applications are invited for the 3-year, fixed-term posi-

tion of Postdoctoral Fellow. The successful candidate will be working on a Marsden-funded research project titled “Are genetic shifts in dispersal ability key to resolving the ”paradox of the great speciators“?” and will involve conducting genetic research on the South Pacific *Zosterops white-eyes*.

The “paradox of the great speciators” has puzzled evolutionary biologists for over half a century. A great speciator requires excellent dispersal ability to explain wide distributions, but reduced dispersal ability to explain high numbers of divergent, isolated forms. Rapidly changing dispersal abilities are assumed, but identifying a mechanism has proved elusive. This project takes a novel approach by examining genetic changes at “migration” genes in a great speciator (the *Zosterops white-eyes*). These genes were recently shown to switch migrants into year-round residents in other species. These genetic switches may simultaneously affect dispersal and behavioural characteristics within populations and individuals leading to differentiation of populations, potentially leading to speciation. The white-eyes of the south Pacific are an ideal study system as repeated island colonisation and divergence has occurred over a range of timescales, from hundreds to hundreds of thousands of years. They also display varying dispersal ability along the continuum from migratory to resident, with some populations containing both migrating and non-migrating individuals, allowing us to examine the genetic switches at the level of the population and individual. The study will be the first to address the role that evolutionary shifts in genes associated with dispersal ability play in speciation and provide a resolution to an enduring paradox.

A PhD and research experience in evolutionary genetics is essential. Experience in analysis of candidate genes associated with migration or animal personality would be an advantage, as would experience with catching, handling and blood sampling small passerine birds.

The appointment is expected to start within the following period: July 2015 to October 2015.

The project is funded by a Marsden grant to Dr Bruce Robertson (University of Otago, <http://www.otago.ac.nz/zoology/staff/otago008933.html>) and Dr Sonya Clegg (University of Oxford, <http://www.zoo.ox.ac.uk/egi/members/dr-sonya-clegg/>) (Principal Investigators) in collaboration with Prof Ian Owens (Natural History Museum, London, <http://www.nhm.ac.uk/our-science/departments-and-staff/staff-directory/ian-owens.html>).

Specific enquiries may be directed to Dr Bruce Robertson, [bruce.robertson@otago.ac.nz](mailto:bruce.robertson@otago.ac.nz)

Applications quoting reference number 1500512 will close on Tuesday, 31 March 2015.

Further details and applications: <https://otago.taleo.net/careersection/2/jobdetail.ft!lang=en&job=1500512> [sonya.clegg@zoo.ox.ac.uk](mailto:sonya.clegg@zoo.ox.ac.uk)

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## UOtago NZ GenomicsComplexCognition

Postdoctoral Opportunity

Fixed term, One year

Genomic Investigation of Complex Cognition

We are currently seeking an outstanding Postdoctoral with experience in genomics and to conduct research into the genetic basis of complex cognition in New Caledonian crows.

**Project Description:** The discovery of complex avian cognitive abilities has revolutionized our understanding of the evolution of intelligence. However, the genetic basis of these abilities is unknown. One possibility is that numerous changes in genes across a wide range of functional domains are required for the evolution of complex intelligence. Alternatively, only a limited number of genetic tweaks might be required. We seek a postdoctoral fellow to undertake genomic comparisons between the tool manufacturing New Caledonian crow and closely related non-tool-using crows to search for genes that underpin a tool-using lifestyle.

The project emerges from a Marsden Grant headed by Dr Gavin Hunt (Auckland) in collaboration with Profs Neil Gemmill (Otago) and Russell Gray (Max Planck Institute for History and the Sciences, Jena; Auckland). The position will be based in the Gemmill laboratory at the University of Otago.

**The Ideal Candidate:** The ideal candidate will possess experience in molecular genetics/genomics, evolutionary biology and bioinformatics. Knowledge of NGS approaches and analyses is essential, while past work in comparative genomics and an interest in neurobiology and cognition may be helpful. The successful candidate will be motivated and organised, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research project.

**Minimum qualifications:** PhD in Genetics, Genomics, Molecular Biology or equivalent.

Eligibility: The position is open to all nationalities.

Salary Level and Range: Postdoctoral Fellow (\$72,046), Fixed term until 2016

How to Apply: Interested applicants are encouraged to make informal enquiries to Professor Neil Gemmell. Please send your Curriculum Vitae, a copy of your academic transcript, a sample of your written scientific work and the names of three referees with a covering letter to:

Professor Neil J. Gemmell e-mail: neil.gemmell@otago.ac.nz

Applications close on the 28th March and it would be desirable if the successful applicant were able to start by mid 2015.

Professor Neil J. Gemmell Head of Department Department of Anatomy University of Otago, PO Box 913 Dunedin 9054 New Zealand

Phone: +64 3 479 6824 Fax: +64 3 479 7254  
e-mail: neil.gemmell@otago.ac.nz Web: <http://gemmell-lab.otago.ac.nz/> Allan Wilson Centre for Molecular Ecology and Evolution: <http://www.allanwilsoncentre.ac.nz/> Gravida - National Centre for Growth and Development: <http://www.gravida.org.nz/> Neil Gemmell <neil.gemmell@otago.ac.nz>

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## UOulu PopulationStatisticalGenomics

Post doc in population and statistical genomics at the University of Oulu

Post doctoral position for two years available in the Population and statistical genomics (PSG) research team <http://www.oulu.fi/popstatgen> at the University of Oulu, in the Genetics and Physiology unit.

The team consists of five different research groups, dealing with genomics of adaptation of plant populations (Outi.Savolainen at oulu.fi), with conservation genetics of especially large carnivores (Jouni.Aspi at oulu.fi), of statistical genomics, especially variable selection methods (Mikko.Sillanpaa at oulu.fi), systematics and evolutionary genetics of Lepidoptera and of social insects (Marko.Mutanen at oulu.fi) and human cancer functional genomics (Gonghong.Wei at oulu.fi).

The post doc will be associated with one of these groups

to conduct research on topics studied in the group. Some 10-20 % of the time will be allocated to shared interests of the whole team. We seek a highly motivated Ph.D. with interest in the topics represented by the groups, expertise in population genomics and bioinformatics and international experience. The position will be based on the Linnanmaa campus, where all groups except for the cancer biology group are based. Applications should include a letter describing your interest, your CV and list of publications, and names of three possible persons to ask for letters of reference. All the materials should be submitted as one single pdf to kirjaamo@oulu.fi, by March 23rd, 2015.

For the official announcement, please see [https://www.saimanet.com/certiahome/-open\\_job\\_view.html?did=5600&jc=1&id=0000863&lang=en](https://www.saimanet.com/certiahome/-open_job_view.html?did=5600&jc=1&id=0000863&lang=en) . For information, please be in touch with Outi.Savolainen@oulu.fi and/or the other PIs.

Outi Savolainen <Outi.Savolainen@oulu.fi>

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## UPernambuco Brazil EvolutionaryBiol

Dear EvolDir members

The PPGBA - Graduate Program in Animal Biology , Zoology Department, Universidade Federal de Pernambuco, Northeastern Brazilian coast - will be selecting 1 PostDoc Fellow (PNPD Capes) to develop scientific and educational activities within the PPGBA . The scholarship will be valid for 12 to 60 months . The scholarship amount is R\$3,800.00 (around USD 1,500.00) monthly. Note that FACEPE - Foundation for Science and Technology of the State of Pernambuco - can supplement the scholarship in R\$ 1,200.00 (USD 600.00) . Candidates should express their interest to participate in the selection by presenting a work plan, stating the research project and discipline plan with simplified menu to be offered in PPGBA UNTIL 03/25/2015. It is still offered to the selected candidate the possibility of co-supervision of Master's Dissertation and/or Doctorate Thesis in the area of the Supervisor.

Thus, the Laboratory of Evolutionary and Environmental Genomics, led by Dr. Rodrigo A. Torres (lagea.com.br) has full interest for hosting an associate researcher with remarkable scientific production. It is preferred but not mandatory applications for Brazilians.

It is offered excellent working infrastructure in the areas of Conservation Genetics, Molecular Systematics, and Conservation of species and ecosystems through analysis of genome damaging. Additionally, our team is now composed of one PostDoc, four PhD students, three MSc. students, and undergraduate students. Our lab expects candidates with at least 5 papers accepted/published at the qualis B1 or higher in the area of BIODIVERSITY-CAPES . For details see the WebQualis ( <http://qualis.capes.gov.br/webqualis/publico/pesquisaPublicaClassificacao.seam?conversationPropagation=3&g in> )

More information by email [rodrigotorres@ufpe.br](mailto:rodrigotorres@ufpe.br) .

Sincerely yours,

Rodrigo A. Torres, D. Sc. - CNPq PQ 2 Laboratory of Evolutionary and Environmental Genomics Department of Zoology, UFPE

[rodrigotorres@ufpe.br](mailto:rodrigotorres@ufpe.br)

pollen identity data; phylogenetically-controlled and community-level statistical analyses and preparation of manuscripts for publication. There is also the ample opportunity to design and implement additional pollination projects of mutual interest.

The postdoc position is for two years, renewable up to two additional years. Start date is negotiable, but Summer 2015 is preferred.

TO APPLY: Please send a CV and a description of your experience and interests as relevant to the position to [tia1@pitt.edu](mailto:tia1@pitt.edu), along with the names and contact information for three referees. In a covering letter clearly highlight skills and experience related to key responsibilities. Informal enquiries are also welcome! Deadline for application materials is April 1, 2015.

Dr. Tia-Lynn Ashman Professor Department of Biological Sciences University of Pittsburgh Pittsburgh, PA 15260-3929 412-624-0984 <http://www.pitt.edu/~tia1/tia1@pitt.edu>

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## UPittsburgh Plant-Pollinator Interactions

Postdoc in Plant-Pollinator Interactions at the University of Pittsburgh

A Postdoctoral fellow position exploring plant-pollinator interactions in diverse flowering plant communities is available in the laboratory of Tia-Lynn Ashman, Department of Biological Sciences at the University of Pittsburgh. Field work will be conducted in the Serpentine seeps of Napa County, California.

Using replicated California wildflower communities, the work will link plant traits with the pattern and costs of heterospecific pollen transfer, and characterize the modifiers of both pre- and post-pollination interactions at a community-wide scale. The work will specifically test the idea that within a co-flowering community tolerance and avoidance of heterospecific pollen receipt are alternate strategies for coexistence, and that tolerance is a stabilizing force that depresses the risks of reproductive failure of rare or facilitated species (e.g., Ashman and Arceo-Gomez 2013 *AJB* 100:1061-1070; Arceo-Gomez and Ashman 2011 *New Phytologist* 192: 738-746).

Responsibilities include characterizing plant-pollinator interactions in the field; greenhouse experiments to assess fitness costs of plant-plant interactions on the style, collection of reproductive trait, pollinator, and

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## USDA ARS Gainesville Population Genomics

Two postdoctoral research positions in population genomics are available in the laboratory of DeWayne Shoemaker, Agricultural Research Service, Gainesville, Florida.

Our current research program largely focuses on functional, population and evolutionary genomics studies of fire ants (genus *Solenopsis*). Examples of current projects include the use of population genetic and genomic tools and approaches to understand the genetic underpinnings of fire ant social behavior, the patterns of genome-wide gene flow and introgression among fire ant species, the genetic architecture of species differences, the consequences of recent invasions of fire ants into new environments and reproductive biology and life history of fire ants and other ants.

We are looking for someone to join us on a project that uses NGS methods (particularly genotyping-by-sequencing) to investigate population structure, gene flow, introgression, and species delimitation in fire ants. Successful candidates will be encouraged to work on additional projects, depending on personal interests and demonstrated abilities. The lab is located within the Fire Ant Research Unit at the Center for Medical, Agricultural and Veterinary Entomology in Gainesville,

Florida and maintains close interactions with labs that work on insect genetics at the University of Florida. Initial appointments are for one year with the possibility of extension based on performance and available funding. Desired qualifications: Ph.D. in genetics, evolutionary genomics or related field, interest and expertise in population and evolutionary genomics, bioinformatics experience of managing and analyzing large-scale genomic data sets, programming experience in any scripting language (e.g. PERL or Python), and evidence of excellence in research and high productivity.

To apply, please send a brief description of research interests (1-2 pages), a CV, and contact information for three references to [dewayne.shoemaker@ars.usda.gov](mailto:dewayne.shoemaker@ars.usda.gov). Start date is flexible and can be immediate. Positions are open until filled.

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

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## USheffield PlantPopGenomics

A three-year postdoc funded by the ERC is available at the University of Sheffield (United Kingdom), in the department of Animal and Plant Sciences. The postdoc will work with Pascal-Antoine Christin (<http://www.shef.ac.uk/aps/staff-and-students/acadstaff/christin>), in collaboration with Patrik Nosil (<http://nosil-lab.group.shef.ac.uk/>) and Colin Osborne (<http://osbornelab.group.shef.ac.uk/people/-colin-osborne/>).

