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# E v o l D i r

February 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 .....	33
Jobs .....	63
Other .....	87
PostDocs .....	103
WorkshopsCourses .....	145
Instructions .....	158
Afterword .....	159

---

## Conferences

Barcelona PlantGenomeEvolution Mar17-18 .....	3	Vienna SMBE Archaea Jul12-16 .....	18
Bonn Systematics Mar18-21 .....	3	Vienna SMBE BiologicalImpactTransposableElements Jul12-16 .....	19
BritishEcolSociety .....	3	Vienna SMBE DemographyAndSelection Jul12-16 .	19
Cairns Behaviour FemaleSongFitnessCosts Aug9-14 .4		Vienna SMBE EvolEcolMicrobialCommunities Jul12-16	20
Cordoba Argentina EvolBiol Jul6-8 .....	4	Vienna SMBE EvolEcolMicrobialCommunities July12- 16 .....	21
CzechRepublic RotiferEvolution Aug30-Sep4 .....	6	Vienna SMBE EvolMulticellularity Jul12-16 .....	21
Goettingen Germany GOEvolIV EvolutionaryBiol Feb18 .....	6	Vienna SMBE EvolutionCancer Jul12-16 .....	22
HarvardU TreeGenomes Jun16-17 .....	7	Vienna SMBE FitnessLandscapes Jul12-16 .....	22
IndianaU Bloomington MidwestEcologyEvolution Mar28-29 .....	8	Vienna SMBE FunctionalApproaches Jul12-16 ....	23
Krakow EvolutionaryConservationMonoamines Aug23- 28 .....	9	Vienna SMBE FungalEvolutionaryGenomics Jul12-16 23	
Lausanne ESEB Aug10-14 DeadlineJan10 .....	9	Vienna SMBE GeneExpressionEvol Jul12-16 .....	24
Lausanne ESEB SpeciationGenomics Aug10-14 Re- minder .....	9	Vienna SMBE GeneFlow Jul12-16 .....	24
Luxembourg MicrobiomeEvolution Mar31-Apr2 ...	10	Vienna SMBE GenomePhylogenies Jul12-16 .....	25
Marseilles 19thEBM Sep15-18 DeadlineJan31 .....	11	Vienna SMBE GenomePhylogenies Jul12-16 2 .....	25
Marseilles 19thEBM Sep15-18 DeadlineJan31 2 .....	11	Vienna SMBE GenomicsOfSexBias Jul12-16 .....	26
Marseilles EvolutionaryBiology Sep15-18 .....	11	Vienna SMBE GoldenAgeArchaea Jul12-16 .....	27
Oxford Systematics Aug26-28 AbstractSubmission .	11	Vienna SMBE HorizontalMicrobialEvolution Jul12-16	27
Porquerolles France MathCompEvolBiol Jun21-25 3 12		Vienna SMBE Jul12-16 .....	28
Porquerolles France MathCompEvolBiol Jun21-25 Ab- stDeadline .....	12	Vienna SMBE MicroEvoDevo Jul12-16 .....	29
RoyalSociety London NervousSystemEvolution Mar9-10 13		Vienna SMBE MolecularInnovation Jul12-16 .....	29
Stockholm MammalEvol Aug16-22 .....	14	Vienna SMBE NetworkEvolution Jul12-16 .....	30
StonyBrook NY Stickleback Jul26-31 .....	14	Vienna SMBE RapidAdaptation Jul12-16 .....	30
Turkey EcolEvolutionaryBiology Aug6-7 .....	15	Vienna SMBE SexChromosomeEvolution Jul12-16 .	31
UCalifornia Berkeley EvoDevo Aug5-8 2 .....	15	Vienna SMBE-Spatial-Population-Genetics Jul12-16	31
UCalifornia Berkeley EvoDevo Aug5-9 .....	16	Vienna SMBE SpeciationGenomics Jul12-16 .....	32
Vienna SMBE2015 AbstractDeadline reminder ....	17	Vienna SMBE ViolationsKingmanCoalescent Jul12-16	32
Vienna SMBE AlternativeSplicingEvolution Jul12-16 17		WesternConnecticutStateU EvolBiol Apr18 .....	33
Vienna SMBE AncientGenomes Jul12-16 .....	18		

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## Barcelona PlantGenomeEvolution Mar17-18

Dear colleagues and friends,

This is to announce the meeting that Jonathan Wendel, Scot Jackson, Olivier Panaud, Michael Purugganan and myself are organizing in Barcelona very soon, in March (17-18), on plant genome evolution. The meeting is entitled "Evolution of plant phenotypes, from genomes to traits" and will be divided in three scientific sessions: 1. Mechanisms generating genome variability, with special emphasis on polyploidy and TEs; 2. Evolution of plant phenotypes: wild and domesticated species; 3. Domestication and plant improvement: Putting science into practice in the aid of the human condition. We have a group of excellent speaker from the US, the EU, Israel and Japan that will ensure a fantastic discussion on these exciting and timely scientific questions.

The registration will be available very soon at the price of only 100 euro (which includes the lunch onsite for the two days of the conference). Please visit the webpage of the meeting (<http://-plantevolutionbarcelona2015.cragenomica.es/>) for more information on the meeting.

Hope to see you in Barcelona!

Best wishes,

Josep

Olivier Panaud <panaud@univ-perp.fr>

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## Bonn Systematics Mar18-21

The next Annual Meeting of the Gesellschaft für Biologische Systematik will take place on March 18-21, 2015, at the Zoologisches Forschungsmuseum Alexander Koenig (ZFMK) in Bonn.

It is now the third time the annual conference of the GfBS ([www.gfbs-home.de](http://www.gfbs-home.de)) takes place in Bonn at the ZFMK, after the meetings in 1998 and 2012. With many participants, these Annual Meetings are a complete success and essential for the promotion of systematics and taxonomy in Germany. The organizers hope for broad interest of systematists in attending the 2015 meeting.

After some large and expensive joint conferences of the GfBS with other societies, the next annual meeting will take place in a more "familiar" circle and at a low conference fee.

As special items on the agenda, special workshops (on Saturday 21. March) will offer for example software training for "Mitogenom-Annotation" and "Target DNA enrichment". For this, a separate registration is necessary later on! In addition, participants will have the chance to visit the Biohistoricum at ZFMK or take part on a tour through the collection.

Registration of posters and talks is possible via the email [gfbs2015@zfmk.de](mailto:gfbs2015@zfmk.de) New registration deadline is January 30. 2015. More Information about the conference: <https://www.zfmk.de/gfbs2015> . All topics of biological systematics are welcome! We especially encourage submission of contributions about the topics "The demand of taxonomic knowledge: for whom and in what form?" .

Key Speakers (status quo) - Florian Leese, Ruhr-UNI Bochum, Improvement of freshwater ecosystem assessment with DNA barcoding - Wolfgang Weisser, TU München, Ecology and Taxonomy - start of a new partnership - Hans-Joachim Mader, Stiftung Naturlandschaften Brandenburg, monitoring in natural landscapes - Peter Zulka, Umweltbundesamt Wien/ Rote Liste, taxonomic problems with classification of endangered species

We look forward to your registration!

The organizers at ZFMK, Prof. Dr. Wolfgang Waegle & Dr. Johannes Dambach

Zoologisches Forschungsmuseum Alexander Koenig - Leibniz-Institut für Biodiversität der Tiere - Adenauerallee 160, 53113 Bonn, Germany [www.zfmk.de](http://www.zfmk.de) Stiftung des öffentlichen Rechts; Direktor: Prof. J. Wolfgang Wägele Sitz: Bonn

Dambach Johannes <[J.Dambach@zfmk.de](mailto:J.Dambach@zfmk.de)>

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## BritishEcolSociety

Conference: Demography Beyond The Population, March 24 - 26 2015. Sheffield, UK: <http://bit.ly/1vmZrMy> @BritishEcolSoc

Conference: Methods in Ecology and Evolution 5th Anniversary Symposium. Live streamed in conjunction with a joint meeting in Canada. 22 April 2015, UK and Canada: <http://bit.ly/1x4c8hw> @BritishEcolSoc

Conference: The Ecology and Evolution of Emerging Plant Pests and Pathogens: Challenges to Global Food Security and Ecosystem Resilience, 13 - 14 July 2015. Cornwall, UK: <http://bit.ly/1CbJHC7> @BritishEcolSoc

Many thanks.

Richard Communications Manager

Richard English British Ecological Society < <http://www.britishecologicalsociety.org/> > Follow us on Twitter < <http://twitter.com/BritishEcolSoc> > @BritishEcolSoc and Facebook < <http://www.facebook.com/pages/British-Ecological-Society/-101064631942?ref=ts> > Charles Darwin House 12 Roger Street London WC1N 2JU, United Kingdom Tel: +44(0)207 685 2500

Our vision: a world inspired, informed and influenced by ecology

Get involved with us < <http://www.britishecologicalsociety.org/getting-involved/> > - there are so many ways!

The BES is Europe's largest ecological society, in terms of membership, services and activities. Our members are central to our work in science and outreach; through them we represent not only ecologists, but the science of ecology as well. Become a member! < [http://www.britishecologicalsociety.org/about\\_bes/membership/index.php](http://www.britishecologicalsociety.org/about_bes/membership/index.php) >

P Think before you print...

Richard English <[richard@britishecologicalsociety.org](mailto:richard@britishecologicalsociety.org)>

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## Cairns Behaviour FemaleSongFitnessCosts Aug9-14

Dear evoldir members,

As a part of the Behaviour 2015 conference that will be held in Cairns, Australia, on 9-14 August 2015 (<http://www.behaviour2015.org/>), 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 15 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](mailto:hall.mATunimelb.edu.au)

Naomi E Langmore - [naomi.langmoreATanu.edu.au](mailto: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.

Dr Michelle L Hall Research Fellow Department of Zoology University of Melbourne Melbourne, Vic, 3010 Australia Email: [hall.mATunimelb.edu.au](mailto:hall.mATunimelb.edu.au) Phone: 03 90359576 Web: <http://michellehall.wordpress.com/hall.m@unimelb.edu.au>

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## Cordoba Argentina EvolBiol Jul6-8

\*I ARGENTINEAN EVOLUTIONARY BIOLOGY MEETING\*

JULY 6 - 8, 2015

VAQUERÁAS, CÁRDABA, ARGENTINA

\* The objective of this meeting is to include all researchers and students interested in Evolutionary Biology in Southern South America. We intend to stimulate future periodic academic meetings in different regions of the country, the development of shared frameworks, the implementation of different methodologi-

cal approaches; bring some reflection to developing this discipline, and promote Evolutionary Biology in Argentina. With this communication we are pleased to announce the key speakers and symposia that will take place during I Argentinean Evolutionary Biology Meeting. The event will take place in the Tourist Center Vaquerías, located in the Natural Reserve Vaquerías (Valle Hermoso, Córdoba). For more information, visit: Web Page: <http://2015rabe.wix.com/rabe-2015> < <http://2015rabe.wix.com/rabe-2015> > Facebook: <https://www.facebook.com/RABE2015?ref=hl> < <https://www.facebook.com/RABE2015?ref=hl> > e-mail : 2015.rabe@gmail.com <2015.rabe@gmail.com> \*

#### \*KEY SPEAKERS\*

\*Using comparative genomics to study the origin of novel phenotypes in vertebrates\*

Dr. Scott Edwards. Museum of Comparative Zoology, and Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA. EEUU.

\*Evolution, natural selection and genomics\*

Dr. Esteban Hasson. Instituto de Ecología, Genética y Evolución de Buenos Aires (IEGEBE/EGE, FCEyN UBA). Buenos Aires. Argentina.