\* The project The goal of this project is to understand the history of mutations and subsequent gene flow under selection that led to the gradual emergence of novel physiological pathways, using C4 photosynthesis as a study system. Genome-wide data will be generated for grasses of the genus *Alloteropsis* collected throughout Africa and Asia and analysed in an ecological context coupled with phenotyping (conducted in parallel by other group members).

\* What we require The postdoc will be responsible for collecting the samples in the field, generating the genome-wide data, and leading hypothesis-driven analyses in an evolutionary context. He will perform innovative data analyses and disseminate the results of the project. Applications are invited from candidates with interests in populations genomics as a tool to address important questions in evolutionary biology. A PhD is required, as well as a demonstrated expertise in population genomics, or bioinformatics. Field work experience is preferred.

\* What we offer A three-year contract is offered, which might be renewed for two extra years. The successful candidate will have the opportunity to conduct fieldwork in Africa, Asia and Oceania. The postdoc will integrate in a dynamic team composed of multiple postdocs and PhD students, and will collaborate with groups studying evolution, genomics, ecology and physiology.

Preferred start date: 1st May 2015. The position will remain open until a suitable candidate is found. For inquiries, contact Pascal-Antoine Christin by email ([p.christin@sheffield.ac.uk](mailto:p.christin@sheffield.ac.uk)) and include a CV and brief (1-page) statement of research interests.

Further reading: Christin PA, et al. 2012. Adaptive evolution of C4 photosynthesis through recurrent lateral gene transfer. *Current Biology* 22: 445-449. Soria-Carrasco V, et al. 2014. Stick insect genomes reveal *Angoum*-selection's role in parallel speciation. *Science* 344: 738-742.

[p.christin@sheffield.ac.uk](mailto:p.christin@sheffield.ac.uk)

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## UToledo FishGenomics

Position or Title: Postdoctoral Researcher in Fish Genomics and Genetics

Agency/State: University of Toledo, Ohio

Responsibilities: The research entails helping to develop, test, and publish a Next-generation sequence assay for detecting and identifying all Great Lakes native and invasive fish species, including those anticipated to invade, from environmental DNA and plankton samples. The postdoc will organize large DNA sequence databases, train and co-supervise students and technicians, and publish results in high-impact journals.

Qualifications: Ph.D. degree required in hand. Publication of Ph.D. results in peer-reviewed journals required. Excellent recommendation from former advisors required. Teaching and supervisory experience preferred. Data management experience, bioinformatics, and data analysis experience in molecular phylogenetics and population genetics required. DNA extraction, PCR, DNA Sequencing (Sanger and Illumina MiSeq), alignment, and GenBank experience required. Familiarity with QIMME, Unix/Linux operating systems and writing Perl is a plus. Strong communication (written, oral) skills required.

Salary: Competitive salary, full benefits.

Ad Closing Date: April 15, 2015 or until filled

Contact/Email: carol.stepien@utoledo.edu

How to Apply

Send (1) cover letter, (2) CV, (3) 2 letters of reference, (4) unofficial copies of graduate and undergraduate transcripts via .pdf to Dr. Stepien at carol.stepien@utoledo.edu.

The University of Toledo is an Equal Access, Equal Opportunity, Affirmative Action Employer and Educator and is committed to increasing the diversity of our campus.

Weblink: <http://www.utoledo.edu/nsm/lec/research/-ggl/index.html> Carol A. Stepien, Ph.D. Distinguished University Professor of Ecology & Director of the Lake Erie Center University of Toledo 6200 Bayshore Rd. Oregon OH 43616 carol.stepien@utoledo.edu 419-530-8362 <http://www.utoledo.edu/nsm/lec/> "Stepien, Carol" <Carol.Stepien@utoledo.edu>

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## UUtah Evolutionary Genetics Genomics Development

Applications are invited for grant-funded postdoctoral positions in the laboratory of Mike Shapiro in the Department of Biology, University of Utah (<http://www.biology.utah.edu/shapiro>).

We seek highly motivated and creative colleagues to study the genetic and developmental basis of phenotypic variation in the rock pigeon (epidermal, skeletal, and muscle identity and patterning). Specific projects will be tailored to the strengths and interests of successful candidates.

Recent publications from our lab on this topic include:

E.T. Domyan, et al. (2014) Epistatic and combinatorial effects of pigmentary gene mutations in the domestic pigeon. *Current Biology* 24: 459-464

M.D. Shapiro, et al. (2013) Genomic diversity and evolution of the head crest in the rock pigeon. *Science* 339: 1063-1067.

S.A. Stringham, et al. (2012) Divergence, convergence, and the ancestry of feral populations in the domestic rock pigeon. *Current Biology* 22: 302-308.

Ideal candidates are recent Ph.D. awardees who demonstrate: 1. A strong background in analysis of genetic

and genomic data (e.g., whole-genome resequencing, GBS/RAD genotyping, QTL mapping) and/or experimental developmental biology (e.g., manipulation of gene expression, transgenesis, genome editing) 2. An ability and willingness to work both independently and collaboratively 3. A strong track record of high-quality research and publication

To apply, please submit the following materials: 1. Cover letter that describes your research interests and goals 2. CV, including a list of publications 3. Names of three referees who will be willing to submit letters of reference upon request

Please email application materials in a single PDF file to Mike Shapiro: shapiro@biology.utah.edu.

Mike Shapiro Associate Professor Department of Biology University of Utah 257 S 1400 E, Room 201 Salt Lake City, UT 84112 (801) 581-5690, fax (801) 581-4668 <http://www.biology.utah.edu/shapiro/> Pigeonetics! pigeon breeder video game: <http://learn.genetics.utah.edu/content/pigeons/pigeonetics/> Michael D Shapiro <mike.shapiro@utah.edu>

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## UUtah Herbivore Microbiome Biodiversity

\*Biodiversity and Metagenomics of the Herbivore Microbiome\*

The Dearing lab at the University of Utah invites applications for a postdoctoral fellow to participate in a collaborative study to understand the gut microbiome of mammalian herbivores with respect to detoxification of plant defensive compounds. Our investigations suggest 1) the microbiome in the foregut of woodrats is critical for the ingestion of dietary toxins, 2) microbial biodiversity is important in this process and 3) previous exposure to toxins shapes the microbiome. For more information on previous research, see:

<http://biologylabs.utah.edu/dearing/Lab/-publications.html> This postdoctoral position will focus on the influences of host evolutionary history and diet in sculpting the diversity and function of the mammalian microbiome. One component of this will be a broad survey of microbiomes and phylogeny across the woodrat genus (\*Neotoma). \*The ideal candidate will have a strong interest and experience in microbial ecology and metagenomics, with experience in gut systems preferably of vertebrates. Basic bioinformatic

and molecular skills are required. Fieldwork for small mammal collection will be necessary; prior experience preferred but not required. The candidate should have a demonstrated record of publication with at least one first authored publication in press, and will be expected to work well in a collaborative environment. The Dearing lab provides a strong training and career development environment for candidates interested in academic positions.

\*Applications will be reviewed as they are received until the position is filled\*. The preferred start date is June 15, 2015. Please send cover letter, C.V., statement of research experience and interests that includes career goals (1-2 pgs), pdfs of papers, and contact information (emails, phone numbers and professional relationship) for at least 3 professional references to Dr. Denise Dearing, denise.dearing@utah.edu; please put 'Microbiome Postdoctoral Applicant' in the Subject Line.  
jaelmalenke@gmail.com

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## UUtah PlantAnimalMolEvol

\*Postdoctoral Fellowship: \*\*Molecular Evolution of Plant-Animal Interactions\*

\*Plant-Animal Interactions\*: The Dearing lab at the University of Utah invites applications for a postdoctoral fellow to participate in a study to understand the co-evolution of mammalian herbivores and plant defensive compounds. This collaborative project will investigate the role of a subfamily of detoxification enzymes with respect to dietary strategy. Few mammalian herbivores are capable of dietary specialization. Our preliminary data suggest the cytochrome P450 2B subfamily is critical in the biotransformation of plant secondary compounds, particularly terpenes. These enzymes may play a key role in dietary specialization since substrate specificity and catalytic efficiency of CYP2B enzymes can be greatly affected by small changes in amino acid sequence. The change of even a single amino acid, particularly in critical regions such as a substrate recognition site, can have notable effects on metabolism of substrates. Thus, the structure and copy number of CYP2B genes may be key in an herbivore's ability specialize on a terpene-rich diet. The future work consists of characterizing and comparing the amino acid sequences of CYP2B enzymes of specialist and generalist woodrats (\*Neotoma spp.\*) and possibly other terpene feeders. We are currently sequencing the genome of \*Neotoma

lepida\* with assembly expected by April 1, 2015. The successful applicant will use this new genomic information to amplify and sequence CYP2B genes from a variety of wild mammalian species, compare predicted protein sequence with respect to degree of dietary specialization, and characterize the function of the proteins purified from heterologous expression systems to determine the structural basis of functional differences. The applicant may also conduct enzyme assays. This research is a collaborative project with Dr. James Halpert, UConn and provides possibilities for interactions with his research group.

For more information on previous research, see:

[http://biologylabs.utah.edu/dearing/Lab/pdf/2012\\_journal\\_pone.pdf](http://biologylabs.utah.edu/dearing/Lab/pdf/2012_journal_pone.pdf) [http://biologylabs.utah.edu/dearing/Lab/pdf/2009\\_expression\\_biotrans\\_magnanou.pdf](http://biologylabs.utah.edu/dearing/Lab/pdf/2009_expression_biotrans_magnanou.pdf)

The ideal candidate will have experience accessing and evaluating genomic data, using molecular techniques, experience with biochemical analyses and have an interest in addressing questions of molecular evolution, molecular ecology or plant-animal interactions. Animal collection fieldwork is possible. The candidate should have at least one first authored publication in press. The Dearing lab provides a strong training and career development environment for candidates interested in academic positions.

Applications will be reviewed as they are received. The preferred start date is July 6, 2015, with an earlier start date possible. Please send a cover letter, C.V., statement of research interests that includes career goals (1-2 pgs), pdfs of papers, and contact information (emails and phone numbers) for at least 3 professional references to Dr. Denise Dearing, \*denise.dearing@utah.edu\*; please put '\*Postdoctoral Applicant CYP2B\*' in the Subject Line.

jaelmalenke@gmail.com

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## UVermont LoyolaU ChagasGenomics

Research/Teaching Post-doc in Bioinformatics with an emphasis on Evolutionary Genomics. The postdoctoral fellow will use bioinformatics of DNA sequence to understand the population and evolutionary relationships of Chagas disease insect vectors and/or parasites. The post-doc will be mentored to develop 10-15 lectures for



an introductory biology major's course and/or an area of candidate's expertise. Ideally, the candidate will spend 50% time each at University of Vermont and Loyola University New Orleans.

**Minimum Qualifications:** A Ph.D. in a relevant area such as bioinformatics, genomics or biology.

**Preferred Qualifications:** Documented theoretical and practical experience with relevant methods in bioinformatics as well as knowledge of evolutionary biology, ecology and host-parasite interactions. Excellent communication skills, written and spoken are anticipated. The ability to work collaboratively in an interdisciplinary research team is desirable.

Position is funded for two years, the preferred start date is May 1, 2015.

Inquiries may be addressed to Lori Stevens at: [Lori.Stevens@uvm.edu](mailto:Lori.Stevens@uvm.edu) or Patricia Dorn at: [Dorn@loyno.edu](mailto:Dorn@loyno.edu). Please include 'Chagas Post-doc' in the subject line.

**How to Apply:** Applications will be reviewed as they are received. Please send a cover letter, C.V., statement of research interests and career goals (1-2 pgs), pdfs of papers, and contact information of 3 references to Dr. Lori Stevens ([lori.stevens@uvm.edu](mailto:lori.stevens@uvm.edu) <<mailto:lori.stevens@uvm.edu>>) with 'Chagas Post-doc' in the subject line.

Lori Stevens Professor 321 Marsh Life Science Building  
Department of Biology University of Vermont Burlington,  
VT 05401 Ph: 802-656-0445 [lori.stevens@uvm.edu](mailto:lori.stevens@uvm.edu)

Chagas project website <http://www.chagasecohealth.com>  
Lori Stevens  
<[lori.stevens@uvm.edu](mailto:lori.stevens@uvm.edu)>

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## UVirginia EvolutionaryGenomics

The Department of Biology at the University of Virginia invites applications for a postdoctoral Research Associate position in the lab of Dr. Benjamin Blackman. The aims of the position will be tailored to the expertise of the successful applicant and complement the Blackman Lab's broad interests in the genetic basis of adaptation and domestication, the ecology and evolution of plant development, and mechanisms of organism-environment interaction.

Applying tools from evolutionary genomics, molecular genetics, and field ecology in sunflowers (*Helianthus*)

and monkeyflowers (*Mimulus*), our research addresses the following questions: How do plants cope with daily and seasonal environmental fluctuations? How and why do these responses evolve along environmental gradients? How are multi-trait adaptations assembled over evolutionary time? Current NSF-funded work is focused on following the history and function of sunflower domestication alleles with ancient DNA and gene expression studies as well as the genetics of natural variation in solar tracking. Additional lab and field work in wild sunflowers and monkeyflowers centers on the genetic changes and ecological pressures contributing to clinal variation in developmental plasticity, with an emphasis on responses to seasonal cues.

The Research Associate will work closely with the PI, collaborators, and lab personnel to design and lead research in the lab and field. The position also involves preparing grant proposals and manuscripts, data management and dissemination, and mentoring graduate and undergraduate students. The ideal candidate will demonstrate the ability to integrate across biological disciplines, identify and troubleshoot promising new methodologies independently, and use the appointment to develop and pursue novel, exciting questions. Demonstrated expertise in evolutionary genetics, including experience with analysis of genomic or transcriptomic datasets and programming for bioinformatics, is essential. Expertise in selection analysis, QTL mapping, transgene construction and plant transformation, or gene expression studies is desirable.

The completion of a PhD degree in Biology or related field by appointment start date is required. Preferred appointment start date is June 2015. This is a one-year appointment; however, appointment may be renewed for an additional two one-year increments, contingent upon available funding and satisfactory performance.

To apply, please submit a candidate profile through Jobs@UVA (<https://jobs.virginia.edu>) and electronically attach: curriculum vitae with list of publications, a cover letter that summarizes research interests and professional goals, and contact information for three (3) references; search on posting number 0615936.

Review of applications will begin March 12, 2015; however, the position will remain open until filled.

Questions regarding this position should be directed to: Dr. Benjamin Blackman ([bkb2f@virginia.edu](mailto:bkb2f@virginia.edu))

Questions regarding the Candidate Profile process or Jobs@UVA should be directed to: Rich Haverstrom ([rkh6j@virginia.edu](mailto:rkh6j@virginia.edu))

The University will perform background checks on all new hires prior to making a final offer of employment.

The University of Virginia is an Equal Opportunity/Affirmative Action Employer. Women, minorities, veterans and persons with disabilities are encouraged to apply.

Benjamin Blackman Department of Biology University of Virginia PO Box 400328 Charlottesville, VA 22904

Tel: 434.924.1930 E-mail: [bkb2f@virginia.edu](mailto:bkb2f@virginia.edu) Web: [http://people.virginia.edu/~bkb2f/Blackman\\_Lab/](http://people.virginia.edu/~bkb2f/Blackman_Lab/) [bkb2f@virginia.edu](mailto:bkb2f@virginia.edu)

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### UWashington PlantFrugivoreCoevolution

A postdoctoral position is available at the Santana and Riffell laboratories at the University of Washington in Seattle (<http://faculty.washington.edu/ssantana/-wordpress/>). The postdoc will be part of the NSF-funded collaborative project “Chance or necessity? Adaptive vs. non adaptive evolution in plant-frugivore interactions”. The project will focus on the mutualism between bats of the genus *Carollia*\* and their primary food source, Neotropical *Piper*\*. The project will integrate tools from analytical chemistry, genomics and behavioral ecology to measure the coevolution between diversity in scent composition of *Piper*\* fruits and the olfactory ability and behavioral preferences of *Carollia*\*. Fieldwork will be based at La Selva Biological Station in Costa Rica.

The postdoc will be involved in: (a) planning, conducting and/or supervising chemical assays of fruit volatile organic compounds (VOCs) in the field and the lab, (b) designing and conducting behavioral experiments on frugivorous bats in Costa Rica, and (c) conducting phylogenetic and other statistical analyses on VOC and behavioral data. The ideal candidate will have a strong background in relevant laboratory and field methods. Proficiency with R, phylogenetic comparative methods and multivariate statistics will be highly regarded. Fieldwork will play a central role in this project, and familiarity with bat research tools will also be viewed favorably. We seek a highly motivated candidate who is able to work both collaboratively and independently. The position will be filled as soon as possible, with October being the latest desired start date.

Applicants must have a Ph.D. Exceptional candidates completing their Ph.D. within the next few months will

also be considered. Applicants should submit:

1. A cover letter describing research experience, interests and goals, and their relevance to the project.
2. A full CV, including publications, and
3. The names and contact information for three individuals willing to serve as references.

Please submit all application materials as a single PDF file to [ssantana@uw.edu](mailto:ssantana@uw.edu) with “Postdoctoral application” as the subject line. Funding is available for three years contingent upon a successful one-year review. Review of applications will begin April 1st and continue until the position is filled.

The postdoc will join a center of excellence in ecology, evolutionary and organismal biology at UW (<http://www.biology.washington.edu>), s/he will have constant interaction with the rest of the project’s collaborative team (Dávalos lab at SUNY Stony Brook), and will have ample opportunities for further development in research, teaching and outreach at the Department of Biology and the Burke Museum of Natural History and Culture.

[ssantana@uw.edu](mailto:ssantana@uw.edu)

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### UWisconsin Madison PlantQuantGenet

A postdoctoral research associate position is available in the laboratory of John Doebley at the University of Wisconsin-Madison to study the quantitative genetics and genomics of teosinte, the progenitor of maize.

The postdoctoral associate will work as a member of the NSF-funded Panzea project ([www.panzea.org](http://www.panzea.org)) and use population genomics to understand the genetic architecture of domestication traits and inbreeding depression in natural populations of teosinte.

We bred 120 teosinte individuals (parent plants) from multiple natural populations to create a set of 10,000 progeny of known pedigree. These progeny are being phenotyped for traits related to domestication and local adaptation. A combination of whole genome sequences for the 120 parents along with GBS data for the 10,000 progeny provides a knowledge of the whole genome sequences of the all 10,000 progeny. These data will be used to address questions about quantitative genetic parameters in teosinte, map genes for trait variation, investigate inbreeding depression, and compare the con-

tributions of different functional classes of genomic variants to trait variation. Potential projects are flexible within the scope of the project.

The postdoctoral associate will work with other team members on the creation and analysis of this large dataset combining phenotypes, pedigrees, and GBS marker data for the 10,000 of teosinte plants. Approximately  $\frac{1}{2}$  of these data are 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 is also an opportunity to collaborate with other Panzea labs to compare teosinte population genomic data to that for maize landraces.

The initial appointment is one year, with the potential for additional years of support conditional on performance. Start dates are open-ended, with preference for earlier dates.

A Ph.D. in statistical genetics, quantitative genetics, or closely related field is required. We seek applicants with proficiency in R and/or SAS programming and a strong background in quantitative genetics. 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 jdoebley@wisc.edu.

SALARY: \$42,840

PROPOSED HIRE DATE: June 1, 2015 or later

jdoebley@wisc.edu

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## Vienna 6 EvolutionaryBiology

**CLOSING DATE MARCH 31 2015 - APPLY NOW!**  
Postdoc positions at the Vetmeduni Vienna 2015

The University of Veterinary Medicine, Vienna (Vetmeduni) is inviting applications for \*six post-doctoral positions\* to be filled this year. Successful candidates will be awarded four-year contracts to undertake basic research in the biological or veterinary sciences. They will be fully integrated in the Vetmeduni's Postdoc-Programme.

Each of the positions will be allocated to one of the 21 research groups listed below.

Candidates should complete the application form and send it together with:

- a full CV (including a list of publications) - a letter detailing why they are applying for a position - two letters of reference

to the Office for Human Resources.

Send E-Mail to Human Resources <bewerbungen@vetmeduni.ac.at> \*Download Application Form (.doc, 654 KB) <<http://www.vetmeduni.ac.at/fileadmin/v/z/forschung/1-Form.doc>>\*

\*Closing date for applications: March 31st 2015\*

Short-listed candidates will be invited to an \*interview in Vienna on May 13th 2015\*. Successful candidates will be expected to take up their positions by the end of 2015. Postdoc Projects Olena Andrukhova: Role of vitamin D in the regulation of cardiovascular function (Code PD0115) <<http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#>> Andrea Jean Betancourt: Population genetics of transposable elements (Code PD0215) <<http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#>> Pamela Burger: Genomic selection for docility in old world camelids - A model for domestication in farm animals (Code PD0315) <<http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#>> Reinhold Erben: Regeneration of articular cartilage and tendon lesions using mesenchymal stem cells (Code PD0415) <<http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#>> Leonida Fusani: Hormonal control of rapid body mass changes in birds (Code PD0515) <<http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#>> Michael Hess: Elucidating pathways of Escherichia coli infections in chickens (Code PD0615) <<http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#>> Lukas Kenner: Dissecting PDGFRB function in NPM - ALK driven lymphoma (Code PD0715) <<http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#>> Carolin Kosiol: Linking genotypic and phenotypic time series data through Gaussian process models (Code PD0815) <<http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#>> Norbert Nowotny: Vector-borne viral infections in central Europe: virological and entomological investigations (Code PD0915) <<http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#>> Dustin Penn: How do animals smell out disease? (Code PD1015) <<http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#>> Friederike Range: Towards understanding physiological measurements underlying animal emotions (Code PD1115)

< <http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#> > Thomas Ruf: Thermogenesis in the wild boar: the role of Ca<sup>2+</sup>-cycling in myocytes (PD1215) < <http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#> > Thomas Rüllicke: CRISPR/Cas9 technology for routine in vitro and in vivo applications (Code PD1315) < <http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/#> >

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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>

## Wageningen MicrobialSyntheticBiol

Vacancy: Postdoc in Synthetic Biology

We are looking for an enthusiastic, motivated Postdoc on Synthetic Biology with a strong background in or affinity with experimental work in microorganisms. Candidates should be proficient in molecular biology, proactive, independent, team player and have the ability to engage with professionals in adjoining fields.

The candidate should apply the concepts of synthetic biology enhance our understanding of the fundamental principles of signalling and regulatory networks in living organism, to generate a mechanistic understanding with the aim of constructing novel synthetic systems. Experience and willingness to interact with colleagues on large-scale genome engineering and re-factoring, and interplay of the circuits designed and the host chassis (eg. through omics and detailed biochemical measurements) will be a substantial bonus. Using an interdisciplinary and integrated approach the candidate should be able to work on a small scale/network level to develop/design, e.g., sensing devices for synthetic signalling networks within and across cells or the design of (opto) signal-sensing systems. The candidate should have working experience or be interested in applying in designing and implementing synthetic networks exhibiting complex dynamic behaviour, such as adjustable time-delayed expression kinetics, tuneable synthetic oscillators or modular logic gates. He/she should be interested in applying mathematical, physical and engineering principles in the design process.

We ask

For this position we request:

- A proficiency in molecular biology (prokaryotic expertise being a bonus);
- A sound knowledge physiology, biochemistry and Synthetic Biology;
- Some computational competences such as scripting and experience in interacting with modelers would be advantageous;
- The candidate is required to have a PhD in Biotechnology, Microbiology, Molecular Life Sciences or related fields;
- Fluent in English, both written and spoken;
- The candidate will collaborate in a team with scientists at departments of Systems and Synthetic Biology and of Microbiology.

We offer We offer you a temporary position for a period of 2 years with possibility for extension or, under specific circumstances, to engage in a Tenure Track systems at the WUR. Gross salary 2855 to 3783, based on a fulltime employment and dependent on expertise and experience.

We not only offer a competitive salary but also good (study) leave and a pension of the ABP Pension Fund.

More information For more information about this position, please contact Prof. Vítor Martins dos Santos, chair Systems and Synthetic Biology, telephone number +31 317482865.

For more information about the contractual aspects, please contact Mrs. J. van Meurs, HR advisor, telephone number +31 317480101.

Interested? You can apply online at [www.wageningenur.nl/career](http://www.wageningenur.nl/career) until 30th April 2015.

We are Systems Biology is one of the spearheads of the Wageningen UR, which invests considerably in this area. The mission of the Laboratory of Systems and Synthetic Biology is to contribute to the elucidation of the mechanisms underlying basic cellular processes, evolution and interactions among microbes and between microbes and their environment (including the human host) and to translate this knowledge into applications of biotechnological, medical and environmental interest.

The Agrotechnology & Food Sciences Group is part of Wageningen UR where fundamental and applied sciences complement each other. As an important European player, we carry out top-level research and work alongside authoritative partners within the international business world as well as the government on 'Healthy food in a biobased society'. We have a crucial role in innovations within the market. Entrepreneurship and professionalism are what define us. In short, we are an interesting, international employer of stature.

Wageningen University and Research centre delivering a substantial contribution to the quality of life. That

is our focus - each and every day. Within our domain, healthy food and living environment, we search for answers to issues affecting society - such as sustainable food production, climate change and alternative energy. Of course, we do not do this alone. Every day, 6,500 people work on 'the quality of life', turning ideas into reality, on a global scale.