\*Southern Andean Altiplano: an historical perspective based on the evolution of co-distributed taxa\*

Dr. Marco Antonio Méndez. Universidad de Chile. Departamento de Ciencias Ecológicas. Facultad de Ciencias. Chile.

\*A race against time: the evolution of plant defenses against herbivores\*

Dr. Juan Fornoni. Instituto de Ecología, Universidad Nacional Autónoma de México.

\*Evolutionary Biology in Argentina: ¿What and how it is researched? \* An analysis of the first Argentinean Evolutionary Biology Meeting and its regional context\*

Dr. Ignacio Soto. Instituto de Ecología, Genética y Evolución de Buenos Aires (IEGEBE/EGE, FCEyN UBA).

#### \*SYMPOSIA\*

\*Evolutionary Genomics\*

\*Coordinator:\* Esteban Hasson. IEGEBE/EGE-CONICET, FCEyN, Universidad de Buenos Aires (UBA).

- \*Metagenomic of microeukaryote communities and its ecological implications.\*

Enrique Lara. Universidad de Neuchatel. Suiza.

- \*Evolutionary Genomics of chemosensory gene families in arthropods.\*

Francisca Cunha Almeida. IEGEBE/EGE-CONICET, FCEyN, UBA.

- \*Transcriptomics of detoxification in Drosophila.\*

Esteban Hasson. IEGEBE/EGE-CONICET, FCEyN, UBA.

\*Current state of phylogeographic knowledge of Southern South America.\*

\*Coordinator\*: Mariana Morando. CENPAT-CONICET, Universidad Nacional de la Patagonia San Juan Bosco, Pto. Madryn. Argentina.

- \*Phylogeography of rodents of Patagonia and central and southern Chile: historical significance and intraspecific diversification. \*

Guillermo D' Elia. Instituto de Ciencias Ambientales y Evolutivas, Universidad Austral de Chile, Chile.

- \*History of herpetofauna intraspecific lineages from mediterranean areas and temperate forests of central and southern Chile.\*

Pedro Victoriano. Universidad de Concepción, Chile.

- \*Diversification patterns and evolutionary histories in lizards from Patagonia.\*

Mariana Morando. CENPAT-CONICET. Universidad Nacional de la Patagonia San Juan Bosco.

- \*Past and present histories of plants from Patagonia and Monte.\*

Alicia Sérsic. IMBIV-CONICET, FCEyN, Universidad Nacional de Córdoba.

\*The analyses of shape in an Evolutionary context \* \*Coordinator: \*Rolando González-José. CENPAT-CONICET. Puerto Madryn, Chubut, Argentina.

- \*Floral shape selection mediated by pollinators.\*

Andrea Cocucci. IMBIV-CONICET, Universidad Nacional de Córdoba. Argentina.

- \*Evolutionary aspects of craneofacial variation in modern humans modernos: an Evo-Devo perspective. \*

Sol de Azevedo. CENPAT-CONICET. Puerto Madryn, Chubut, Argentina.

- \*The coastal patagonian environment as shape-modeller of the marine invertebrates: snails, crabs and bivalves as study models. \*

Federico Márquez. CENPAT-CONICET. Puerto Madryn, Chubut, Argentina.

- \*The importance of shape in Primate diversification at

different phylogenetic scales\*\*. \*Ivan Pérez. CONICET-Universidad Nacional de La Plata. Buenos Aires, Argentina.

\*Extinctions and niche construction.\*

\*Coordinator:\* José Luis Lanata. IIDYPCA-CONICET, Universidad Nacional de Río Negro. Río Negro. Argentina.

- \*Extinctions and humans.\*

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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>

you can learn how to use these techniques in rotifer studies.

\*<http://www.rotifera.org/how-ordinate-rotifers> \*Workshop on dormancy\*

Discussing the ecological and evolutionary role of rotifer resting eggs.

\*Workshop on bdelloid rotifers\*

To know more about the taxonomy, ecology, and genetics of these fascinating organisms.

\*Flyer of the meeting\*

\*<http://www.rotifera.org/files/second-announcement-rotifera-xiv.pdf> Diego Fontaneto <diego.fontaneto@gmail.com>

## CzechRepublic RotiferEvolution Aug30-Sep4

\*14th International Rotifer Symposium\*

The 14th International Rotifer Symposium will be held in Ěeské Budějovice, Czech Republic, from August 30th to September 4th, 2015.

All researchers interested in rotifers, as well as researchers working on topics that relate to rotifer biology should join us. Related topics include, but are not limited to the following: Acanthocephalans; Aging; Aquaculture; Anhydrobiosis; Asexuals; Biogeography; Diapause; Dispersal; Evolution; Population dynamics; etc.

All research topics relating to rotifers will be discussed, including their ecological roles in aquatic systems, their evolutionary processes and adaptations, their use in ecotoxicology, the surprising asexual genomes of bdelloids, and more.

Need more information about the symposium? Visit the IRS14 webpage!

\*<http://www.rotifera.org/>\* \*Additional highlights\*

\*Invited speakers\*

Nelson Hairston, Claudia Ricci, Karine Van Doninck, Scott Monks, Holger Herlyn

\*<http://www.rotifera.org/speakers>\* \*Workshop on multivariate statistics\*

Petr ©milauer and Jan ©uspa Lep<sup>1</sup> will provide an introduction to advanced multivariate statistics in which

## Goettingen Germany GOEvolIV EvolutionaryBiol Feb18

Dear colleagues and friends,

herewith we would like to remind you of the fourth GOEvol meeting on February 18th, 2015 at the University of Göttingen, Germany. Please note that the registration deadline is extended until February, 6th 2015.

GOEvol is a local network of PhD students and postdocs working on various evolutionary questions in Göttingen. The major aim of the network is to provide a platform for exchange.

More information about GOEvol, a preliminary program for the upcoming meeting and the online registration are available on the GOEvol website:

<http://goevol.uni-goettingen.de> This year's meeting aims at building on the already established U4 network (<http://www.u4network.eu/>), a strategic partnership between Ghent University (Belgium), the University of Göttingen (Germany), the University of Groningen (Netherlands), and Uppsala University (Sweden). Our upcoming meeting will give an overview of evolutionary research at these four Universities followed by a discussion about shared teaching possibilities.

Please consider to present your data (contributed talk or poster) and specify your decision during the registration process.

Registration and abstract submission deadline is February, 6th 2015. The registration fee of 5 EUR will be

paid at the registration desk.

Feel free to contact us if you have any queries or questions.

We are looking forward to welcome many of you at the GOEvol meeting 2015!

The GOEvol Team

Jens Bast

Juliane Germer

Lukas Geyrhofer

Ines Herlitzke

Nico Posnien

Natascha Zhang

Digest:

What?

GOEvol IV Meeting

When?

February 18, 2015

Where?

Georg-August-University Göttingen

Ernst-Caspari-Haus (GZMB)

Justus-von-Liebig-Weg 11

37077 Göttingen

Germany

Information and registration:

<http://goevol.uni-goettingen.de> –

Nico Posnien

Georg-August-University Göttingen Johann-Friedrich-Blumenbach Institute for Zoology and Anthropology Department of Developmental Biology Ernst-Caspari-Haus (GZMB) Justus-von-Liebig-Weg 11 37077 Göttingen Germany

Phone: +49 (0) 55139 20817 E-mail: [nposnie@gwdg.de](mailto:nposnie@gwdg.de)

web: <http://www.evolution.uni-goettingen.de/-posnienlab/index.html> web: <http://www.uni-goettingen.de/en/44993.html> [nico.posnien@gmail.com](mailto:nico.posnien@gmail.com)

## HarvardU TreeGenomes Jun16-17

35th New Phytologist Symposium: The genomes of forest trees - new frontiers of forest biology Arnold Arboretum of Harvard University, Boston, MA, USA. 16-17 June 2015

<http://www.newphytologist.org/symposiums/view/37> — On behalf of the New Phytologist Trust and symposium organisers we are pleased to invite you to participate in a symposium entitled 'The genomes of forest trees - new frontiers of forest biology'. The symposium will cover a range of topics but of particular interest to this list will be the session on 'Evolution' which will be headlined by our keynote speaker Sir Peter Crane. Programme, registration and further details can be found on the website <http://www.newphytologist.org/symposiums/view/37> Travel grants are available for students and early career scientists. Application deadline 13th MARCH 2015.

Poster abstract submissions are open. Submission deadline 10th APRIL 2015

— SCOPE New genomic technologies are bringing previously intractable but fascinating aspects of forest tree biology to the forefront of plant biology. Completed and ongoing sequencing projects are providing extensive expressed gene and even full genome sequence resources for tree species from diverse taxa. At the same time, creative applications of genomic and sequencing technologies are producing tools capable of probing the fundamental processes responsible for woody growth and other unique biological processes in trees. Among the most promising but largely unexplored areas of research is the use of comparative evolutionary genomics approaches that can illuminate key regulatory processes and how they have evolved over macro- and micro-evolutionary history. For example, the evolutionary innovations leading to the vast array of woody growth forms in extant plants are almost entirely unknown at the genetic level, but could soon be elucidated using comparative genomics approaches.

We will bring together researchers who are exploring the frontiers of tree evolution, ecology, and development using next generation sequencing, genomics, and systems biology approaches. Together, we hope to inspire new ideas for collaborative research that will bring together currently disjoint research communities, and usher in a new era of genome-based forest biology. Ultimately,

the approaches and insights from genome-based forest biology will inform us how to address problems ranging from forest conservation during climate change to tailoring of tree-based biofuels feedstocks.

— **FORMAT** The symposium will take place over two days at the Arnold Arboretum of Harvard University, Boston, MA, USA. There will be dedicated time for discussions, posters, selected poster talks, a conference dinner and a tour of the Arboretum's collections.

— **ORGANISING COMMITTEE** William Friedman Arboretum of Harvard University, Boston, USA Andrew Groover USDA Forest Service and University of California, Davis, USA

— **KEYNOTE SPEAKER** Peter Crane Yale University, New Haven, USA

**SPEAKERS** Siobhan Brady University of California, Davis, USA Taku Demura Nara Institute of Science and Technology, Nara, Japan Steve DiFazio West Virginia University, Morgantown, USA Carl Douglas University of British Columbia, Vancouver, Canada William Friedman Arnold Arboretum of Harvard University, Boston, USA Andrew Groover USDA Forest Service and University of California, Davis, USA Ykä Helariutta University of Helsinki, Helsinki, Finland Isabelle Henry University of California, Davis, USA Nathalie Isabel Natural Resources Canada, Canadian Forest Service, Québec, Canada Catherine Kidner University of Edinburgh, Edinburgh, UK Francis Martin INRA, Nancy, France David Neale University of California, Davis, USA Nathaniel Street Umeå University, Umeå, Sweden Jill Wegrzyn University of Connecticut, Storrs, USA Matthew Zinkgraf USDA Forest Service, Davis, USA

**DISCUSSION LEADER** Steve Strauss Oregon State University, Corvallis, USA

— Programme, registration and further information available at <http://www.newphytologist.org/-symposiums/view/37> Contact: Helen Pinfield-Wells np-symposia@lancaster.ac.uk

New Phytologist Trust website:  
[www.newphytologist.org](http://www.newphytologist.org) Twitter: @NewPhyt  
 Facebook: fb.com/NewPhytologist G+: <https://www.google.com/+NewphytologistOrgplantscience>  
 m.panagopulos@lancaster.ac.uk

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## IndianaU Bloomington MidwestEcologyEvolution Mar28-29

Dear colleagues,

We are pleased to announce that this year (March 28-29, 2015) The Midwest Ecology and Evolution Conference (MEEC) will be held at Indiana University Bloomington!