Met vriendelijke groet, Kind regards,

Carolien Pinkster Secretary

Wageningen University Laboratory of Systems and Synthetic Biology Wageningen Centre for Systems Biology (WCSB) Laboratory of Microbiology Building 316 Dreijenplein 10 6703 HB WAGENINGEN the Netherlands phone +31 317 482105 fax +31 317 483829 email carolien.pinkster@wur.nl

In the office at: Tuesday / Thursday / Friday 08.30 - 17.00 hours

"Pinkster, Carolien" <carolien.pinkster@wur.nl>

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## Workshops Courses

Arizona Lepidoptera Aug16-25 ..... 117	Sicily SystemsBiol Jul5-9 ApplDeadlineMar31 .... 126
Aveiro Portugal AmphibianConservation May18-22 118	StPierredOleron France EvoEpigen May16-22 .... 127
Bialowieza Poland MetaBarcoding Jun1-5 ..... 119	SwissAlps Adaptation Jun17-20 ..... 128
CSIC Spain MacroevolutionPhylogenies Sep28-Oct2 120	UAzores EvolutionMicroorganisms Aug31-Sep5 ... 128
Debrecen Hungary Myrmecology Jul24-27 ..... 120	UBonn CrypticSpeciation Jun5-6 ..... 129
FridayHarbor ComparativeEmbryology Jun15-Jul17 120	UBremen EvolutionStatisticsUsingR ..... 129
Guaruji Brazil Metaanalysis Jun25-26 ..... 121	UExeter EvolutionaryBehaviour Jul6-9 ..... 130
Ilhabela Brazil PhylogeneticComparativeMethods Jul2-5 ..... 121	UMaryland Bioinformatics ..... 130
Lausanne ESEB2015 ActivelyTeachingEvolution Aug9 122	UMichigan EvolutionFieldCourses ..... 130
LipariIsland Italy Bioinformatics Jul19-25 ..... 122	UMichigan Evolution May24-Aug22 ..... 131
NIMBioS EvolutionaryQuantGenetics Aug10-15 .. 123	UNewHampshire BioinformaticsForUndergrads Jul27-30 ..... 131
NorthCarolina EvolutionDisease May4-6 ..... 124	UWestIndies Trinidad ViralEvolution Aug9-14 ... 132
Raleigh NC BioinformaticsPractical May18-22 .... 125	UWestIndies VirusEvolution Aug9-14 ..... 132
Raleigh NC BioinformaticsPracticalTools May18-22 125	UYork EvolutionOfEvolution Jul24 ..... 133
Roscoff MarineEvolutionaryGenomics May31-Jun12 126	Venice EvoDevo Sep28-Oct1 ..... 134

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### Arizona Lepidoptera Aug16-25

Announcing the Sixth Annual Lepidoptera Course, 16 V 25 August, 2015.

Held at the Southwestern Research Station (SWRS) in the Chirichahua Mountains in SE Arizona (a 2 1/2 hour drive from Tucson), the focus of the Lep course is to train graduate students, post-docs, faculty, state and federal employees, and serious citizen-scientists in the classification and identification of adult Lepidoptera and their larvae. Topics to be covered include the biology

and systematics of major families of Lepidoptera, an introduction to adult and larval morphology with a focus on taxonomically-important traits, extensive field work that concentrates on both collecting and photographing adults and larvae, collecting and curatorial techniques, genitalic dissection, larval classification, use (and abuse) of DNA barcoding, and general topics in Lepidoptera systematics, ecology, and evolution.

With its extensive series of Sky-Island mountain ranges, SE Arizona has the highest Lepidoptera diversity in the US. With low desert scrub, oak and mixed oak-pine woodland, lush riparian, juniper, Douglas fir, and mountain meadow habitats all within a 40 minute drive from the station, the SWRS is an ideal location from which to sample this diversity (of both habitats and species).

If you want to interact with other Lepidoptera enthusiasts, see a spectacular Dysschema, identify the Organ of vom Rath, sort through trap samples with hundreds of species, learn about diversity of Lepidoptera, and enjoy the vistas of the SE Arizona, then this course will provide a unique experience.

Partial list of Invited instructors (subject to change) Rich Brown (Mississippi Entomological Museum), Jennifer Bundy (RD4AG), Chris Grinter (Illinois Natural History Survey), Don Harvey (Smithsonian), Sangmi Lee (Arizona State University), Chris Schmidt (Canadian National Collection), Bruce Walsh (University of Arizona)

For more information, see <http://research.amnh.org/-swrs/education/lepidoptera-course> or [www.lepcourse.org](http://www.lepcourse.org) or contact Bruce Walsh at [jbwalsh@u.arizona.edu](mailto:jbwalsh@u.arizona.edu) You can also see photos and comments from students in the 2011 course at their facebook site, "2011 Lep Course, SWRS SEAZ".

"Walsh, James Bruce - (jbwalsh)" [<jbwalsh@email.arizona.edu>](mailto:jbwalsh@email.arizona.edu)

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## Aveiro Portugal Amphibian Conservation May18-22

The 1st Course on Amphibian Conservation and Husbandry (ACH) is an interesting and intensive course to researchers or technical staff working with amphibians and looking for more complete basis on Amphibian Conservation and Husbandry. The course will be held from 18th to 22nd May. Registrations for this edition already available (<http://ach2015.wix.com/ach2015>).

The course explores the principles of amphibians husbandry, nutrition and dietary needs, captive reproduction, population management, veterinary aspects (diseases, pathology, and necropsy), biosecurity and quarantine, conservation, threats and global action. Hands on demonstrations, practical and group exercises are also included (enclosure demonstrations: tank drilling, false bottoms and plumbing, filters).

Speakers:

Luis Carrillo, University of Mexico City, AArk

Isabel Lopes, University of Aveiro, CESAM

To be confirmed.

To be confirmed.

Important note: the course will not start if a minimum of 10 participants will not be reached; similarly the maximum number of participants is 15.

Inscription fees include: attending at the course and the use of all the materials provided by University of Aveiro and the AArk.

The course will be held in partnership with the organization of the Advanced Course Ecotoxicology of Amphibians and Reptiles: from theory to practice± (<https://sites.google.com/site/ecotoxamre/>). Registration in both courses have reduced fees (through Ecotox course payment proof).

Fees:

ACH Course only

General: 350 euros

Student: 250 euros

UA Student: 250 euros

ACH Course (with Ecotox Registration)

General: 230 euros

Student: 170 euros

UA Student: 250 euros

Applications should be sent to: [emanuele.fasola@ua.pt](mailto:emanuele.fasola@ua.pt) till the 10th of April 2015.

Applications results and the instructions for payment will be notified to participants no later than 48h after. The payment proof must be sent to us for the registration to be valid.

Sara

Sara Costa <[sara\\_d\\_a\\_costa@hotmail.com](mailto:sara_d_a_costa@hotmail.com)>

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## Bialowieza Poland MetaBarcoding Jun1-5

Dear Colleagues,

We are pleased to announce that this year the fifth DNA Metabarcoding Spring School will be held in Bialowieza (Poland) and will be organized in collaboration with Rafal Kowalczyk and Jan Wójcik from the Bialowieza Mammal research institute.

Please take care that this year the registration period is really short and will end by April the 15th, 2015.

<http://metabarcoding.org/spip.php?article70> Best regards

Eric Coissac

Dr Eric Coissac Associate professor Laboratoire d'Ecologie Alpine UMR CNRS-UJF 5553 / UMR CNRS 5553 Université J. Fourier Domaine de Saint Martin d'Hères 2233, rue de la piscine Bât. D Biologie BP 53, 38041 Grenoble Cedex 9 France

The fifth DNA metabarcoding Spring School at Białowieża

DNA metabarcoding is a rapidly evolving method for assessing biodiversity from environmental DNA. It has a wide range of applications: biodiversity monitoring, animal diet assessment, reconstruction of paleo communities, among others. DNA metabarcoding relies on molecular techniques such as PCR and next generation sequencing, and requires bioinformatics and biostatistics competence to analyze sequencing results. This approach integrates several scientific areas and requires a broad range of skills, in addition to the classical ecological knowledge related to the considered research topic.

The DNA metabarcoding spring school is now in its fifth edition and this year it is co-organized by the metabarcoding.org team and the Mammal Research Institute, Polish Academy of Sciences in Białowieża, Poland.

The DNA metabarcoding spring school will hold from the 1st to 5th of June 2015.

Participants can register for the school (24 places) by sending an email to the following address :

[bialowieza2015@metabarcoding.org](mailto:bialowieza2015@metabarcoding.org)

The email must contain a brief curriculum vitae and

a letter of motivation indicating how your researches are related to DNA metabarcoding and what you are hoping from this school. As part of the course program, each participant is required to give a flash talk (5 minutes) about its research and how it is related to DNA metabarcoding.

Registration deadline is 15 April 2015

Main lecturers

- Marta de Barba (LECA, CNRS, France) - Aurélie Bonin (LECA, CNRS, France) - Frédéric Boyer (LECA, CNRS, France) - Antony Chariton (CSIRO, Australia) - Eric Coissac (LECA, CNRS, France) - Håvard Kauserud (University of Oslo, Norway) - Dorota Porazinska (University of Florida, USA) - Pierre Taberlet (LECA, France) - Lucie Zinger (EDB, CNRS, France)

Course Schedule

The school will consist of a series of lectures and practicals introducing different aspects of DNA metabarcoding. Bioinformatics practicals will introduce data analysis from raw sequences to basic ecological conclusions. Molecular ecology practical will present basic techniques for DNA extraction in field condition and DNA amplification by PCR. More details are available on the following web page

<http://metabarcoding.org/spip.php?article70> Travel and accommodation

To join Białowieża, the easiest way is to reach Warsaw airport. According to the number of participant, we will propose to you the most convenient solution to travel from Warsaw to Białowieża the Sunday 31h of March afternoon.

Accommodation will be provided in double bedrooms at the guesthouse located in the park close to the place of the school. Meals will be served at the same place at the Parkowa restaurant.

Workshop Costs

There are no registration fees for the workshop. Participants will have to pay for their accommodation, meals and travel expenses. The cost for accommodation and meals for 6 days is estimated to 1500 PLN ( 360€).

[eric.coissac@inria.fr](mailto:eric.coissac@inria.fr)

soledad.esteban@transmittingscience.org

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**CSIC Spain**  
**MacroevolutionPhylogenies**  
**Sep28-Oct2**

Dear colleagues,

Registration is open for the course “THE USE OF PHYLOGENIES IN THE STUDY OF MACROEVOLUTION - 3rd edition”, Septiembre 28-October 2, 2015. Instructor: Dr. Juan López Cantalapiedra (Museo de Ciencias Naturales, CSIC, Spain).

New phylogenetic methods would allow us to draw on the information encapsulated in phylogenetic trees in order to address a wide range of questions on macroevolution. First, this course will introduce participants to the use, modification and representation of phylogenetic trees. Then, we will focus on the use of phylogenetic information to reconstruct ancestral characters and biogeographic histories, learning how to apply phylogenetic comparative methods. This course will also tackle trait evolution modelling and the assessment of phylogenetic signal. Finally, we will learn about the shape of phylogenetic trees and its evolutionary causes and how to estimate the rates of diversification throughout the evolutionary history of groups. Participants are encouraged to bring their data sets to use in the practical class.

Important note: Please bear in mind that this course is not about reconstructing (building) phylogenetic trees.

Software: Mesquite, TreeEdit, FigTree, BayesTraits (using BayesTraits Wrapper in R), Tracer, RASP and R (ape, TreeSim, TreePar, Geiger, OUwie, BioGeoBEARS).

Place: Facilities of the CRIP at Els Hostalets de Pierola, Barcelona (Spain).

Organized by: Transmitting Science, the Centre de Restauració i Interpretació Paleontològica and the Institut Català de Paleontologia Miquel Crusafont.

More information: <http://www.transmittingscience.org/courses/evol/-phylogeny-and-macroevolution/> or writing to [courses@transmittingscience.org](mailto:courses@transmittingscience.org)

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Soledad De Esteban Trivigno, PhD.

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**Debrecen Hungary Myrmecology**  
**Jul24-27**

Dear Colleagues,

We kindly invite you to the 6th Central European Workshop of Myrmecology held in Debrecen, Hungary between 24-27 July 2015. Please visit our webpage: [cewm2015.unideb.hu](http://cewm2015.unideb.hu) for details and subscribe to our newsletter: <http://cewm2015.unideb.hu/news> PLEASE NOTE, the extended deadline of registration and Abstract submission is the midnight of 23rd of March! We are sorry if you received this newsletter a bit late.

Best Regards,

the Organisers

Contact info: [cewm-info@unideb.hu](mailto:cewm-info@unideb.hu) Homepage: <http://cewm2015.unideb.hu/> Registration: <http://regisztracio.unideb.hu/en/cewm2015> List archives: <http://levlista.unideb.hu/cgi-bin/mailman/private/-cewm2015/> Thank you very much in advance,

András Tartally and the other Organisers

CEWM 2015 contact <[cewm-info@unideb.hu](mailto:cewm-info@unideb.hu)>

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**Friday Harbor**  
**Comparative Embryology Jun15-Jul17**

Hello,

There are still spots open in the Comparative Invertebrate Embryology course at the Friday Harbor Labs (June 15 to July 17, 2015). It's a great course for anyone interested in the evolution of development, animal evolution, developmental mechanisms, life histories, or anything else involving early animal life stages. The Friday Harbor Labs is also a wonderful place to experience: not only does it have a truly amazing diversity of organisms, but it is in a beautiful location, and provides opportunities to interact with a broad community of biologists from all over.