MEEC is an annual student-hosted research conference held at various institutions within the Midwestern United States. The conference provides an outstanding opportunity for graduate and undergraduate students to showcase their research and network with students and faculty from nearby institutions. MEEC provides a great environment for emerging scientists to discuss new ideas, hone presentation skills, and make connections in the local science community.

MEEC will include oral and poster sessions, panel sessions on outreach and career development, as well as what promise to be extraordinary plenary talks by Dr. Cathy Pfister (University of Chicago) and Dr. Alan Templeton (Washington University in St. Louis). The abstract call and registration are both from February 1-28. Registration for MEEC is only \$50!

Moreover, the annual IU Animal Behavior Conference (ABC), hosted by the IU Center for the Integrative Study of Animal Behavior, will take place right before MEEC, from March 26-28. We encourage people with a research interest in behavior to attend both conferences (plus, registration for ABC is free).

Get excited for one of the most enjoyable conferences of the year! You can find more information about the conference and how to register at our website (<http://meec2015.wordpress.com>), Facebook (<https://www.facebook.com/MEEC.conference>), or Twitter (@MidEcoEvoCon).

Best,

The MEEC Planning Committee Contact: MidEcoEvoCon@gmail.com

Midwest Ecology and Evolution Conference  
 <midcoevocon@gmail.com>



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**Krakow Evolutionary Conservation-  
Monoamines  
Aug23-28**

We are organizing a symposium titled 'The role of monoamines in modulating behavior' at the Ninth International Conference of Comparative Physiology and Biochemistry, to take place in Krakow, Poland from August 23-28, 2015. The description of the symposium is pasted below, at the end of this message.

The conference registration opens on January 25, and we would like to be able to include a list of confirmed speakers by that date. At this time, the conference fees have not been announced. There may be fee waivers available to invited speakers on a limited basis, but there are no funds available to cover travel expenses. More information about the conference can be found at <http://www.iccpb2015.confer.uj.edu.pl/>. Please respond with a tentative title and abstract by January 21 to ensure your inclusion as an invited speaker in both the general announcement for the conference, and in our symposium. Later replies may still be considered for inclusion in the symposium as regular (non-invited) attendees. Replies should be sent to [jaime.grace@ucdenver.edu](mailto:jaime.grace@ucdenver.edu)

Best wishes, John Swallow Jaime Grace Andrew Bubak  
Organizing committee

Symposium: The role of monoamines in modulating behavior

Monoamines, such as serotonin, dopamine, and norepinephrine, have a variety of essential physiological roles in modulating animal behavior. Furthermore, the evolutionary conservation of these aminergic systems spans across both vertebrates and invertebrates, having comparable effects in such diverse processes as learning and memory, aggression, mating behaviors and reproduction, stress responses, and locomotion. Outstanding research is currently being conducted in this field, uncovering remarkable similarities in neural circuitries even among highly divergent taxa, such as *Drosophila* and humans. Investigating the neural mechanisms involved in the monoaminergic modulation of behavior across a variety of taxonomically distant species can provide researchers with a better understanding of the origins and functions of these systems. The goal of this symposium is to provide a venue in which colleagues, researching invertebrates and vertebrates, both model and nonmodel, can

present their recent and groundbreaking work in this exciting area of biology. We hope this symposium will encourage and stimulate a dialogue on the similarities of monoaminergic function in a wide variety of animals and ultimately promote future comparative approaches when investigating behavioral modulation.

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

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**Lausanne ESEB Aug10-14  
Deadline Jan10**

Dear EvolDir colleagues,

for some bizarre reason the website address for abstract submission to the next ESEB meeting was not transmitted correctly in my previous reminder e-mails. Sorry for the problem.

The correct address is

[www.unil.ch/eseb2015](http://www.unil.ch/eseb2015) Hopes it works correctly this time

This mail was to remind you that the deadline for abstract submission is approaching fast:

(coming Saturday, Jan 10).

thanks and all the best

Nicolas Perrin

[Nicolas.Perrin@unil.ch](mailto:Nicolas.Perrin@unil.ch)

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**Lausanne ESEB Speciation Genomics  
Aug10-14 Reminder**

ESEB 2015 SYMPOSIUM ON SPECIATION GENOMICS

Dear colleagues,

This is a final reminder of the abstract deadline (10th January) for our symposium CHARTING THE GENOMIC LANDSCAPE OF SPECIATION which will be held at the 15th Congress of the European Society for Evolutionary Biology (ESEB) in Lausanne, Switzerland, 10th - 14th August 2015.

INVITED SPEAKERS - Nicolas Bierne (Institut de Sciences de l'Evolution- Montpellier, France) - Mohamed

Noor (Duke University, USA)

ORGANIZERS - Anja Westram (Sheffield, UK) - Mark Ravinet (NIG, Japan) - Juan Galindo (Vigo, Spain) - Rui Faria (Porto, Portugal)

NB: Although only two organisers are officially listed, the idea for the symposium was conceived by a group of four people who are all contributing to its organisation.

WEBSITE (Symposium No. 34) <http://www3.unil.ch/wpmu/eseb2015/symposium.list/> DESCRIPTION:

Understanding how speciation with gene flow works at the genomic level is currently a major focus of speciation biology. Genome scans between diverging populations have become widespread, demonstrating that the extent of differentiation can be quite variable across the genome. Highly differentiated regions are often interpreted as resulting from divergent selection, therefore playing an important role in speciation. This view is prominently expressed in the striking metaphor of 'speciation islands'. Yet some debate remains. Is differentiation generated by divergent natural selection acting as a barrier to otherwise homogenising gene flow? Or by recombination rate variation and/or intrinsic incompatibilities? Might differentiation occur when gene flow ceases and local adaptation increases the rate of lineage sorting in some parts of the genome but not others? And what genomic features affect homogenising gene flow? Being able to distinguish these alternative explanations is fundamental for understanding the genomic basis of speciation with gene flow. This symposium will explore this debate, bringing together empirical evidence from different perspectives and focusing on emerging approaches for identifying the processes that cause the rugged landscape of genomic differentiation.

DETAILS:

Registration for ESEB 2015 and abstract submission for all symposiums is now available at: <http://www3.unil.ch/wpmu/eseb2015/>. Please be aware the deadline for submitting abstracts for both talk and posters is 10th January 2015. Please be sure to state your preference for a talk or poster when submitting your abstract. All four organisers will evaluate the submissions and we hope to finalise our selections by early March. When selecting presentations, we aim to take into account gender balance.

Please don't hesitate contact us if you have any further questions (mravinet@nig.ac.jp; a.westram@sheffield.ac.uk)

We look forward to reading your abstracts and discussing speciation with you at ESEB 2015!

Mark, Anja, Juan and Rui

mravinet@nig.ac.jp

## Luxembourg MicrobiomeEvolution Mar31-Apr2

I thought that maybe the contents of Day 1 would be interesting for evolutionary biologists, especially PL1 "The Microbiome and Human Evolution" <http://www.ihmc2015.org/en/scientific-programme/day1>  
Thank you and happy New Year!

Julia

After 4 successful past congresses held in Europe, Canada, China and the United States, the International Human Microbiome Consortium (IHMC) is pleased to announce that the 5th International Human Microbiome Congress will take place from March 31st to April 2nd, 2015 in Luxembourg.

Entitled « Future Directions for Human Microbiome Research in Health and Disease », the congress agenda will reflect this focus and will gather 50 internationally renowned speakers from around the world, who will present the cutting edge approaches, which advance new knowledge for this field.

For this 5th congress, every effort has been made through concurrent sessions, poster sessions and workshops to provide opportunities for all scientists to learn about state-of-the-art research methods and clinical protocols for conducting microbiome work, while offering plenty of opportunity for discussion and networking over 3 days.

Co-organized with the support of our local host, IBBL (Integrated BioBank of Luxembourg), a leading biobank with a strong focus on microbiome research, the congress will also feature a dedicated session on biobanking of human microbiome samples, which will stress the importance of biobanking for research and disease intervention.

With such a comprehensive agenda, this 5th IHMC promises to be a truly outstanding congress for the field of human microbiome research and will attract over 500 participants from all around the world. Don't miss out, register now!

We would appreciate if you could advertise our congress on your website and circulate the details to your colleagues and network. A PDF invitation is also attached to this letter.

We can provide a banner or an image at the most convenient format you may need to insert on your website.

Please do not hesitate to contact us for any further information or clarification you may need.

We thank you in advance for your kind attention.

\*The IHMC Organising and Scientific Committees\*

Julia Schroeder MCO  
<julia.schroeder@mcocongres.com>

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### Marseilles 19thEBM Sep15-18 DeadlineJan31

Dear all the 19th EBM early deadline (as usual) is January 31st see <http://sites.univ-provence.fr/evol-cgr/> or [http://aeeb.fr/?page\\_id=333](http://aeeb.fr/?page_id=333) all the best Pierre

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

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### Marseilles 19thEBM Sep15-18 DeadlineJan31 2

Dear all the Evolutionary biology meeting at marseilles web site is open again it was close due to an internet attack of the web site of the Marseille University . <http://sites.univ-provence.fr/evol-cgr/> please Note that the early dead line is the end of january

best regards Pierre

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

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### Marseilles EvolutionaryBiology Sep15-18

Dear all the information concerning the Evolutionary biology meeting at Marseilles can be found at the AEEB web site: [www.aeeb.fr](http://www.aeeb.fr) best regards Pierre

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

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### Oxford Systematics Aug26-28 AbstractSubmission

Want to give a talk or a poster at the Systematics Association Biennial meeting (Oxford, UK 26-28 August 2015)?

There is an exciting programme that includes both plenaries and thematic symposia, as well as contributed sessions. Scheduled symposia include:

- The value of long term monitoring plots for plant systematics and ecology in the tropics - Comparative approaches to the origin of biodiversity - Accelerating the pace of taxonomy - Rooted in deep time: Palaeontological contributions to systematics

Abstract submission now open: <http://systass.org/-biennial2015/#abstract> Registration for attendees is open too.

The website for registration & accommodation bookings is here: [http://www.oxforduniversitystores.co.uk/-browse/extra\\_info.asp?compid=3D1&modid=-2&deptid=187&catid=119&prodid=299](http://www.oxforduniversitystores.co.uk/-browse/extra_info.asp?compid=3D1&modid=-2&deptid=187&catid=119&prodid=299) \*Registration Rates\*

£220 Full 3 day rate SA member £250 Full 3 day rate non-member £130 Student 3 day rate SA member £160 Student 3 day rate non-member £85 Full 1 day rate £60 Student 1 day rate

The 3 day rate includes sandwich lunch (meat, fish and vegetarian) and 2 drinks receptions. The day rate includes sandwich lunch.

\*Accommodation\*

All accommodation, if desired must be booked for three nights. The accommodation is at Christchurch for 25th, 26th and 27th August with breakfast included. Prices shown are for all 3 nights.

£186 Single standard room £261 Single ensuite room £384 Twin ensuite room £306 Twin set room (would suit two students sharing)

£40 Conference dinner (menu choice available at conference)

For further contact / queries, email: [sabiennial2015@systass.org](mailto:sabiennial2015@systass.org)

rcpm20@bath.ac.uk rcpm20@bath.ac.uk

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## Porquerolles France MathCompEvolBiol Jun21-25 3

NEW UPDATED ANNOUCEMENT MCEB - Mathematical and Computational Evolutionary Biology 21-25 June 2015 - Porquerolles Island, South of France.