Please see <http://depts.washington.edu/fhl/-studentSummer2015.html#SumA-4> for the course



description.

Thanks for taking a look.

–Mickey

Michelangelo von Dassow <mvondass@gmail.com>

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## Guaruji Brazil Metaanalysis Jun25-26

Subject line: \*Workshop @ Evolution meeting in meta-analysis\*

\*Short Workshop: Introduction to Meta-Analysis and Systematic Reviews\*

\*June 25 “ June 26, 2015\*

Instructors:

\*Jessica Gurevitch\* (Stony Brook University, State University of New York)

\*Marc Lajeunesse \*(University of South Florida)

A 1.5 day workshop will be held before the Evolution meeting in Guarujá, Brazil, starting on the afternoon of June 25. The cost is \$60 U.S. per participant. Some scholarships may be available. Applications and registration details are available at:

[http://lajeunesse.myweb.usf.edu/-ASN\\_workshop\\_2015.html](http://lajeunesse.myweb.usf.edu/-ASN_workshop_2015.html) Participation is limited to 24 people. Sponsored by the \*American Society of Naturalists\*.

\*Introduction/Objectives\*

\*Synopsis:\* Participants will become familiar with what meta-analysis is, where it comes from, some examples of how it has been used in ecology and evolution, and its major strengths, weaknesses, advantages and limitations as a tool for the quantitative summary of research results. They will be introduced to the formal methods for carrying out a systematic review, which may (or may not) be combined with a meta-analysis, and to the problems and issues involved in carrying out systematic reviews. They will become familiar with carrying out the calculations involved in typical ecological meta-analyses, and learn how to interpret the results. We will look very briefly at some of the areas of current development in meta-analysis in ecology, evolution, and conservation, including integrating phylogenetic information in analyses and imputation methods. We also introduce criteria for evaluating and critiquing the results of meta-analyses

in the literature.

Workshop participants should have a general background in statistics (anova, regression, etc.) and graduate-level understanding of experimental design, ecology, evolution and/or conservation research. No real familiarity with meta-analysis is necessary.

\*Format of the course:\*

Lectures, demonstrations of methods, hands-on computational experience with ample opportunities for questions and feedback, group discussions and presentations, and peer critiques.

\*Prerequisites\*: An introductory statistics course covering up to regression and ANOVA. Background in ecology and evolutionary biology. Familiarity with experimental design and more advanced statistics and probability desirable but not necessary.

\*Software:\*

OpenMEE (open meta-analysis software for ecology and evolution). Freely available at: [http://www.cebm.brown.edu/open\\_mee](http://www.cebm.brown.edu/open_mee). Familiarity and experience with \*R\* is not necessary but will prove useful.

[jessica.gurevitch@stonybrook.edu](mailto:jessica.gurevitch@stonybrook.edu)

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## Ilhabela Brazil PhylogeneticComparativeMethods Jul2-5

Intensive short course on 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. The course will be four days in length and will take place at the Hotel Ilha Flata (<http://www.ilhaflat.com>) in Ilhabela, Sao Paulo State, Brazil, from the 2nd to the 5th of July, 2015. This course is funded by the National Science Foundation. The course is free of cost, and accommodation at the course venue, as well as breakfast & lunch on all course days, is included for all accepted students. There will be a small number of travel stipends available for qualified students and post-docs. Applicants are welcome from any country, but are especially encouraged from the Latin American region.

Topics covered will include: an introduction to the R environment and programming language, tree manipula-

tion, independent contrasts and phylogenetic generalized least squares, ancestral state reconstruction, models of character evolution, diversification analysis, and community phylogenetic analysis. Course instructors will include Dr. Liam Revell (University of Massachusetts Boston), Dr. Luke Harmon (University of Idaho), and Dr. Mike Alfaro (University of California, Los Angeles).

Instruction in the course will be primarily in English, thus all students must have a basic working knowledge of scientific English. To apply for the course, please submit your CV along with a short (maximum 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. Applications should be submitted by email to [ilabela.phylogenetics.course@gmail.com](mailto:ilabela.phylogenetics.course@gmail.com) by May 1st, 2015. Questions can be directed to [liam.revell@umb.edu](mailto:liam.revell@umb.edu).

– Liam J. Revell, Assistant Professor of Biology University of Massachusetts Boston web: <http://faculty.umb.edu/liam.revell/> email: [liam.revell@umb.edu](mailto:liam.revell@umb.edu) blog: <http://blog.phytools.org> [Liam.Revell@umb.edu](mailto:Liam.Revell@umb.edu)

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### Lausanne ESEB2015 Actively Teaching Evolution Aug9

\*Workshop: Actively teaching evolution 9<sup>th</sup> August, ESEB 2015, Lausanne. \*

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As part of the 15th ESEB congress, we are organising a workshop to explore methods and resources available for the enquiry-based teaching of evolution.

An understanding of evolution is crucial in order to make informed decisions on important issues ranging from antibiotic resistance to the consequences of climate change. However, teaching evolution is often challenging because there can be a number of social challenges and misconceptions about evolutionary theory both among teachers and their students.

After the success of the ESEB 2013 workshop in Lisbon, the aim of this event is to further promote dialogue among evolutionary biology researchers and local teachers. The day will include plenary talks on education and outreach, research talks by evolutionary biologists interested in outreach and hands-on activities that build on the concepts addressed during the talks.

Poster presentations are encouraged, but not mandatory. The language of the event will be decided according to participant capabilities and needs.

The event will take place at the “*Àprouvette*”, a public science laboratory situated at the heart of the University of Lausanne campus.

<http://wp.unil.ch/mediationscientifique/activites/-eprouvette/> Please note that the event will take place on Sunday the 9<sup>th</sup> August, a day before the official start of the congress.

\*\*

A contribution towards the costs of this event is \*25 Swiss Francs\*. This includes two coffee breaks, lunch and a cheese and wine session. The rest of the event is funded by the ESEB Outreach Fund, with a participation from the Cercle FSER.

For further information:

<http://wp.unil.ch/eseb2015/satellite-workshops/> Applications are open and places are limited to 15 researchers. Participants will be selected based on their interest in outreach. Deadline for applications is May 31<sup>st</sup> 2015.

To apply:

[https://docs.google.com/forms/d/-1\\_uD9vAoAcgF6fACIwuW\\_4H4vh1OPfB7luB2JELMNNEo/-viewform](https://docs.google.com/forms/d/-1_uD9vAoAcgF6fACIwuW_4H4vh1OPfB7luB2JELMNNEo/-viewform) For information on other outreach events at ESEB and registration see here:

<http://outreachateseb2015.tumblr.com/> If you have any questions please contact Tania Jenkins ([tania.jenkins@unil.ch](mailto:tania.jenkins@unil.ch))

Tania Jenkins <[tania.jenkins@unil.ch](mailto:tania.jenkins@unil.ch)>

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### Lipari Island Italy Bioinformatics Jul19-25

Computational Dynamic Analysis of Biological Processes <http://lipari.cs.unict.it/LipariSchool/Bio> July 19 - July 25, 2015 Lipari Island, Italy

Aim and scope:

Processes is one of the most challenging research areas in modern life science. Topics such as Disease Dynamics, Drug Resistance, Immune System Analysis, Emerging Mutations, Microbiome Analysis, and Biological Networks Evolution involve intriguing and still unsolved problems. On the other hand, the availability of Next

Generation Sequencing and other High-throughput techniques provide a strong support for scientists working in this field. Our main and special guest lectures will address the scope focusing on algorithms, computational models, biomedical and biotechnological results on this field. From the enclosed bibliography, it appears that the selected themes have received much attention in the scholarly literature ranging from Nature and Science to Bioinformatics Journals.

#### Speakers

Peer Bork Network Dynamics European Molecular Biology Laboratory (EMBL), Heidelberg, GERMANY

Jeff Gore Evolutionary Game-Theoretic Models MIT, Massachusetts, USA

Laxmi Parida Evolutionary Dynamics IBM, Thomas J. Watson Research Center, Yorktown Heights, NY, USA

Stephen Quake NGS and Cancer Dynamics Stanford University, California, USA

#### Guest speakers

Eric Jonasch Molecular Determinants of Renal Cell Carcinoma Ontogeny and Progression MD Anderson Cancer Center, Houston, Texas, USA

Michael Levitt Stanford University, California, USA

Participants will be arranged in a comfortable hotel at very special rates. The conference room (in the same hotel) is air-conditioned and equipped with all conference materials. Special areas are reserved to students for the afternoon coursework and study. The island of Lipari can be easily reached from Milazzo, Palermo, Naples, Messina and Reggio Calabria by ferry or hydrofoil (50 minutes from Milazzo). Two kinds of participants are welcome. Students: Participants who are expected to do afternoon courseworks and take a final exam (The grades will be given following the ECTS grading scale). The course will involve a total of 24 hours of teaching. According to our university rules passing the final exam gives right to an equivalent of 6 ECTS credits in any Ph.D. program. Auditors: participants who are not interested in taking the final exam. Registration fee is 470 Euros. The fee covers the course material, bus+hydrofoil Catania airport-Lipari-Catania airport, social event. Late registration is 570 Euros.

Applications can be submitted from November 1, 2014 up to May 29, 2015. Late registrations will be accepted until July 14th. Admission notification will start on March 2nd, according to registration time. Applicants must include a short curriculum vitae.

The official language is English.

School Directors Prof. Alfredo Ferro (University of Cata-

nia) Prof. Raffaele Giancarlo (University of Palermo) Prof. Concettina Guerra (Georgia Institute of Technology) Prof. Michael Levitt (Stanford University)

Dr. Rosalba Giugno (co-director, University of Catania) Prof. Alfredo Pulvirenti (co-director, University of Catania)

People interested in receiving further information about the school can contact:

Lipari School Organization Prof. Alfredo Ferro – Lipari School secretary Università degli Studi di Catania - Dipartimento di Matematica e Informatica Città Universitaria - Viale A.Doria, 6 - 95125 Catania - ITALY Tel: +39 095 7383071 Fax: +39 095 7337032 / +39 095 330094 E-mail: liparischool@dm.unict.it

Alfredo Ferro <liparischool@dm.unict.it>

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## NIMBioS EvolutionaryQuantGenetics Aug10-15

Please distribute to interested colleagues.

The National Institute for Mathematical and Biological Synthesis (NIMBioS) is now accepting applications for its Tutorial, “Evolutionary Quantitative Genetics,” to be held August 10-15, 2015, at NIMBioS.

**OBJECTIVES:** Quantitative genetic theory has been applied to a wide range of phenomena including the evolution of differences between the sexes, sexual preferences, life history traits, plasticity of traits, as well as the evolution of body size and other morphological measurements. This tutorial is for evolutionary biologists interested in how quantitative genetics theory can be tested with data, both from single species and with multiple-species phylogenies. Participants – graduate students, postdocs, and junior faculty – will learn how to use R to build and test evolutionary models. There is a need for evolutionary biologists to understand the field of evolutionary quantitative genetics because of the ability to collect large amounts of data by computer, the development of statistical methods for changes of traits on evolutionary trees and for changes in a single species through time, and the realization that quantitative characters will not soon be fully explained by genomics.

The content of this tutorial will be similar to the workshop held at NIMBioS in 2014. For information

about the Evolutionary Quantitative Genetics 2014 tutorial held at NIMBioS, visit [http://www.nimbios.org/tutorials/TT\\_eqg](http://www.nimbios.org/tutorials/TT_eqg). LOCATION: NIMBioS at the University of Tennessee, Knoxville

CO-ORGANIZERS: Stevan J. Arnold, Integrative Biology, Oregon State Univ. and Joe Felsenstein, Genome Sciences, Univ. of Washington, Seattle

INSTRUCTORS: Patrick Carter, Evolutionary Physiology, Washington State Univ., Pullman; Tyler Hether, Biological Sciences, Univ. of Idaho, Moscow; Adam Jones, Biology, Texas A&M Univ.; Emilia Martins, Biology, Indiana Univ., Bloomington; Brian O'Meara, Ecology & Evolutionary Biology, Univ. of Tennessee; Liam Revell, Biology, Univ. of Massachusetts, Boston; and Michael Whitlock, Zoology, Univ. of British Columbia

CO-SPONSOR: The American Society of Naturalists

For more information about the tutorial and a link to the online application form, go to [http://www.nimbios.org/tutorials/TT\\_eqg2015](http://www.nimbios.org/tutorials/TT_eqg2015). There are no fees associated with this tutorial. Tutorial participation in the tutorial is by application only. Individuals with a strong interest in the topic, including post-docs and graduate students, are encouraged to apply, and successful applicants will be notified within two weeks of the application deadline.

FOOD AND LODGING: Breakfast and lunch will be provided at NIMBioS each day of the tutorial, as well as coffee and mid-morning and mid-afternoon snacks. NIMBioS is not covering other expenses for participants, but a block of rooms will be reserved at a nearby hotel. More information will be available on our website soon about lodging, room rates, and how participants can make reservations.

APPLICATION DEADLINE: May 1, 2015

The National Institute for Mathematical and Biological Synthesis (NIMBioS) (<http://www.nimbios.org>) brings together researchers from around the world to collaborate across disciplinary boundaries to investigate solutions to basic and applied problems in the life sciences. NIMBioS is sponsored by the National Science Foundation, with additional support from The University of Tennessee, Knoxville.

Catherine Crawley, Ph.D. Communications Manager National Institute for Mathematical and Biological Synthesis (NIMBioS) University of Tennessee 1122 Volunteer Blvd, Ste. 106 Knoxville, TN 37996 e [ccrawley@nimbios.org](mailto:ccrawley@nimbios.org) t +1 865 974 9350 f +1 865 974 9461 <http://www.nimbios.org> <http://www.facebook.com/nimbios> <http://twitter.com/nimbios> To receive email notifications of blog updates, click here <http://www.nimbios.org/wordpress/subscribe2updates/> To

subscribe to our bi-monthly newsletter, click here <http://visitor.r20.constantcontact.com/manage/optin/ea?v=001RgvbKVL7a4Psoj8H7c43A%3D%3D> Joe Felsenstein <[joe@gs.washington.edu](mailto:joe@gs.washington.edu)>

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## North Carolina Evolution Disease May 4-6

Call for Participants: Catalysis Meeting on “Biodiversity, Conservation and Infectious Disease”

On May 4-6, 2015, the Triangle Center for Evolutionary Medicine (TriCEM), the National Evolutionary Synthesis Center (NESCent) and the Duke Tropical Conservation Initiative (DTCI) will be hosting a Catalysis Meeting on “Biodiversity, Conservation and Infectious Disease.” The organizers are Charles Nunn, Hillary Young, Gavin Smith and Jeffrey Vincent.

The goal of the meeting is to understand how changes in biodiversity impact infectious disease risk in humans and wildlife. Remarkably little effort has synthesized either theory or data on the efficacy of biodiversity and conservation practices as a disease management strategy, the effects of different anthropogenic changes on infectious disease risk in the tropics, or the impacts of different conservation strategies on human health. We will take a broad view on this important issue by examining the many potential links between changes in biodiversity and infectious disease risk, and by considering the diversity of ways to investigate these questions using empirical and theoretical approaches. We will also engage with the conflicting views that natural systems appear to buffer some disease risks, yet they can also serve as the source of new infectious diseases.

The meeting will be composed of approximately 10 researchers from Research Triangle universities (Duke, UNC-Chapel Hill, NC State, and NC Central), with another 25 participants from outside the Triangle. All travel expenses will be covered for non-Triangle participants, and meeting-associated meals covered for all participants. In building the participant list, we seek a wide range of interests, approaches, and experience levels. Thus, we welcome modeling approaches, field biologists, and those with expertise in meta-analysis, and graduate students, postdocs, and faculty. At the meeting, we will work toward specific outputs, which will include a special “theme” issue in a high-impact journal that synthesizes diverse views on this important topic, and development of future working groups

to investigate specific questions in greater depth.

For those wishing to participate in the Catalysis Meeting “ including scientists from the Research Triangle Universities ” we ask that you fill out a brief application at this link: <http://goo.gl/forms/LuCWB5Vhgm> .We will begin inviting participants after March 14.

For questions, please contact Charles Nunn at [clnunn@duke.edu](mailto:clnunn@duke.edu).

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

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## Raleigh NC Bioinformatics Practical May18-22

We still have space! Please contact us if you have any questions or need additional info. Hope to see you in Raleigh.

Spring workshop in Bioinformatics

Raleigh, North Carolina May 18 - 22, 2015

The handling of large datasets has become intractable without some level of bioinformatic literacy. Many biologists find that there is a steep learning curve to develop the confidence required to explore their genomics datasets effectively. This bioinformatics short course includes a rich collection of hands-on instruction and lectures specifically intended to help novice users become comfortable with a range of tools currently used to analyze next-generation data. There is no prerequisite for this course other than a willingness to learn and to work hard throughout the week. All workshop exercises will be implemented via VirtualBox and focus on Illumina data.

Course participation is limited to 25 students to ensure an intimate learning environment. Course instructors: Nic Blouin, PhD & Ian Misner PhD

Full course information/topics, contact, instructor info, and application instructions at <https://biodatatraining.wordpress.com> [nblouin69@gmail.com](mailto:nblouin69@gmail.com)

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## Raleigh NC Bioinformatics Practical Tools May18-22

Hi Everyone-

We have 5 spots left! <https://biodatatraining.wordpress.com> I am writing to provide and update on our workshop:

We have booked into a conference space at HQ Raleigh (<http://hqraleigh.com/>) and believe it will provide us with the space and resources we need for a terrific workshop.

Please contact us if you have any questions or need additional info. Hope to see you in Raleigh. Nic and Ian

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The handling of large datasets has become intractable without some level of bioinformatic literacy. Many biologists find that there is a steep learning curve to develop the confidence required to explore their genomics datasets effectively. This bioinformatics short course includes a rich collection of hands-on instruction and lectures specifically intended to help novice users become comfortable with a range of tools currently used to analyze next-generation data. There is no prerequisite for this course other than a willingness to learn and to work hard throughout the week. All workshop exercises will be implemented via VirtualBox and focus on Illumina data.

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Full course information/topics, contact, instructor info, and application instructions at <https://biodatatraining.wordpress.com> nic blouin <[nblouin69@gmail.com](mailto:nblouin69@gmail.com)>

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**Roscoff**  
**Marine Evolutionary Genomics**  
**May31-Jun12**

SUMMER COURSE ON MARINE GENOMICS AT THE MARINE BIOLOGICAL STATION OF ROSCOFF (F)

Second announcement

>From May 31st - June 12th, 2015 the 11th Summer Course on Marine Evolutionary & Ecological 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, metagenomics 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

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 Collén, SB-Roscoff, FR Simon Creer, Univ. Bangor, UK Yves Desdevises, OO-Banyuls, FR Jakob Hemmer-Hansen, DTU-Aqua, DK Erica Leder, Univ. Turku, Fi Frédéric Partensky, SB-Roscoff, FR Daniel Vaultot, SB-Roscoff Filip Volckaert, Univ. Leuven, BE Mathias Wegner, AWI-Sylt, GE

Organizing committee Jonas Collén, 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 Filip Volckaert, Univ. Leuven, BE

For information, a flyer and application please check <http://meeg2015.sciencesconf.org> . The application deadline is March 10 2015.

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

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**Sicily SystemsBiol Jul5-9**  
**ApplDeadlineMar31**

Call for Participation (apologies for multiple copies) Please forward to anybody who might be interested.

Synthetic and Systems Biology Summer School - 2nd Edition Taormina - Sicily, Italy, July 5-9, 2015

<http://www.taosciences.it/ssbss2015/> ss-  
bss.school@gmail.com

\* News \* New Speaker! Ron Weiss, MIT, USA

\*\* Deadlines \*\* Student Application: March 31, 2015  
 Oral/Poster Submission: March 31, 2015

\*\* List of Speakers \*\* \* Adam Arkin, University of California Berkeley, USA \* Jef Boeke, New York University, USA \* Angela DePace, Harvard University, USA \* Forbes Dewey, MIT, USA \* Karmella Haynes, Arizona State University, USA \* Richard Kitney, Imperial College London, UK \* Timothy Lu, MIT, USA \* Philip Maini, Oxford University, UK \* Giancarlo Mauri, University of Milano - Bicocca, Italy \* Steve Oliver, Cambridge University, UK \* Velia Siciliano, MIT, USA \* Ron Weiss, MIT, USA \* Nicola Zamboni, ETH, Switzerland

\*\* Industrial Panel \*\* \* Jon D. Chesnut, Life Sciences Solutions Group -Thermo Fisher Scientific, USA \* Speaker TBA, Autodesk Inc., USA \* Zach Serber, Zymergen, Inc. USA

School Directors Jef D. Boeke, New York University, USA Giuseppe Nicosia, University of Catania, Italy Mario Pavone, University of Catania, Italy Giovanni Stracquadanio, University of Oxford, UK

\*\* Short Talk and Poster Submission \*\* Students may submit a research abstract for presentation. School directors will review the abstracts and will recommend for poster or short-oral presentation. Abstract should be submitted by March 31, 2015. The abstracts will be published on the electronic hands-out material of the summer school.

<http://www.taosciences.it/ssbss2015/-index.html#applicationForm> <http://www.taosciences.it/ssbss2015/ssbss.school@gmail.com>

Apologies for multiple copies. Please forward to anybody who might be interested.

cfp.ssbss@dmi.unict.it

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## StPierre d'Oleron France EvoEpigen May16-22

Bonjour,

Rappel: les inscriptions pour l'école thématique Eco-Evo-Epigen le 18-22 Mai 2015 à St.Pierre d'Oléron sont ouverts sur le site

<http://rtp-3e.wix.com/rt3e#!et-3e/cwad> L'école est organisé par le Réseau thématique pluridisciplinaire (RTP) 3E Epigénétique en Ecologie et Evolution. La participation à l'école thématique est gratuit pour les membres CNRS. Pour les membres externes: thesards 150, Post-Doc/IE/IR/ 300. Le nombre de participants est limité à 40.

Date limite est le 20 mars 2015.

A très bientôt - Christoph Grunau

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Dear Colleagues,

Reminder: I am happy to announce that the enrollments for the CNRS "summer" school Eco-Evo-Epigen the 18-22 Mai 2015 in St.Pierre d'Oléron (France) are now open on our website

<http://rtp-3e.wix.com/rt3e#!et-3e/cwad> This event is organised by the research network 3E (Epigenetics in Ecology and Evolution). Inscription is free for CNRS members. Non-CNRS are asked to contribute 150 for PhD students and 300 for PostDocs etc. The number of participants is limited to 40.

Official languages are French and English.

Deadline for inscription is March 20, 2015.

Please don't hesitate to contact me for further information.

Very best regards - Christoph Grunau

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Programme:

- Aspects historiques et épistémologiques de l'épigénétique Francesca Merlin (CR2, CNRS-IHPST), Antonine Nicoglou (PostDoc Labex "Who Am I?", CRPMS & Institut Jacques Monod, IHPST) Conférence/débat

- Bases épigénétiques de la plasticité et variabilité phénotypiques Stéphane Maury (Pr. Univ Orléans), Marie Mirouze (CR2, IRD) Cours interactif

- Rôle de l'épigénétique dans la structuration et l'évolution des génomes Marie Mirouze (CR2, IRD), Clémentine Vitte (CR1, CNRS) Cours interactif

- Concepts et modèles de l'héritabilité Frank Johannes (Pr. Univ of Groningen), Etienne Danchin (DR CNRS) Cours interactif

- Techniques d'épigénétique moléculaire: quels outils pour quelles questions Stéphane Maury (Pr. Univ), Marie Mirouze (CR2, IRD), Clémentine Vitte TD/TP

- Analyse et traitement des données (BS-Seq, Me-DIP, ChIP-Seq) Christoph Grunau (Pr. Univ), Clémentine Vitte (CR1, CNRS) TD/TPbioinfo

- Techniques spécifiques à l'analyse ADN répétées et ARNs « non-codants » Cristina Vieira (Pr. Univ), Emmanuelle Lerat (CR1, CNRS) TD/TPbioinfo

- Définition de l'épigénétique Frank Johannes (Pr. Univ of Groningen), Antonine Nicoglou (PostDoc Labex "Who Am I?", CRPMS & Institut Jacques Monod, IHPST) table ronde

- Vers une nouvelle conception de l'hérédité, implications évolutives Francesca Merlin (CR2, CNRS-IHPST), Etienne Danchin (DR CNRS) table ronde

Christoph Grunau Prof. des Universités/Professor (HDR) IHPE UMR 5244 Université de Perpignan Via Domitia 58 Avenue Paul Alduy Bât R F-66860 Perpignan Cedex, France Tel 33 (0)4.68.66.21.80 Fax

33 (0)4.68.66.22.81 <http://ihpe.univ-perp.fr/> <http://methdb.univ-perp.fr/epievo/> Christoph Grunau <grunau@methdb.net>

## SwissAlps Adaptation Jun17-20

Workshop announcement - registration deadline approaching (15 April 2015)

A few places are still available in our workshop on “Theoretical and empirical evidence of adaptations” to be held in La Fouly (Valais, Switzerland) on June 17-20, 2015.

The aim of the proposed symposium is to bring together experimental, empirical and theoretical evolutionary biologists, all working to resolve fundamental questions at the center of a century-old debate.

For example: What is the distribution of fitness effects of new, segregating, and fixed mutations? What is the relative importance of adaptation vs. genetic drift in the evolution of natural populations? What are the genetic and genomic bases of adaptations and speciation(s)?