Webpage: <http://www.lirmm.fr/mceb2015/> Pre-registration deadline: February 10th Notification to applicants: February 28th Final list of attendees: April 1st

Scope: Mathematical and computational tools and concepts form an essential basis for modern evolutionary studies. The goal of the MCEB conference (at its 7th edition) is to bring together scientists with diverse backgrounds to present recent advances and discuss open problems in the field of mathematical and computational evolutionary biology. The theme of this year's edition will be new data, new questions, new methods. New generation sequencing techniques have multiplied not just the amount, but also the types of genetic data produced, giving rise to new questions, and new methodologies to answer them. These methodologies are often cross-disciplinary, with applications to diverse research topics. General concepts, models, methods and algorithms will also be presented and discussed, just as during the previous conference editions.

Where and when: Porquerolles Island, near Hyères, in the South of France, 21-25 June 2015.

Cost: Conference fees including accommodation for four nights, meals, coffee breaks, etc., will be between 300 and 630 euro, all inclusive, and will vary depending on the room. PhD students and postdocs will benefit of the cheapest rooms.

Keynote speakers:

David Bryant - <http://www.maths.otago.ac.nz/~dbryant/> University of Otago, NZ Recovering phylogeny and demographics from SNPs: prospects and limitations

Jukka Corander - <http://www.helsinki.fi/bsg/> Bayesian Statistics Group, University of Helsinki, FI ABC meets machine learning - fitting intractable models to genome data

Asger Hobolth - <http://www.daimi.au.dk/~asger/> Bioinformatics Research Center (BiRC), Aarhus University,

DK Modelling DNA sequence evolution within and between species

Philippe Lemey <https://rega.kuleuven.be/cev/ecv/lab-members/PhilippeLemey.html> Rega Institute, Clinical and Epidemiological Virology, BE Data integrating in viral evolutionary inference: from spatial dynamics to trait evolution

Bernard Moret - <http://lebb.epfl.ch/> Laboratory for Computational Biology and Bioinformatics, EPFL, CH Phylogenetic Transfer of Knowledge

Ludovic Orlando - [http://geogenetics.ku.dk/-research\\_groups/palaeomix\\_group/](http://geogenetics.ku.dk/-research_groups/palaeomix_group/) Center for GeoGenetics, Natural History Museum of Denmark, DK Ancient DNA: from very old molecules to genomes and epigenomes

Molly Przeworski - <http://przeworski.c2b2.columbia.edu/> Columbia University, New York, USA A population-genetic approach to the study of mutation and recombination in humans

For more information, visit the website at: <http://www.lirmm.fr/mceb2015/> Please forward this announcement.

Olivier Gascuel <[gascuel@lirmm.fr](mailto:gascuel@lirmm.fr)>

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## Porquerolles France MathCompEvolBiol Jun21-25 AbstDeadline

Reminder: Don't forget to submit your abstracts for the 4th Mathematical and Computational Evolutionary Biology Meeting!

Deadline for abstract submission is approaching: \*February 10th, 2015\*.

Conference: MCEB - Mathematical and Computational Evolutionary Biology 21-25 June 2015 - Porquerolles Island, South of France.

Webpage: <http://www.lirmm.fr/mceb2015/> Pre-registration deadline: February 10th Notification to applicants: February 28th Final list of attendees: April 1st

WHAT/Scope: Mathematical and computational tools and concepts form an essential basis for modern evolutionary studies. The goal of the MCEB conference (at its 7th edition) is to bring together scientists with diverse backgrounds to present recent advances and dis-

cuss open problems in the field of mathematical and computational evolutionary biology. The theme of this year's edition will be new data, new questions, new methods. New generation sequencing techniques have multiplied not just the amount, but also the types of genetic data produced, giving rise to new questions, and new methodologies to answer them. These methodologies are often cross-disciplinary, with applications to diverse research topics. General concepts, models, methods and algorithms will also be presented and discussed, just as during the previous conference editions.

WHERE and WHEN: Porquerolles Island, near Hyères, in the South of France, 21-25 June 2015.

Cost: Conference fees including accommodation for four nights, meals, coffee breaks, etc., will be between 300euro and 630euro, all inclusive, and will vary depending on the room. PhD students and postdocs will benefit of the cheapest rooms.

Keynote speakers (to be completed):

David Bryant - <http://www.maths.otago.ac.nz/~dbryant/> University of Otago, NZ

Jukka Corander - <http://www.helsinki.fi/bsg/> Bayesian Statistics Group, University of Helsinki, FI

Asger Hobolth - <http://www.daimi.au.dk/~asger/> Bioinformatics Research Center (BiRC), Aarhus University, DK

Philippe Lemey <https://rega.kuleuven.be/cev/ecv/lab-members/PhilippeLemey.html> Rega Institute, Clinical and Epidemiological Virology, BE

Bernard Moret - <http://lcbp.epfl.ch/> Laboratory for Computational Biology and Bioinformatics, EPFL, CH

Ludovic Orlando <http://geogenetics.ku.dk/research-groups/palaeomix-group/> Center for GeoGenetics, Natural History Museum of Denmark, DK

Molly Przeworski - <http://przeworski.c2b2.columbia.edu/> Columbia University, New York, USA

For more information, visit the website at: <http://www.lirmm.fr/mceb2015/> Please forward this announcement.

raphael.leblois@supagro.inra.fr

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## Royal Society London Nervous System Evolution Mar9-10

“Origin and evolution of the nervous system”

9:00 am on Monday 09 March 2015 “ 5:00 pm on Tuesday 10 March 2015 at The Royal Society, London

<https://royalsociety.org/events/2015/03/nervous-system/> Scientific discussion meeting organised by Professor Nicholas Strausfeld FRS and Dr Frank Hirth

Event details The origin of brains and central nervous systems is thought to have occurred before the Paleozoic era. Yet in the absence of tangible evidence there has been continued debate whether today's brains derive from one ancestral origin or whether similarities amongst them are due to convergent evolution. This meeting will consider the origin of nervous systems, integrating knowledge ranging from evolutionary theory and palaeontology to comparative developmental genetics and phylogenomics. It will cover discoveries of fossil brains, as well as correspondences of neural circuit organisation and behaviours, all of which allow evidence-based debates for and against the proposition that the nervous systems and brains of animals all derive from a common ancestor.

Attending this event This event is intended for researchers in relevant fields and is free to attend. There are a limited number of places and registration is essential. An optional lunch is offered and should be booked during registration (all major credit cards accepted).

This meeting is immediately followed by a related, two-day satellite meeting, “Homology and convergence in nervous system evolution“ (<https://royalsociety.org/events/2015/03/nervous-system-satellite/>), at the Royal Society at Chicheley Hall, home of the Kavli Royal Society International Centre.

List of Speakers for the following sessions are available on the Webpage:

Session 1: Evidence from palaeontology

Session 2: Evolution of the nervous system ” evidence from non-bilateria and protostomia

Session 3: Evidence from protostomia and deuterostomia

Session 4: Evidence from protostomia and deuterostomia: is a unifying synthesis possible?

andreas.hejnol@sars.uib.no

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## Stockholm MammalEvol Aug16-22

Dear Colleagues,

We would like to invite you to participate in the 7th European Congress of Mammalogy (ECM7) in Stockholm, on 16-22 August 2015.

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.

For more information, and to register and submit abstracts for oral presentations as well as posters, please visit: [www.zoologi.su.se/ecm7](http://www.zoologi.su.se/ecm7) Early Registration will be between mid-February until April 15, and Late Registration will be between 16 April and 16 June.

Preliminary list of Plenary & Keynote speakers: David MacDonald, Oxford University Anjali Goswami, University College London Heikki Henttonen, Finnish Forest Research Institute Xavier Lambin, University of Aberdeen Henrik Andrén, Swedish University of Agricultural Sciences Mike Bruford, Cardiff University Ian Barnes, Natural History Museum London Bodil Elmhagen, Stockholm University Kjell Danell, Swedish University of Agricultural Sciences

The first day of the conference will be dedicated to workshops. If you are interested in suggesting and organizing a workshop session on any aspect of mammal biology, please contact the conference organizers.

ECM7 is organized by Anders Angerbjörn (Stockholm University), Lars Werdelin (Swedish Museum of Natural History) and Love Dalén (Swedish Museum of Natural History).

Love.Dalen@nrm.se

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## StonyBrook NY Stickleback Jul26-31

The Eighth International Conference on Stickleback Behavior and Evolution will be held from Sunday, July 26 through Friday, July 31, 2015 at Stony Brook University in Stony Brook, New York, USA. Contributed papers and posters will be scheduled, and the invited speakers are John A. Baker (Clark University), Theo C. M. Bakker (University of Bonn), William A. Cresko (University of Oregon), David M. Kingsley (Stanford University), Nadia Aubin-Horth (University of Laval), Juha Merilä (University of Helsinki), and Katie Peichel (Fred Hutchinson Cancer Research Center). Please visit the Conference website at <http://life.bio.sunysb.edu/ee/stickleback/index.html> for further information. The website will begin to accept registration payments and reservations for housing on about February 1.

**VENUE, ACTIVITIES, AND COSTS:** Talks will be given in the Charles B. Wang Center theater, and the posters will be displayed throughout the Conference in the theater lobby. Early registration through April 22, 2015 will be US\$285, and late registration until July 1, 2015 will be US\$315. Registration includes attendance of all talks, breakfasts (5), morning (5) and afternoon (3) coffee breaks, and food at the welcoming reception, poster session, and closing banquet, plus beverages at some social events.

**HOUSING:** The daily charge for dormitory housing (3 bedrooms per suite with shared bathroom and lounge) will be US\$73.50 for a private room and US \$60.00 per person for a room for two. Dormitory housing will be in the new Noble Dormitories about 15 minutes' walk from the Wang Center. Hotel rooms adjacent to the Wang Center will cost US \$140 plus tax per day. Information on off-campus hotels is provided on the Conference website. The Wang Center and Nobel Dormitories are about 15 minutes' walk from the rail road station. Lunches and most dinners will not be included in the registration fees, but meals will be available on or near campus. Dormitory housing will be available for at least two days before and after the Conference to allow participants to visit New York City or destinations on Long Island.

**TRANSPORTATION:** Stony Brook can be reached easily by air, automobile, or train. International flights come into John F. Kennedy (JFK) and Newark Liberty (EWR) international airports, which connect to Stony

Brook by train. LaGuardia (LGA) and Long Island MacArthur (ISP) airports have only domestic flights and lack train service to Stony Brook. The Stony Brook station of the Long Island Railroad is on the edge of campus. The Conference website provides more details on transportation.

**GRADUATE STUDENT SUPPORT:** Thanks to the efforts of Katie Peichel and Matt Wund, we have received a generous award from the American Genetic Association to support Conference registration and housing for about 20 graduate students. The deadline for submission of applications for support is March 2, 2015. Guidelines for application for support are posted on the Conference website.

**CONTACT:** Please contact Mike Bell (mabell@life.bio.sunysb.edu) if you have colleagues who should be added to the Conference email list, if you would prefer not to receive future notices, or if you have any questions about the Conference.

– Mike Bell

Michael A. Bell, Professor Department of Ecology and Evolution Stony Brook University Stony Brook, NY 11794-5245, USA Office Phone: 1-631-632-8574 <http://life.bio.sunysb.edu/ee/belllab/> “Michael A. Bell” <mabell@life.bio.sunysb.edu>

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## Turkey EcolEvolutionaryBiology Aug6-7

Dear Colleagues,

We are pleased to announce the 2nd Ecology and Evolutionary Biology Symposium - 2015, Turkey (EEBST 2015, <http://eebst2015.bio.metu.edu.tr/Home.html>). The symposium will be convening on August 6-7 2015 at the Middle East Technical University, Ankara. This will be the second international ecology-evolution symposium organized in Turkey, after EEBST 2014 (<http://www.eebst2014.boun.edu.tr/-EEBST-2014/Home.html>) held last year at Bogazici University, Istanbul.