By combining expertise across wet and dry lab biology, and due to the progress of new genomic technologies, it is becoming increasingly possible to gain traction on these questions which are fundamental to any basic understanding of the very mode and tempo of the evolutionary process.

The workshop will bring together top researchers in the field with graduate students and junior researchers in La Fouly, a remote and beautiful location in the Swiss Alps (see [www.lafouly.net](http://www.lafouly.net)), allowing for close interactions and vivid exchanges due to the very limited number of participants (max. 35). The scientific program will consist in 2 1/2 days of a mixture of talks by invited speakers and students, and poster sessions. The workshop will end with a hike to some nearby magnificent view points over the Mont Dolent and Mont-Blanc region.

Confirmed invited speakers:

Prof. Peter Andolfatto, Princeton University (US) Prof. Joachim Hermisson, University of Vienna (AT) Dr. Felicity Jones, Friedrich Miescher Laboratory of the Max Planck Society, Tübingen (DE) Prof. Hanna Kokko, University of Zurich (CH) Prof. Bret Payseur, University of Wisconsin (US) Prof. Ole Seehausen, University of Bern & EAWAG (CH) Prof. Olivier Tenaillon, Institut national de la santé et de la recherche médicale, Paris

(FR)

Cost:

400 CHF, including conference fees, all meals and accommodation (with sleeping bags). Free attendance for CUSO students.

Web site and registration:

<http://www.cuso.ch/activity/?p=3D1128&id=3D2243>

The organizers:

Laurent Excoffier Jeff Jensen Stephan Peischl Claudia Bank

Dr. Claudia Bank School of Life Sciences École Polytechnique Fédérale de Lausanne (EPFL), Switzerland and Swiss Institute of Bioinformatics

Email: [claudia.bank@epfl.ch](mailto:claudia.bank@epfl.ch) Webpage: <http://people.epfl.ch/claudia.bank> Jensen lab: <http://jensenlab.epfl.ch> [klaudiebank@gmail.com](mailto:klaudiebank@gmail.com)

## UAzores EvolutionMicroorganisms Aug31-Sep5

Dear EvolDir community,

The Deep Carbon Observatory (DCO) is an international, multidisciplinary initiative aimed at exploring all aspect of carbon science. The Deep Carbon Observatory is trying to integrate different aspect of carbon science from all disciplines (including evolutionary biologist), and one of the main interest is to integrate knowledge through time (in the evolutionary sense). Relevant questions are linked to the evolution of microorganisms and their metabolism, the origin of life and the co-evolution of biosphere with the geosphere.

The Deep Carbon Observatory is hosting its second Early Career Scientist Workshop at the Centro De Vulcanologia e Avaliação de Riscos Geológicos ( <http://www.cvarg.azores.gov.pt/>), University of the Azores, São Miguel (Portugal), 31 August-5 September 2015. This workshop will bring together the next generation of researchers active in deep carbon studies from around the world. This relatively small workshop (~40 scientists) of early career researchers will continue to foster collaboration and community within the growing DCO Science Network. This workshop is funded by the Deep Carbon Observatory, and aims to support financially as many participants as possible. There is no registration fee for this workshop (accommodation and meals will



be provided), and successful applicants will be eligible for up to 100% reimbursement of travel costs.

Applications are encouraged from senior graduate students, postdoctoral researchers, fellows, and newly appointed assistant professors working on all aspect of carbon science (visit the DCO website for major details, <https://deepcarbon.net/>).

More informations on the workshop and the application procedure are available at this link <https://deepcarbon.net/feature/second-dco-early-career-scientist-workshop#.VOZv2DVMekA> Deadline for the application is May 1, 2015.

Please pass this message along to those that may be interested.

Donato Giovannelli, PI Second DCO Early Career Scientist Workshop [image: Imagine in linea 1]

Donato Giovannelli, PhD

a: Department of Marine and Coastal Science - IMCS Rutgers University 71 Dudley Rd, suite 208 08901 New Brunswick, NJ - USA

\*Follow me on Twitter @d.giovannelli < [https://twitter.com/d\\_giovannelli](https://twitter.com/d_giovannelli) >\*

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Skype: Given95 Google Scholar Profile <http://scholar.google.com/citations?user=-3DeYxwQpkAAAAJ&hl=3Den> giovannelli@marine.rutgers.edu

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## UBonn CrypticSpeciation Jun5-6

Graduate Meeting of the Zoological Systematics group of the German Zoological Society

June 5th to 6th 2015

Institute of Evolutionary Biology and Ecology of the University of Bonn, Germany

To whom it may concern,

On behalf of the Zoological Systematics group of the German Zoological Society Thomas Bartolomaeus and Torsten Struck invite you to participate at the graduate meeting at the Institute of Evolutionary Biology and Ecology of the University of Bonn. The topic of the meeting are the challenges that cryptic speciation

poses to taxonomic, evolutionary biological and ecological research. The invited speakers will speak about the specific requirements to taxonomically describe cryptic species, the foundations and problems of automatic species delineation, the pros and cons of different marker systems with respect to cryptic species and the impact of cryptic species on ecological and evolutionary biological studies. For more detailed informations see the flyer of the meeting (link to the flyer is below). Besides the invited speakers there is plenty of time and opportunity to present the own research as a presentation and poster as well as for discussion.

Please register inclusive an abstract for presentations or posters till May 8th 2015 by E-Mail to: [graduate.meeting.2015@annelida.de](mailto:graduate.meeting.2015@annelida.de) <<mailto:graduate.meeting.2015@annelida.de>> Best wishes by the speakers of the Systematics group,

Sven Bradler & Torsten Struck

Flyer with Information about graduate meeting: [http://www.dzg-ev.de/de/veranstaltungen/2015/-graduierentreffen\\_zoolsyst2015.pdf](http://www.dzg-ev.de/de/veranstaltungen/2015/-graduierentreffen_zoolsyst2015.pdf)

Torsten Struck <[torsten.struck.zfmk@uni-bonn.de](mailto:torsten.struck.zfmk@uni-bonn.de)>

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## UBremen EvolutionStatisticsUsingR

\*BRESSS V BRemen Ecological Statistics Summer School 2015\*

\*Date: June 02 V 05, 2015\*

\*Place: University of Bremen, Germany\*

Application deadline: 17th of April, 2015

Data obtained in research in ecology and evolution are often not normally distributed. Within the workshop we will use the unifying concept of generalized linear models (GLM) to deal with such data. Besides short lectures, exercises will be offered using the open source software R.

\*For further information please visit our website: \*<https://sites.google.com/site/statisticsbremen/>\* Topics covered: Linear Models, Generalized Linear Models (Poisson, Negative binomial, Gamma and Binomial distribution), Zero-inflated/-truncated Models, Generalized Linear Mixed Models

Thanks to the funding of the \*Deutsche Zoologische Gesellschaft\*, registration is free for all DZG members (The course fee for non-members is 20€ / 50€ for PhD

students/PostDocs).

We hope to welcome you soon in Bremen!

The organizing committee,

Katharina Merkel, Mareike Koppik and Thomas Hoffmeister

Statistics Bremen <statisticworkshopbremen@gmail.com>

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## UExeter EvolutionaryBehaviour Jul6-9

Omics for evolutionary/behavioral ecologists Reply-To: DJ Hosken <D.J.Hosken@exeter.ac.uk> X-Mailer: Apple Mail (2.1510)

The University of Exeter's Cornwall Summer Science Institute is open for this years registration. This years Summer School will be held from July 6th to 9th 2015. It is primarily directed at students of behavioural and evolutionary ecology and will provide guidance and training in the implementation of:

multivariate phenotypes (phenomics); transcriptomics; and genomics) into their work.

World-leading researchers from within and outside the Centre will attend; sharing their expertise to provide training and networking opportunities. Talks covering cutting-edge techniques and innovative science are intended to be pedagogical, and will be interspersed with workshop style sessions on problem solving, publishing and grant writing.

See: <http://www.exeter.ac.uk/summerscience/about/>  
CSSI events are held at the Centre for Ecology and Conservation. The Centre hosts unrivalled strength in depth of organismal biologists working in a friendly and collegiate environment. Delegates interested in discussing their research with particular CEC members while visiting are strongly encouraged to make contact prior to the workshop. The Summer School is hosted by the University of Exeter, Cornwall (UK).

Prof DJ Hosken University of Exeter, Cornwall Tremough, Penryn TR10 9FE UK

01326 371843 D.J.Hosken@exeter.ac.uk [http://biosciences.exeter.ac.uk/staff/index.php?web\\_id=-david\\_hosken](http://biosciences.exeter.ac.uk/staff/index.php?web_id=-david_hosken) DJ Hosken <D.J.Hosken@exeter.ac.uk>

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## UMaryland Bioinformatics

The Institute for Genome Sciences (IGS) is an internationally known research center located at the University of Maryland School of Medicine in Baltimore. IGS offers five different workshops as part of a professional development program organized by Dr. Michelle Giglio, a faculty member at IGS with over 17 years of experience in genomics and bioinformatics. Dr. Giglio has recruited IGS faculty and staff to form a highly experienced instruction team to provide workshop participants with the knowledge and skills needed to engage in numerous 'omics applications. All IGS workshops are hands-on, providing attendees with real-world challenges and experience.

Please see our workshop dates listed below.

### IMPORTANT DATES:

Metagenome Analysis October 13th - 16th, 2015  
Introduction to Programming for Bioinformatics March 16th - 20th, 2015

Transcriptome Analysis May 18th - 20th, 2015

Prokaryotic Comparative Genomics September 29th - October 1st, 2015

Introduction to Genomics and Bioinformatics November 2nd - 6th, 2015

FOR MORE INFORMATION & REGISTRATION:  
[www.igs.umaryland.edu/workshops](http://www.igs.umaryland.edu/workshops) EMAIL: Renee Nathaniel Workshop Administrative Coordinator  
rnathaniel@som.umaryland.edu

"Nathaniel, Renee" <rnathaniel@som.umaryland.edu>

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## UMichigan EvolutionFieldCourses

We invite undergraduate and graduate students interested in ecological research and hands-on study of the natural world to take our Spring and Summer 2015 field classes at the University of Michigan Biological Station. You will join a community of researchers on the shores of Douglas Lake near Pellston, Michigan.

Spring classes are 2-4 weeks long (2-5 credits) and in-

clude Great Lakes Oceanography, Biology of Birds and Ethnobotany.

Summer classes are 8 weeks long and feature organismal- (Biology of Insects, Biology of Fishes, Algae) and ecosystem- (Rivers, Lakes and Wetlands, Limnology, Field Botany and Forest Ecosystems) focused classes as well as Ecology, Evolution and Behavioral Ecology.

We have rolling course admissions, but the DEADLINE for priority consideration for our FINANCIAL AID is March 16, 2015.

More information available at: <http://lsa.umich.edu/umbs> . farmeral@umich.edu

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## UMichigan Evolution May24-Aug22

Course Announcement: Natural History and Evolution

The University of Michigan Biological Station (UMBS) offers a diverse set of courses in both a four-week spring term (May 24 to June 20) and an eight-week summer term (June 27 to August 22). One of the summer courses is a field course in evolutionary biology (EEB 390, Natural History and Evolution). This course is intended for undergraduate biology majors or first-year graduate students who want a strong foundation in evolutionary biology and exposure to methods of studying evolution in the field. The class meets all day twice a week, Tuesdays and Fridays. Mornings include lectures and afternoons are devoted to fieldwork either for demonstration or for individual research projects. Lecture topics include all aspects of evolution, from theory, molecular evolution, and phylogenetics to aspects of evolutionary biology that are amenable to observation in the field, including speciation, coevolution, sexual selection, sex ratio, and social behavior. Students conduct independent projects, which in the past have focused on plants, crayfish, aquatic invertebrates, damselflies and dragonflies, and birds. Numerous field trips will be taken to study the biological diversity of northern Michigan and to understand the importance of human modifications of the environment. Northern Michigan is a fabulous place to spend the summer and there are many opportunities for outdoor activities when not in the classroom.

Application material and other details can be found at the station's web site (<http://www.lsa.umich.edu/umbs/>). Students attending taking courses during the summer term typically take two courses, and details

of the other courses being offered are available at the web site above. Need and merit-based financial aid is available.