These symposia series started out as a project by the Ecology & Evolution Network of Turkey (“evoeko”). Our goal is to promote cutting edge research in ecology, evolutionary biology, and related interdisciplinary areas in Turkey and in the region.

This year’s keynote speakers will be:

- Resit Akcakaya (Stony Brook University),
- Sergey Gavrilets (University of Tennessee),
- Rasmus Nielsen (University of California, Berkeley), and
- Daniel Simberloff (University of Tennessee).

We invite talks and poster presentations in all areas of ecology and evolutionary biology. All presentations will be in English and we welcome international participation.

Important Dates for registration and abstract submission are:

- Registration open: March 1
- Abstract submission for oral and poster presentations: March 1 - May 15
- Symposium program announced: June 1
- Registration closes: July 15

This will be a unique opportunity for meeting Turkey’s evolutionary biologist and ecologist research community and setting up collaborations.

For any questions, contact [wwwebst@metu.edu.tr](mailto:wwwebst@metu.edu.tr) or visit the website at: <http://eebst2015.bio.metu.edu.tr/-Home.html> We look forward to seeing you in Ankara!

On behalf of the Organizing Committee

Aysegul Birand ([birand@metu.edu.tr](mailto:birand@metu.edu.tr)) and

Mehmet Somel ([somel.mehmet@gmail.com](mailto:somel.mehmet@gmail.com))

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

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## UCalifornia Berkeley EvoDevo Aug5-8 2

Calling Evolutionary Developmental Biologists:

On behalf of the Council for the new \*Pan-American Society for Evolutionary Developmental Biology\*, we invite you to visit our new website [www.evodevopanam.org](http://www.evodevopanam.org) and join this new and exciting society! We welcome scientists from all over the world who are interested in evolutionary developmental questions spanning all levels of biological diversity.

Our mission as a society is to provide a voice for and promote evolutionary developmental biology in the America’s, to provide a forum for establishing communication and collaboration, and to promote training and edu-

cation. We hope to accomplish our mission through a number of community building activities, including organizing a bi-annual conference that alternates with our sister society \*The European Society of Evolutionary Developmental Biology\*, organizing training and education workshops, hosting evo-devo sessions and symposia in conjunction with other evolutionary and developmental biology societies, and facilitating the exchange of educational and training materials between researchers and among academic institutions.

The society will hold bi-annual conferences (alternating with our sister society \*The European Society of Evolutionary Developmental Biology\*). At these meetings, we will recognize and celebrate the careers of pioneers in the field of evolutionary developmental biology through the \*Pioneers Award,\* and early career contributions to the field via our \*Early Career Award\*. Both recipients will present a plenary lecture at the meeting. A number of awards presented at the meeting will our highly promising students and postdocs.

The inaugural meeting will be held in Berkeley, California from August 5-9, 2015. Register early at [www.evodevopanam.org](http://www.evodevopanam.org) because space is limited to 350 participants.

2015 Pioneers Award recipient: Professor Rudolf Raff (Indiana University)

2015 Early Career Award recipient: Dra. Natalia Pabon-Mora (Universidad de Antioquia)

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](mailto:cdspecht@berkeley.edu) <http://spechtlab.berkeley.edu/>  
[cdspecht@berkeley.edu](mailto:cdspecht@berkeley.edu)

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**UCalifornia Berkeley EvoDevo**  
**Aug5-9**

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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

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[cdspecht@berkeley.edu](mailto:cdspecht@berkeley.edu)



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## Vienna SMBE2015 AbstractDeadline reminder

Hello evoldir community,

abstract submission for oral presentations at SMBE 2015 (July 12-16) in Vienna, Austria, closes on February 8.

Join us 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 though 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.smbel.org/smbel/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)

Early bird registration by March 1 will also benefit from up to 30% reduced registration fee and full consideration of submitted abstracts.

All details about registration, accommodation options and travel discounts are available at the conference website: [www.smbel2015.at](http://www.smbel2015.at) The Local Organising Committee is looking forward to welcome you to Vienna in July!

julia.hosp@gmail.com

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## Vienna SMBE AlternativeSplicingEvolution Jul12-16

Dear Colleagues,

We are writing to advertise our symposium on \*the evolution of alternative splicing\*, which will be held as part of the Society for Molecular Biology and Evolution (SMBE) meeting, July 12-16 in Vienna, Austria.

\* Confirmed speakers: Chris Burge, MIT (<http://genes.mit.edu/burgelab/>) Michael Tress, Spanish National Cancer Research Centre (<http://ubio.bioinfo.cnio.es/people/mtress/>)

\* Symposium description: Post-transcriptional modifications of mRNAs by alternative splicing (AS) are thought to be an important road for evolutionary innovation. The advent of RNA-seq has enabled deep surveys of the splicing complexity across species. However, there are still large gaps in our understanding of the significance of AS evolution. This symposium aims at moving beyond simple comparisons of AS events across species to the study of the functional impact of new isoforms during evolution. We will highlight the latest advances in the field, notably related to the following questions: - How did splicing evolve between species? What use can be made of the last sequencing technologies (e.g., long-reads) to describe the evolution of AS at an unprecedented resolution? - Recent studies have highlighted that many isoforms are low-abundance and species-specific. What portion of AS might just represent “noise”? How could it influence the evolution of transcriptomes? - What is the functional impact of AS on the evolution of proteins? E.g., does AS modulate protein-protein interaction networks? What are the changes induced by AS on protein structures?

\* SMBE website and registration: <http://smbel2015.at/> Abstracts for oral presentations should be sent by February 8, 2015. Abstracts for poster presentations should be sent by March 29, 2015. Travel awards and child-care support are available to allow young scientists and parents to attend the conference.

Please do not hesitate to contact us with any questions. We hope to see you this summer in Vienna!

Julien Roux (julien.roux@unil.ch)    Âlodie Laine (elodie.laine@upmc.fr)    Hugues Richard (hugues.richard@upmc.fr)

Julien Roux Marie-Curie postdoctoral fellow Department of Ecology and Evolution, University of Lausanne, Switzerland <http://www.unil.ch/dee/home/menuinst/-people/post-docs-associates/dr-julien-roux.html>  
julien.roux@unil.ch

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## Vienna SMBE Ancient Genomes Jul12-16

SMBE SYMPOSIUM ON DETECTING SELECTION USING ANCIENT GENOMES - VIENNA JULY 12-16TH 2015.

We are pleased to invite you to participate in the symposium “Ancient genomes: A time machine for investigating natural selection”, which will take place at the annual meeting of the Society for Molecular Biology and Evolution (Vienna, July 12-16th 2015).

Symposium abstract: ‘Detecting natural selection and processes underlying genetic adaptations are core objectives of evolutionary biology and ecology. A number of statistical approaches have been developed in recent years to detect signatures of natural selection in modern genetic data. However, they all have poor temporal resolution, most are confounded by past demographic processes, and many are insensitive to selection acting on standing variation.

Ancient genomics has gained considerable momentum in recent years but its application to selection studies is still in its infancy. Sequencing ancient genomes from fossil material provides a unique snapshot of past genetic variation, thus providing a powerful tool for investigating adaptation hypotheses directly, and the only means of assessing temporal heterogeneity in natural selection.

In this Symposium we will explore new methods and the potentials of using heterochronic data to study natural selection, whether comparing ancient genomes to modern variation and/or ancient genomes from different time periods. We will discuss the principles, examples and potential limitations of detecting selection in any organism for which ancient genomes are available, including prokaryotes, plants, animals, and humans.’

Confirmed keynote speakers: Johannes Krause (<http://www.geo.uni-tuebingen.de/?id=2106>) and Ludovic Orlando (<http://geogenetics.ku.dk/research-groups/-palaemix-group/>).

Submit your abstracts for oral presentations (ABSTRACT SUBMISSION DEADLINE: 8TH OF FEBRU-

ARY 2015 - Check submission details on SMBE’s annual meeting webpage <http://smbe2015.at/>). Other important dates: Abstract submission for poster presentations, March 29, 2015 - Early bird registration, March 1, 2015.

See you in Vienna!

Zuzana Faltyskova, Yoan Diekmann, David Díez-del-Molino, Pascale Gerbault and Mark Thomas. Research Department of Genetics, Evolution and Environment, University College London, London, UK.

d.molino@ucl.ac.uk

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## Vienna SMBE Archaea Jul12-16

Dear colleagues,

We are pleased to invite you to submit an abstract to a symposium titled “The Golden age of Archaea: unveiling the diversity and evolution of the third Domain of Life” which will be hosted at the 2015 Meeting of the Society for Molecular Biology and Evolution (SMBE) in July 12-16, Vienna, Austria.

Our confirmed invited speakers are Graeme Nicol (University of Aberdeen, UK) and Manolo Gouy (CNRS, France)

Please note that the deadline of abstract submission for oral presentation is February 8th.

You can submit your abstract here:

[http://smbe2015.univie.ac.at/Abstract\\_Submission](http://smbe2015.univie.ac.at/Abstract_Submission)  
Symposium description:

Since their discovery nearly 40 years ago, the Archaea have not stopped being one of the major challenges of Evolutionary Biology. From a cell biology and genomic point of view they represent chimeras of prokaryotic and eukaryotic features, which places them in a key position in the Tree of Life. They thrive in a wide variety of contrasted environments, from deep oceans to the human gut, and have occupied key roles in the setup of major biogeochemical cycles of the early Earth. The development of culture-independent genomics techniques is providing access to an ever-larger and so far inaccessible fraction of archaeal diversity. This leads to a number of exciting discoveries that are revolutionizing our vision of archaeal evolution, generating novel challenges to dissect the nature of the last common archaeal ancestor and the evolutionary trajectories that shaped this domain of life. The archaeal tree is being rapidly filled up with new branches constituting entire phyla and orders with novel

characteristics. Genomic data has highlighted the existence of additional eukaryotic-like characters previously unsuspected in the archaea and re-launched the issue of their role in eukaryogenesis. A symposium specifically focused the diversity and evolution of the Archaea will be a timely occasion to present these exciting new data for this major prokaryotic domain, still widely unknown by the large audience.

Looking forward to seeing you in Vienna this summer!  
Simonetta Gribaldo Institut Pasteur (Paris, France) [simonetta.gribaldo@pasteur.fr](mailto:simonetta.gribaldo@pasteur.fr)

and

Celine Brochier-Armanet Claude Bernard University (Lyon, France)

[celine.brochier-armanet@univ-lyon1.fr](mailto:celine.brochier-armanet@univ-lyon1.fr)

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## Vienna SMBE Biological Impact- Transposable Elements Jul12-16

Dear all,

We are looking forward to receive your abstracts for the SMBE Symposium on The biological impact of transposable elements. Vera Gorbunova (University of Rochester) and Nelson Lau (Brandeis University) are the invited speakers in this symposium.

Best, Josefa

SMBE2015 Symposium: The biological impact of transposable elements

INVITED SPEAKERS: Vera Gorbunova. Department of Biology. University of Rochester. Nelson Lau. Department of Biology. Brandeis University.

ORGANIZERS: Josefa González. Institute of Evolutionary Biology. Barcelona. Ellen Pritham. Department of Human Genetics. The University of Utah.

SUMMARY: Transposable elements are a diverse set of genetic elements able to integrate and often propagate within and between genomes. They engender genome variation and novelty directly from integration and incidentally over a longer evolutionary timeframe by providing platforms for recombination and via the exaptation of sequences that they carry. Transposable elements are found in nearly all organisms and often account for the bulk of genetic material. As with so many

areas of genetics, the advent of genomic technologies has revolutionized the study of transposable elements, the mutation spectrum and their biological impact. This has led to an avalanche of important discoveries revealing new mechanisms through which transposable elements have shaped the chromosomal and regulatory architecture of genomes. This symposium will showcase the impressive array of mechanisms by which the evolutionary trajectory of the host is influenced by transposable elements. By focusing on the biological impact of transposable elements, we aim to showcase the diversity of ways that eukaryotic genomes have been shaped therefore appealing to researchers beyond the transposable element community.

Josefa González, PhD Ramón y Cajal Researcher Institut de Biologia Evolutiva (CSIC-Universitat Pompeu Fabra) Passeig Marítim de la Barceloneta 37-49 08003 Barcelona +34 932309637

[www.biologiaevolutiva.org/gonzalez.lab](http://www.biologiaevolutiva.org/gonzalez.lab)

[www.lacienciaalteumon.cat](http://www.lacienciaalteumon.cat) “GONZALEZ PEREZ, JOSEFA” <[josefa.gonzalez@ibe.upf-csic.es](mailto:josefa.gonzalez@ibe.upf-csic.es)>

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## Vienna SMBE Demography And Selection Jul12-16

Dear Colleagues,

We are please to invite you to our symposium on “Reframing the demography vs. selection debate using 21st century models and data,” which will be held at the Annual Meeting of the Society for Molecular Biology and Evolution (SMBE) in Vienna on July 12-16, 2015. The deadline for submission of abstracts is February 8th, 2015.

Symposium summary:

The importance of natural selection versus population history at shaping genetic variation is at the core of population genetics and has been debated for decades. However, there is a deep interplay between these two evolutionary forces. For example, recent studies have determined that demographic processes have shaped patterns of segregating deleterious variation in humans and that ancient admixture has provided new adaptive alleles on which selection has acted. Further, it is becoming increasingly clear that natural selection can confound demographic inference from genomic data. Due to the wealth of DNA sequence data from multiple model and non-model taxa, ancient and modern genomes, it is now

possible to study the interplay between selection and demography at a higher resolution than was previously feasible. However, even with more data, these topics are not without controversy. This symposium will feature theoretical and empirical advances in studying the interplay between demography and selection using genomic data. It will include a timely discussion of complex population genetic models that simultaneously model both processes. This symposium will be of interest to a broad audience because it will provide fresh perspectives on a classic and highly relevant topic in population genetics.

Invited speakers:

Anna Di Rienzo (<http://genapps.uchicago.edu/-index.html>)

Brenna Henn (<https://ecoevo.stonybrook.edu/hennlab/>)

Deadline: Submissions of abstracts are open until February 8th, 2015.

For more information about SMBE 2015, please go to <http://smbe2015.at/>

Hope to see you there!

Emilia Huerta-Sanchez, PhD Assistant Professor Molecular Cell Biology, School of Natural Sciences University of California, Merced [emiliahsc@ucmerced.edu](mailto:emiliahsc@ucmerced.edu)

Kirk Lohmueller, PhD Assistant Professor Department of Ecology and Evolutionary Biology University of California, Los Angeles [klohmueller@ucla.edu](mailto:klohmueller@ucla.edu)

[klohmueller@ucla.edu](mailto:klohmueller@ucla.edu)

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**Vienna SMBE**  
**EvolEcolMicrobialCommunities**  
**Jul12-16**

SYMPOSIUM ON EVOLUTION AND ECOLOGY OF MICROBIAL COMMUNITIES

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Dear colleagues,

We are glad to introduce the symposium **BEvolution and Ecology of Microbial Communities** that will be held during the annual SMBE conference in Vienna, Austria on July 12th-16th, 2015 (<http://smbe2015.univie.ac.at/program/symposia/-#c518157>).

It focuses on the evolutionary dynamics of microbial

communities and their interactions with their (changing) environment. We invite contribution of works involving metagenomics and genomics of key community isolates geared to understand the evolutionary processes in microbiomes at the taxonomic, genomic and functional levels, along with methodological developments aiming at tackling these issues.

We are delighted to announce that Peer Bork (EMBL, Heidelberg) and Nancy Moran (Uni. Texas, Austin) will be featured as invited speakers, and we wish to invite all interested evolutionary microbiologists to come along and contribute talks and posters.

Abstract submissions will be opened until February 8th.

Looking for seeing you in Vienna!

Florent Lassalle and Mathieu Groussin

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Symposium description:

The study of microbial community ecology and evolution has been advancing at a rapid pace for a few years, benefiting from the possibility to analyze metagenomic sequence data. Microbial communities in diverse environments have been characterized, with major impact on our understanding of microecology and human health. However, the complex nature of a microbial community makes it challenging to identify the ecological and evolutionary processes driving its multi-level structure. A community comprises dozens to hundreds of species interacting together, sharing or competing for goods, cooperating for or antagonizing in niche occupation. It can also be seen as a loosely compartmentalized gene pool structured by the pattern of genetic exchange among its members. These species and genetic interactions evolve in time along with the surrounding environment. Revealing the evolutionary processes linking these aspects of microbiomes is critical to understanding how microbes adapt to various environments and, in turn, how environments are impacted. This symposium aims at presenting new empirical results on evolution and ecology of microbial communities and the dynamics of their taxonomic composition, genomic diversity and functional repertoires. Methodological advances allowing us to infer these dynamics will also be presented.

INVITED SPEAKERS: Peer Bork (EMBL, Heidelberg) Nancy Moran (University of Texas, Austin)

ORGANIZERS: Mathieu Groussin (MIT, Cambridge, USA) [mgroupssi@mit.edu](mailto:mgroupssi@mit.edu) Florent Lassalle (University College London, UK) [florent.lassalle@ucl.ac.uk](mailto:florent.lassalle@ucl.ac.uk)

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

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**Vienna SMBE**  
**EvoEcolMicrobialCommunities**  
**July12-16**

SYMPOSIUM ON EVOLUTION AND ECOLOGY OF MICROBIAL COMMUNITIES

INVITES SPEAKERS: Peer Bork (EMBL, Heidelberg)  
Nancy Moran (University of Texas, Austin)

ORGANIZERS: Mathieu Groussin (MIT, Cambridge, USA) [mgroussi@mit.edu](mailto:mgroussi@mit.edu) Florent Lassalle (University College London, UK) [florent.lassalle@ucl.ac.uk](mailto:florent.lassalle@ucl.ac.uk)

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Dear colleagues,

We are glad to introduce the symposium “Evolution and Ecology of Microbial Communities” that will be held during the annual SMBE conference in Vienna, Austria on July 12th-16th, 2015 (<http://smbe2015.univie.ac.at/-program/symposia/#c518157>).

It focuses on the evolutionary dynamics of microbial communities and their interactions with their (changing) environment. We invite contribution of works involving metagenomics and genomics of key community isolates geared to understand the evolutionary processes in microbiomes at the taxonomic, genomic and functional levels, along with methodological developments aiming at tackling these issues.

We are delighted to announce that Peer Bork (EMBL, Heidelberg) and Nancy Moran (Uni. Texas, Austin) will be featured as invited speakers, and we wish to invite all interested evolutionary microbiologists to come along and contribute talks and posters.

Abstract submissions will be opened until February 8th.

Looking for seeing you in Vienna!

Mathieu Groussin and Florent Lassalle

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Symposium description:

The study of microbial community ecology and evolution has been advancing at a rapid pace for a few years, benefiting from the possibility to analyze metagenomic sequence data. Microbial communities in diverse environments have been characterized, with major impact on our understanding of microecology and human health. However, the complex nature of a microbial commu-

nity makes it challenging to identify the ecological and evolutionary processes driving its multi-level structure. A community comprises dozens to hundreds of species interacting together, sharing or competing for goods, cooperating for or antagonizing in niche occupation. It can also be seen as a loosely compartmentalized gene pool structured by the pattern of genetic exchange among its members. These species and genetic interactions evolve in time along with the surrounding environment. Revealing the evolutionary processes linking these aspects of microbiomes is critical to understanding how microbes adapt to various environments and, in turn, how environments are impacted. This symposium aims at presenting new empirical results on evolution and ecology of microbial communities and the dynamics of their taxonomic composition, genomic diversity and functional repertoires. Methodological advances allowing us to infer these dynamics will also be presented.

[florent.lassalle@ucl.ac.uk](mailto:florent.lassalle@ucl.ac.uk)

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**Vienna SMBE EvoMulticellularity**  
**Jul12-16**

SMBE 2015 Symposium on Evolution of Multicellularity, July 12-16, Vienna

Dear evoldir colleagues,

We are pleased to announce the symposium entitled “The origins of multicellularity under the light of functional genomics±, as part of the annual SMBE meeting that will be held in Vienna on July 12-16 2015 (<http://smbe2015.univie.ac.at/home/>). We encourage you to submit your abstracts for oral presentations before February 8th (<http://smbe2015.univie.ac.at/-registration/>).

Symposium summary: The origin of multicellularity is one of the major evolutionary transitions in the history of life. But unicellular to multicellular transitions have occurred independently several times during eukaryote evolution. In the last decade, the sequencing of the genomes of multicellular species and their closest unicellular relatives allowed for the first time to investigate the molecular basis of the multicellular transitions by using comparative genomics. Nowadays, the rapid advance of functional genomics and the development of key species as model systems are pushing the question into a new level, going beyond genome content description. This offers a unique opportunity to functionally test hypotheses about the origin of multicellularity regarding

genome regulation, gene function and the fundamentals of embryonic development. In this symposium we will cover these new approaches to the question of the multicellular transition from a multidisciplinary perspective, including recent advances from several fields (transcriptomics, cell biology, epigenomics) in different eukaryotic lineages.

Invited speaker: Professor Nicole King (<https://kinglab.berkeley.edu/>).

For more details, please don't hesitate to contact us.

Arnau Seb-Pedrs (arnau.sebe@ibe.upf-csic.es) Alex de Mendoza (alexmendozasoler@gmail.com)

Arnau Seb Pedrs, PhD Multicellgenome lab Institut de Biologia Evolutiva. CSIC-UPF Passeig de la Barceloneta 37-49 08003 Barcelona

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Arnau Seb Pedrs <arnau.sebe@ibe.upf-csic.es>

framework that makes testable predictions as to how interventions will influence therapeutic outcomes. This symposium will bring together researchers with different perspectives - cancer researchers, mathematical oncologists, and evolutionary biologists and ecologists - to explore how mathematical approaches can be used to understand tumor initiation and progression as well as how evolutionarily informed approaches can be used to gain new insights in cancer research. The work presented will provide a basis for future research into cancer as an evolutionary process.

Confirmed invited speaker is Dr. Natalia Komarova.

The abstract submission deadline is February 8, 2015.

We hope to see you this summer!

Oana Carja

Department of Biology, University of Pennsylvania

Oana Carja <oana.carja@gmail.com>

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## Vienna SMBE EvolutionCancer Jul12-16

Dear colleagues,

We would like to encourage you to apply for our upcoming symposium “\*Cancer as a Darwinian process\*,” which will be held at the July 2015 meeting of the Society for Molecular Biology and Evolution (\*SMBE 2015\*) in Vienna [[\\*http://smbe2015.at/\\*](http://smbe2015.at/)]. The symposium will focus on the evolutionary dynamics that govern the process of tumor initiation and progression.