For more information please contact: Stephen Pruett-Jones (pruett-jones@uchicago.edu) or the UMBS office (umbs@umich.edu)

aspj@uchicago.edu

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## UNewHampshire BioinformaticsForUndergrads Jul27-30

Dear Colleagues,

I wanted to bring your attention to the following summer workshop opportunity for undergraduate students - \*accepted students will be fully funded to attend the workshop\*, courtesy of an NSF Research Coordination Network award. Application deadline is April 13th, and full details can be found here: <https://eukhits.wordpress.com/2015/03/02/applications-now-open-for-the-summer-2015-bioinformatics-biodiversity-undergraduate-workshop/> \*'Bioinformatics & Biodiversity' Undergraduate Workshop\* \*July 27-30, 2015\* \*University of New Hampshire, Durham, NH\*

Microscopic eukaryotes (meiofauna e.g. nematode worms, copepods, protists, fungi, etc.) are some of the most abundant animals on Earth, but species within these groups are often overlooked by the general public and even many biologists. This NSF-sponsored workshop will explore the field of environmental DNA sequencing, including collection and analysis of data. Students will learn how high-throughput approaches (rRNA gene surveys, metagenomics) are being used to investigate the biodiversity of microbial eukaryotes and deepen our knowledge of ecosystem function. The workshop program will be a combination of lectures and practical exercises, where students will learn about traditional taxonomic approaches and also gain experience using the command line and bioinformatics tools to analyze environmental DNA datasets.

For more information please contact Holly Bik (holly.bik@gmail.com)

holly.bik@gmail.com

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## UWestIndies Trinidad ViralEvolution Aug9-14

'20th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology'

The University of the West Indies (UWI), St. Augustine Campus, Trinidad and Tobago

Sunday, August 9 - Friday, August 14, 2015

Dear colleague,

We are announcing the organization of the international workshop on Virus Evolution and Molecular Epidemiology (VEME) in 2015, hosted by the University of the West Indies (UWI), St. Augustine, Trinidad and Tobago on behalf of our main sponsor the International Committee for Genetic Engineering and Biotechnology. The workshop is co-organised by the University of Leuven (Belgium) and the J. Craig Venter Institute (USA).

We plan to organize a 'Phylogenetic Inference' module that offers the theoretical background and hands-on experience in phylogenetic analysis for those who have little or no prior expertise in sequence analysis. An 'Evolutionary Hypothesis Testing' is targeted to participants who are well familiar with alignments and phylogenetic trees, and would like to extend their expertise to likelihood and Bayesian inference in phylogenetics, coalescent and phylogeographic analyses ('phylogenetics') and molecular adaptation. A 'Large Dataset Analysis' module will cover the more complex analysis of full genomes, huge datasets of pathogens including Next Generation Sequencing data, and combined analyses of pathogen and host. Practical sessions in these modules will involve software like, PHYLIP, PAUP\*, PHYML, MEGA, PAML or HYPHY, TREE-PUZZLE, SplitsTree, BEAST, MrBayes Simplot and RDP3.

We recommend participants to buy The Phylogenetic Handbook < <http://www.thephylogeneticshandbook.org> > as a guide during the workshop, and to bring their own data set.

The abstract and application deadline is March 15th

Selections will be made by the beginning of May.

The registration fee of 850 Euro covers attendance, lunches and coffee breaks. Participation is limited to 30 scientists in each module and is dependent on a selection procedure based on the submitted abstract and

statement of motivation. A limited number of grants are available for scientists who experience difficulties to attend because of financial reasons.

Selection criteria: (in order of importance)

1. Quality of the abstract: abstracts will be reviewed and priority will be given to applicants who are first author on the abstract.
2. Letter of motivation: how urgent/important is your need for training?
3. Each module is preferably restricted to 1 participant from the same lab.
4. Priority will be given to participants from countries with limited resources.

Grant criteria: (in order of importance)

1. Priority to countries with limited resources.
2. Ranking according to the abstract quality.

Additional information and application forms are available on our website: <http://www.rega.kuleuven.be/cev/-veme-workshop/2015> We are confident that this course meets the needs of many molecular virologists and epidemiologists, and hope we can assist you in your search for training in Bioinformatics methods.

Yours sincerely,

Christine Carrington, Karen Nelson and Annemie Vandamme Organizers of the workshop Contact: [veme2015@sta.uwi.edu](mailto:veme2015@sta.uwi.edu)

"Foley, Brian Thomas" <[btf@lanl.gov](mailto:btf@lanl.gov)>

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## UWestIndies VirusEvolution Aug9-14

20th International Bioinformatics Workshop on Virus Evolution & Molecular Epidemiology (VEME)

Dates: 9th - 14th August 2015

Venue: University of the West Indies, Trinidad and Tobago

DEADLINE FOR APPLICATIONS IS EXTENDED TO 31 MARCH 2015

The International Bioinformatics Workshop on VEME workshop is recognized as one of the best international virus bioinformatics courses in the world and has so far been organized in Belgium, Brazil, Finland, Greece, Portugal, the USA, South Africa, The Netherlands, Serbia and Italy. The 20th edition will be held from 9 - 14 August 2015 at the University of the West Indies in the Caribbean island of Trinidad and Tobago.

The workshop will provide 90 participants with intensive training in the mathematical principles and computer applications used in the study virus evolution and for conducting detailed molecular epidemiological investigations. The workshop will include lectures and computer practical session where students will have the opportunity to analyse their own research data. Each student will also present a poster about their research.

The target group are trainee scientists starting their scientific career, i.e. graduate research student, post-doctoral researchers and specialised research technicians (bio informaticians). The workshop teachers will be 24 world-renowned researchers from top international universities and research institutions. Interaction among participants and teaching staff is a key element, so the ratio of teachers to students will be maintained at no less than 1:4. A limited number of scholarships will be provided. There is no country restriction to attend, but scholarships are restricted to resource limited countries.

Participants will have the opportunity to attend one of the three 4-day modules and their choice of two of the 6 half-day modules:

Three 4-day modules

- 'Phylogenetic Inference' offers the theoretical background and hands-on experience in phylogenetic analysis for those who have little or no prior expertise in sequence analysis
- 'Evolutionary Hypothesis Testing' is targeted to participants who are well familiar with alignments and phylogenetic trees and would like to extend their expertise to likelihood and Bayesian inference in phylogenetics, coalescent and phylogeographic analyses ('phylogenetics')
- 'Large Dataset Analysis' will cover the more complex analysis of full genomes, huge datasets of pathogens including Next Generation Sequencing data, and combined analyses of pathogen and host.

Six 1/2-day modules:

- Morning - 'Large Phylogenies', 'Transmission Chain Investigation' and 'Molecular Adaptation'
- Afternoon - 'Visualization of Large Phylogenies with Metadata', 'Recombination and Networks' and 'Virus Analysis Tools'

Practical sessions in these modules will involve various software packages, including PHYLIP, PAUP\*, PHYML, MEGA, PAML or HYPHY, TREE-PUZZLE, SplitsTree, BEAST, MrBayes, Simplot, RDP3, QuRE.

Detailed information and online applications may be accessed at: <http://rega.kuleuven.be/cev/veme-workshop/2015> OR <http://www.icgeb.org/trinidad-and-tobago-veme-bioinformatics-2015.html>

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

[a.rambaut@ed.ac.uk](mailto:a.rambaut@ed.ac.uk)

## UYork EvolutionOfEvolution Jul24

### CALL FOR PAPERS/ABSTRACTS

EvoEvo workshop

Satellite workshop of the 13th European Conference on Artificial Life (ECAL 2015)

Friday July 24th 2015, University of York, York, UK

Variation and Selection are the two core processes of Darwinian Evolution. Yet, both are directly regulated by many processes that are themselves products of evolution (e.g. DNA repair, mutator genes, transposable elements, horizontal transfer, stochasticity of gene expression, sex, network modularity, niche construction...). This results in the ability of evolution to self-modify its operators, hence its dynamics. We call this process "Evolution of Evolution" or EvoEvo. Different EvoEvo strategies have been proposed in the literature, including regulation of variability, robustness/evolvability strategies, bet-hedging... However, most of these strategies are poorly characterized and the conditions under which they evolve as well as their consequences are generally unknown.

The aim of the EvoEvo workshop is to seek for a unified theory of Evolution of Evolution by studying its biological mechanisms, evolutionary consequences and possible applications to bioinspired computation. The workshop will take place as a satellite workshop of ECAL 2015: the 13th European Conference on Artificial Life (<http://ecal2015.alife.org>), University of York, York, UK. The EvoEvo workshop is an initiative of the EvoEvo consortium (<http://www.evoevo.eu>) funded by the FP7 EU-FET grant EvoEvo (ICT-610427).

### AREAS OF INTEREST

We are seeking submissions that explore all aspects of "Evolution of Evolution", including theoretical and experimental works (including in vivo, in vitro and in silico experiment). Topics include but are not limited to:

- Evolution of robustness and evolvability, evolution of pleiotropy
- Evolution of mutation rates, regulation of variability, mutators, transposable elements, chromosomal rearrangements
- Open-ended evolution
- Evolution

of the genotype-to-phenotype mapping - Niche construction, evolution of trophic networks, evolution of cooperation - Evolution of genes and metabolic networks, evolution of modularity - Evolution of stochastic gene expression and bet-hedging - Modeling and simulation of EvoEvo, EvoEvo and fitness landscapes/seascapes - Experimental characterization of EvoEvo - Application of EvoEvo to evolutionary computation - Philosophical, theoretical and practical aspects of EvoEvo

#### SUBMISSIONS

EvoEvo will accept full papers (10-15 pages) and extended abstracts (up to 3 pages). All submissions (either full papers and abstracts) will be peer reviewed, and accepted full papers and abstracts will appear in the workshop proceedings. Accepted papers will be selected for long or short oral presentation during the workshop.

- Full papers submission of 10 to 15 pages of Lecture Notes in Computer Sciences (LNCS) format. Full papers must present original researches. - Abstract submission will be less than 3 pages of LNCS format. Abstract may present work-in-progress or already published results.

Papers should be submitted via EasyChair (<https://easychair.org/conferences/?conf=evoevo2015>).

LNCS formatting details can be found at < <http://www.springer.com/computer/lncs?SGWID=0-164-7-72376-0> >.

#### IMPORTANT DATES

- Paper Submission: 24 April 2014 - Notification of acceptance: 15 May 2014 - Camera-ready copies: 29 May 2014 - EvoEvo Workshop: 24 July 2014

#### WORKSHOP CHAIRS

- Guillaume Beslon, INSA, Université de Lyon (FR), LIRIS/Beagle team - Santiago Elena, CSIC and Polytechnic University of Valencia (SP), IBMCP - Paulien Hogeweg, Utrecht University (NL), Bioinformatics group - Dominique Schneider, Université Joseph Fourier, Grenoble (FR), LAPM - Susan Stepney, University of York (UK), Centre for Complex Systems Analysis

Prof. Santiago F. Elena Evolutionary Systems Virology Group IBMCP (CSIC-UPV) Campus UPV, CPI 8E, lab. 2.04 Ingeniero Fausto Elio s/n, 46022 Valencia, Spain Phone: +34 963 877 895

Fax: +34 963 877 859 E-mail: [sfelena@ibmcp.upv.es](mailto:sfelena@ibmcp.upv.es)  
 Web: <http://bioxeon.ibmcp.upv.es/EvolSysVir> The Santa Fe Institute 1399 Hyde Park Road Santa Fe, NM 87501 USA Web:[www.santafe.edu/about/people/-profile/Santiago%20F.%20Elena](http://www.santafe.edu/about/people/-profile/Santiago%20F.%20Elena) "Santiago F. Elena" <[sfelena@ibmcp.upv.es](mailto:sfelena@ibmcp.upv.es)>

### Venice EvoDevo Sep28-Oct1

Summer School on Evolutionary Developmental Biology  
 Conceptual and Methodological Foundations

4th Edition: The Evolution of Developmental Processes  
 Venice, 28 September - 1 October 2015

Organizers: Alessandro Minelli, Gerd B. Müller and Giuseppe Fusco School director: Johannes Jaeger

School sponsors: Istituto Veneto di Scienze, Lettere ed Arti, Venice and Konrad Lorenz Institute for Evolution and Cognition Research, Vienna. Location: Istituto Veneto di Scienze, Lettere ed Arti, Palazzo Franchetti, Venice

Taching panel: J. Jaeger (School Director, CRG Barcelona), P. Beldade (Gulbenkian Institute, Lisbon), G.E. Budd (University of Uppsala), G. Fusco (University of Padova), R. Jenner (Natural History Museum, London), A. Khila (Institut de Génomique Fonctionnelle de Lyon), A. McGregor (Oxford Brookes University), A. Minelli (University of Padova), C. Mirth (Istituto Gulbenkian de Ciencia, Oeiras, Portugal), G.B. Müller (Konrad Lorenz Institute, Vienna, and University of Vienna), A. Peel (University of Leeds)

Deadline for applications: May 30th 2015

For details, visit <http://www.istitutoveneto.org/-EDB2015/> Giuseppe Fusco Department of Biology University of Padova Via U. Bassi 58/B I-35131 Padova Italy tel. +39.049.827.6238 fax +39.049.827.6230 e-mail [giuseppe.fusco@unipd.it](mailto:giuseppe.fusco@unipd.it) webpage <http://dept.bio.unipd.it/fusco>

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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](mailto:Golding@McMaster.CA). In addition, if it originates from ‘blackballed’ addresses it will be sent to me at [Golding@McMaster.CA](mailto: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](mailto: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](mailto: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 send to me at [Golding@McMaster.CA](mailto: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.