\*Symposium description:\*

Cancer, one of the worlds biggest killers, is fundamentally a Darwinian process. Heritable genetic and epigenetic changes can disrupt the systems regulating cell replication, which can, in turn, break down the mechanisms of cooperation between cells that are fundamental to multicellularity. In this sense, tumors are nothing more than populations of cells with an evolutionary advantage. In order to understand and eradicate cancer, we must first understand the evolutionary dynamics that govern the process of tumor initiation and progression. This understanding requires an evolutionary and ecological perspective that can integrate vast amounts of biological and clinical data as well as an evolutionary

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## Vienna SMBE FitnessLandscapes Jul12-16

Dear Colleagues,

We are writing to announce a symposium on “Inferring fitness landscapes from experimental evolution”, which will be held as part of the Society for Molecular Biology and Evolution (SMBE) meeting, July 12-16 in Vienna, Austria. Applications to give a talk as part of this symposium will be accepted through February 8; for details concerning how to submit an abstract see the conference website (<http://smbe2015.at/>).

Symposium Description:

What can we learn about the structure of a fitness landscape from observations in evolving laboratory populations? Despite the potential power of massively replicated laboratory evolution experiments, we remain ignorant about the large-scale structure of fitness landscapes, even in simple, fixed environments. The central difficulty is that we do not know how best to draw inferences from the data generated in such experiments. To make matters worse, we do not even know what types of inferences can be made, in principle, from which types of data that is, which feature of the fitness landscape, such as epistasis, are identifiable. This symposium will showcase recent efforts to provide a firm statistical and population-genetic grounding for drawing

inferences about the forces shaping adaptation using data from replicate experimental populations.

Olivier Tenaillon and Michael Desai are confirmed as the two invited speakers for this symposium.

Please do not hesitate to contact us with any questions.

Sincerely,

David McCandlish davidmc@sas.upenn.edu

Joshua Plotkin jplotkin@sas.upenn.edu

Department of Biology University of Pennsylvania  
Philadelphia, PA 19104

david.mccandlish@gmail.com

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## Vienna SMBE Functional Approaches Jul12-16

Dear Colleagues, We are writing to invite you to submit abstracts to our symposium on \*novel functional approaches to evolutionary genomics\*, which will be held as part of the Society for Molecular Biology and Evolution (SMBE) meeting, July 12-16 in Vienna, Austria.

\*Confirmed Speakers Rick Livesey - <http://www2.gurdon.cam.ac.uk/~liveseylab/fj13/index.html>  
Greg Wray - <http://sites.biology.duke.edu/wraylab/>

\*Symposium description Formal testing of many evolutionary hypotheses, especially in closely related mammals, has been difficult until now due to practical and ethical constraints. However, recent advances in cellular biology, such as the development of induced pluripotent stem cell and genome editing technologies and genomics, like single cell sequencing, can open the door to powerful new ways of studying evolution. These technologies are bringing together multiple groups with diverse interests and perspectives, and transforming studies of functional evolution that were previously intractable in non-model organisms like the great apes. Our symposium will highlight research that incorporates these novel approaches to enrich our understanding of evolutionary function and process, such as mechanisms of gene regulation or the importance of developmental contributions to phenotypic divergence.

\*Registration Abstracts for oral presentations should be sent by February 8, 2015. Abstracts for poster presentations should be sent by March 29, 2015. Travel awards and childcare support are available. <http://smb2015.univie.ac.at/> Please contact us with any

questions. We look forward to seeing you in Vienna!

Nicholas Banovich (nbanovich@uchicago.edu) Irene Gallego Romero (ireneg@uchicago.edu)

Nicholas Banovich <nbanovich@uchicago.edu>

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## Vienna SMBE Fungal Evolutionary Genomics Jul12-16

Dear colleagues,

We are pleased to invite you to submit abstracts for a SMBE2015 symposium, "Fungal Evolutionary Genomics: Unravelling Mysteries from the Forgotten Kingdom." The symposium will occur at the annual meeting of the Society for Molecular Biology and Evolution in Vienna, Austria on 12-16 July 2015. Complete conference details can be found at <http://smb2015.at>. Fungal Evolutionary Genomics: Unravelling Mysteries from the Forgotten Kingdom

Fungi have small and compact genomes, yet they retain the key features of other eukaryotes, including introns, centromeres, telomeres, sexual cycles, and complex regulatory networks. They arose in the Precambrian and have radiated to perform a wide array of heterotrophic ecosystem functions, such as the parasitism of animals and plants, tissue decay, and sugar fermentation. Fungi have evolved remarkably different carbon utilization strategies, allowing different species to store excess nutrients and energy as riboflavin, oils, ethanol, and even octane. Thus, they are superlative models of metabolic and genome evolution across even deep evolutionary timescales. Fungal genomes have provided fundamental insights into how functions are partitioned among paralogs following whole genome duplications, how life cycles evolve, and how ecological shifts lead to changes in genome content and metabolism. Several large-scale evolutionary genomics projects, including the Dikaryome (iGénol evures Consortium), F1000 Fungal Genomes, and Y1000+ Saccharomycotina Yeasts projects, make this a timely symposium, which promises to illuminate general principals of genome evolution while providing tractable model systems that enable rigorous experimental tests.

Jason Stajich (University of California-Riverside; <http://lab.stajich.org/home/people/jason-stajich>) is the confirmed, invited speaker. We encourage abstract submission and participation from diverse backgrounds.

Important deadlines include:

- Abstract submission for oral presentations: February 8, 2015 - Early bird registration: March 1, 2015 - Abstract submission for poster presentations: March 29, 2015

Please consider attending and submitting an abstract.

Best wishes,

Chris Todd Hittinger University of Wisconsin-Madison  
cthittinger@wisc.edu

Joseph Schacherer University of Strasbourg / CNRS  
schacherer@unistra.fr

Kenneth H. Wolfe University College Dublin  
kenneth.wolfe@ucd.ie

Chris Todd Hittinger, Assistant Professor of Genetics Genome Center of Wisconsin University of Wisconsin-Madison 425-G Henry Mall, 2434 Genetics/Biotechnology Center Madison, WI 53706-1580 cthittinger@wisc.edu, (608) 890-2586 <http://hittinger.genetics.wisc.edu> cthittinger@wisc.edu

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## Vienna SMBE GeneExpressionEvol Jul12-16

Dear evoldir members,

As a part of the Annual Meeting of the Society for Molecular Biology and Evolution (SMBE), that will be held in Vienna on July 12-16 2015, we are pleased to announce a symposium on the topic "Adaptive and non-adaptive evolution of gene expression and regulation". Abstract submissions for oral presentations are open until February 8th.

Symposium summary:

Identifying the substrate of adaptive evolution is a key question in evolutionary biology. It was proposed early on that much of adaptive evolution may occur at the level of gene expression, by means of positive selection acting on the genetic variation naturally occurring at regulatory elements. Comparisons of gene expression patterns and regulatory mechanisms are now possible within and between species, allowing evolutionary biologists to reveal the genetic mechanisms of adaptations. However, non-adaptive forces are also expected to shape the genetic variation of regulatory modules and to drive the evolution of gene expression. Therefore, mechanisms such as genetic drift, biased gene conversion, variability in mutation rates have to be carefully taken into account

when reconstructing the evolutionary history of gene expression and regulation. In this symposium we propose to bring together researchers from the fields of population genetics, functional and evolutionary genomics and systems biology to discuss issues related to the functional characterization of the genetic variation within regulatory elements and the statistical inference of evolutionary forces driving the evolution of gene expression. We encourage submissions that examine adaptive and non-adaptive mechanisms underlying different aspects of gene expression evolution, including alternative splicing, non-coding RNA expression, as well as transcriptional and post-transcriptional regulation.

Invited speakers: Prof. Laurent Duret (<http://lbbe.univ-lyon1.fr/~Duret-Laurent-.html?lang=en>) and Prof. Yoav Gilad (<http://giladlab.uchicago.edu/>).

Please note that travel awards and childcare support are available to allow young scientists and parents to attend the conference. Please go to <http://smbe2015.at/> for additional information and registration.

For more details, please don't hesitate to contact us.

Stefan Laurent [stefan.laurent@epfl.ch](mailto:stefan.laurent@epfl.ch) Jeffrey Jensen [jeffrey.jensen@epfl.ch](mailto:jeffrey.jensen@epfl.ch) Anamaria Necsulea [anamaria.necsulea@epfl.ch](mailto:anamaria.necsulea@epfl.ch) Mehmet Somel [msomel@metu.edu.tr](mailto:msomel@metu.edu.tr)

- Anamaria Necsulea SNSF-Ambizione fellow Swiss Institute for Experimental Cancer Research (ISREC) Ecole Polytechnique Fédérale de Lausanne (EPFL) EPFL-SV-ISREC-UPDUB SV2842 Station 19 CH-1015 Lausanne Switzerland

Phone +41 21 693 06 05 [anamaria.necsulea@epfl.ch](mailto:anamaria.necsulea@epfl.ch)

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## Vienna SMBE GeneFlow Jul12-16

SMBE 2015 Symposium on the Consequences of Gene Flow, July 12-16, Vienna

Dear Colleagues,

I'm writing to let you know about a symposium we are organizing at this year's SMBE in Vienna on the Functional Consequences of Gene Flow. Here's the info:

Title: Exploring the consequences of ancient and contemporary gene flow

Description: One reason why species are notoriously hard to define is that gene flow often continues in the face of emerging reproductive barriers. Genomic data



has revealed that introgression is ubiquitous; in particular, ancient DNA sequencing has uncovered evidence of ancient gene flow from archaic hominins into anatomically modern humans. The distribution of introgressed alleles in modern human genomes suggests that selection has acted both to eliminate deleterious foreign material and to retain locally adaptive archaic variation related to phenotypes including keratin filament structure, adaptation to high altitude, and lipid metabolism. In addition, contemporary introgression has affected the evolutionary trajectories of many plants and animals, particularly as anthropogenic environmental alteration spurs changes in species' geographic ranges including colonization of new habitats and alteration of life history traits such as migration timing. Gene flow can be adaptive and even rescue populations threatened by inbreeding depression, but always at the risk of inducing outbreeding depression or displacing endemic genetic variation. This symposium will bring together recent work on archaic hominin admixture with studies of gene flow in other species, focusing on the fitness consequences of introgression over long and short timescales.

Confirmed speakers: Philip Hedrick, Josh Akey

Organizers: Kelley Harris, Tyler Linderoth, John A. Capra, Corinne Simonti

Important Dates: 2015 Feb 8 abstract submission for oral presentation closes 2015 March 1 early bird registration closes 2015 Mar 29 abstract submission for poster presentation closes

For submission instructions and more info see: <http://smbe2015.at/> Feel free to contact me <tony.capra@vanderbilt.edu> with any questions.

Thanks, Tony Capra

tony.capra@vanderbilt.edu

2015 abstract submission website.

A brief summary of the theme of the symposium:

Phylogenetic information and noise are central components in successful tree reconstruction as they can invariably impact tree resolution, support, and accuracy. As we attempt to resolve deeper, shorter internodes and estimate short branch lengths in the tree of life with genome-scale data sets, the magnitude of impact of these two components is accentuated considerably, as is the prevalence of conflicts among gene trees. These phylogenetic issues are greatly entangled with intrinsic gene features, e.g. gene mode and tempo of evolution, and are exacerbated by historic depth. A high rate of nucleotide substitution can obscure phylogenetic information, and sometimes yields noise at deep historic times. However, fast rates and genome-scale datasets also potentially yield much more information if modeled accurately, taxa are sufficiently sampled, and substitution rate is not so fast. Thus, our symposium will be relevant to molecular evolution, phylogenetics and genomics. Recruited speakers will address theoretical and empirical studies relating to:

- 1) assessment of suitability of genomic regions across a spectrum of nucleotide substitution rates and selection pressure to resolve phylogenetic trees;
- 2) comparison between whole genome vs. 'optimal genes' approaches;
- 3) evaluation of the effectiveness of current approaches/algorithms used in discerning sources of signal, noise and conflicts among phylogenetic trees;
- 4) fast methods and algorithms for dating and phylogenetic reconstruction of large genomic data.

Best regards, Arindam

"RoyChoudhury,  
<ar2946@cumc.columbia.edu>

Arindam"

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## Vienna SMBE GenomePhylogenies Jul12-16

Untangling information, noise, and phylogenetic reconstruction in genome scale data: A Symposium in SMBE 2015 at Vienna.

Abstracts for oral presentations are being sought for a phylogenetics symposium titled "Untangling information, noise, and phylogenetic reconstruction in genome scale data", a part of SMBE 2015 (July 12-16) at Vienna, Austria. Abstracts are due Feb 8, 2015 at SMBE

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## Vienna SMBE GenomePhylogenies Jul12-16 2

Dear Colleagues,

Abstracts for oral presentations are being sought for a phylogenetics symposium titled "Untangling information, noise, and phylogenetic reconstruction in genome scale data", a part of SMBE 2015 (July 12-16) in Vienna, Austria. Abstracts are due Feb 8, 2015 at the SMBE 2015 submission website (<http://smbe2015.univie.ac.at/>-

)

Invited Speakers: Tandy Warnow (University of Illinois, Champaign-Urbana) Olivier Gascuel, Le Laboratoire d'Informatique, de Robotique et de Microelectronique de Montpellier, France

Organizers: Khidir Hilu, Virginia Tech (hilukw@vt.edu) Jeffery Townsend, Yale University (jeffrey.townsend@yale.edu) Arindam RoyChoudhury, Columbia University (ar2946@cumc.columbia.edu)

A brief summary of the symposium theme:

Phylogenetic information and noise are central components in successful tree reconstruction as they can invariably impact tree resolution, support, and accuracy. As we attempt to resolve deeper, shorter internodes and estimate short branch lengths in the tree of life with genome-scale data sets, the magnitude of impact of these two components is accentuated considerably, as is the prevalence of conflicts among gene trees. These phylogenetic issues are greatly entangled with intrinsic gene features, e.g. gene mode and tempo of evolution, and are exacerbated by historic depth. A high rate of nucleotide substitution can obscure phylogenetic information, and sometimes yields noise at deep historic times. However, fast rates and genome-scale datasets also potentially yield much more information if modeled accurately, taxa are sufficiently sampled, and substitution rate is not so fast. Thus, our symposium will be relevant to molecular evolution, phylogenetics and genomics. Recruited speakers will address theoretical and empirical studies relating to:

- 1) assessment of suitability of genomic regions across a spectrum of nucleotide substitution rates and selection pressure to resolve phylogenetic trees;
- 2) comparison between whole genome vs. optimal genes± approaches;
- 3) evaluation of the effectiveness of current approaches/algorithms used in discerning sources of signal, noise and conflicts among phylogenetic trees;
- 4) fast methods and algorithms for dating and phylogenetic reconstruction of large genomic data.

Best regards,

Arindam RoyChoudhury

“RoyChoudhury,

<ar2946@cumc.columbia.edu>

Arindam”

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## Vienna SMBE GenomicsofSexBias Jul12-16

Dear Colleagues,

We would like to invite you to register to present in the upcoming symposium titled “Genomics of sex bias: Addressing questions with or without genomes”. Our symposium will be a part of the 2015 Society for Molecular Biology and Evolution Meeting (<http://smbe2015.at/>). The meeting will be held in the Hofburg Palace in Vienna, Austria. More details about the destination can be found here: <http://smbe2015.univie.ac.at/destination/>

The deadline for registration is Feb. 8, 2015. You may find registration information and a link to the registration portal here: <http://smbe2015.univie.ac.at/-registration/> We have confirmed the following speakers:

Dr. Deborah Charlesworth: “The molecular evolution of plant sex chromosomes” Dr. Jennifer A.M. Graves: “Evolution of vertebrate sex chromosomes and dosage compensation” Dr. Sevinc Ercan: “Comparative analysis of X chromosome expression in nematodes” Dr. Beatriz Vicoso: “Using the surprising diversity of fly sex chromosomes to systematically test evolutionary hypotheses”

The following is a description of the symposium.

Next-generation sequencing technology permits the study molecular evolution of sex chromosomes even in the absence of reference genomes. Longstanding questions are now amenable to systematic large-scale study, including the analysis of gene movements between the sex chromosomes and autosomes, Y chromosome degeneration, and transcriptome analyses of sex-linked genes, including changes in the expression pattern of the X compared to the Y, as well as stage dependent expression of sex-linked genes (e.g. meiotic sex chromosome inactivation).

Comparative genomics studies highlight divergent and convergent patterns of sex chromosome evolution in a range of taxa (e.g., XY versus ZW systems, as well as between vertebrates, invertebrates and plants), with new sequencing technologies expediting the investigation of non-model organisms. Such studies highlight substantial and functionally important variation, and provide insights into the evolutionary mechanisms that drive sex chromosome evolution. This symposium highlights the ability of technology to allow investigation of previously

unattainable questions in sex-biased molecular biology and evolution.

We look forward to seeing you in Vienna!

Sincerely,

Melissa A. Wilson Sayres, PhD Assistant Professor of Genomics, Evolution, and Bioinformatics The Biodesign Institute Arizona State University

J.J. Emerson, PhD Assistant Professor, Department of Ecology & Evolutionary Biology Center for Complex Biological Systems University of California Irvine

melissa.wilsonsayres@asu.edu

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**Vienna SMBE GoldenAgeArchaea  
Jul12-16**

Dear colleagues,

We are pleased to invite you to submit an abstract to a symposium titled “The Golden age of Archaea: unveiling the diversity and evolution of the third Domain of Life” which will be hosted at the 2015 Meeting of the Society for Molecular Biology and Evolution (SMBE) in July 12-16, Vienna, Austria.

Our confirmed invited speakers are Graeme Nicol (University of Aberdeen, UK) and Manolo Gouy (CNRS, France)

Please note that the deadline of abstract submission for oral presentation is February 8th.

You can submit your abstract here:

<http://smbe2015.univie.ac.at/Abstract.Submission>

Symposium description:

Since their discovery nearly 40 years ago, the Archaea have not stopped being one of the major challenges of Evolutionary Biology. From a cell biology and genomic point of view they represent chimeras of prokaryotic and eukaryotic features, which places them in a key position in the Tree of Life. They thrive in a wide variety of contrasted environments, from deep oceans to the human gut, and have occupied key roles in the setup of major biogeochemical cycles of the early Earth. The development of culture-independent genomics techniques is providing access to an ever-larger and so far inaccessible fraction of archaeal diversity. This leads to a number of exciting discoveries that are revolutionizing our vision of archaeal evolution, generating novel challenges to dissect the nature of the last common archaeal ancestor and the

evolutionary trajectories that shaped this domain of life. The archaeal tree is being rapidly filled up with new branches constituting entire phyla and orders with novel characteristics. Genomic data has highlighted the existence of additional eukaryotic-like characters previously unsuspected in the archaea and re-launched the issue of their role in eukaryogenesis. A symposium specifically focused the diversity and evolution of the Archaea will be a timely occasion to present these exciting new data for this major prokaryotic domain, still widely unknown by the large audience.

Looking forward to seeing you in Vienna this summer!

Simonetta Gribaldo Institut Pasteur (Paris, France) [simonetta.gribaldo@pasteur.fr](mailto:simonetta.gribaldo@pasteur.fr)

and

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**Vienna SMBE  
HorizontalMicrobialEvolution  
Jul12-16**

SMBE 2015: SYMPOSIUM ON THE HORIZONTAL COMPONENT OF MICROBIAL EVOLUTION

INVITED SPEAKERS: Bill Martin (University of Düsseldorf, Germany) Uri Gophna (Tel-Aviv University, Israel)

Dear Colleagues,

We are pleased to invite you to attend our symposium on the horizontal component of microbial evolution to be held during the annual conference of the society for molecular biology and evolution (SMBE) in Vienna, July 12th-16th 2015.

\* Symposium description: Microbes are found everywhere: in clouds and rain drops, on tree leaves, in soil and oceans, on and in our body. Bacteria are interesting research subjects not only due to their impact on human health dynamics and ecological transitions but also because of their genetic characteristics. Unlike eukaryotes, their evolution comprises both vertical and horizontal components. Recombination at the species level plays a role in selective sweeps through the population, while inter-species lateral gene transfer has important implications to microbial adaptation and evo-

lutionary transitions. The advance in high throughput sequencing methods has enabled to study the impact the horizontal component on microbial genome evolution at an unprecedented resolution. Research in this field covers a broad range of topics including the biology of DNA transfer mechanisms, the ecology of mobile genetic elements, experimental evolution of rapid adaptation, and phylogenetics of reticulation events. We aim to include speakers presenting recent advance in the study of microbial evolution by horizontal gene transfer including both computational and experimental approaches.

SMBE 2015 website: <http://smbe2015.univie.ac.at/> \* The abstract submission deadline for oral presentations is February 8, 2015.

\* Abstracts for poster presentations should be sent by March 29, 2015.

\* Early bird registration fees are charged until March 1, 2015.

Looking forward to meeting you in Vienna this summer!

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Peter Gogarten University of Connecticut, USA [gogarten@uconn.edu](mailto:gogarten@uconn.edu)

\* For a summary of the recent SMBE satellite meeting on microbial reticulated evolution read the report in GBE (2014) 6:2206.

[tdagan@ifam.uni-kiel.de](mailto:tdagan@ifam.uni-kiel.de)

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## Vienna SMBE Jul12-16

Dear evoldir community,

Join us in one of the most beautiful cities at the spectacular Imperial Palace (Hofburg) in the heart of Vienna!

Submit your abstract by February 8 to be considered for oral presentations at one of the following exciting symposia:

- Adaptive and non-adaptive evolution of gene expression and regulation.
- Ancient genomes: A time machine for investigating natural selection.
- Beyond the Equilibrium Paradigm: The role of temporal processes in population genetics and evolution.
- Cancer as a Darwinian process.
- Evolution and ecology of microbial communities.
- Evolution of molecular pathways and networks: Molecular evolution meets systems biology.
- Exploring the consequences of ancient and contemporary

- gene flow.
- Fungal evolutionary genomics: Unravelling mysteries from the Forgotten Kingdom.
- Genomic and epigenomic evolution of sex chromosomes: Broad patterns and intriguing cases.
- Genomics of sex bias: Addressing questions with or without genomes.
- Inference of demography and selection under violations of the Kingman coalescent assumptions.
- Inferring fitness landscapes from experimental evolution.
- Micro-evo-devo: using natural variation to explain the how and why of phenotypic evolution.
- Novel functional approaches to evolutionary genomics.
- Open Symposium.
- Origins and evolution of molecular innovation.
- PopGen in space! Theory and inference in spatial population genetics.
- Population genomics of rapid adaptation.
- Reframing the demography vs. selection debate using 21st century models and data.
- Short tandem repeats in the post-genomics age: Accurate typing, variability, evolution, and function.
- Speciation genomics.
- The biological impact of transposable elements.
- The evolution of alternative splicing.
- The golden age of Archaea: unveiling the diversity and evolution of the third Domain of Life.
- The horizontal component of microbial evolution.
- The origins of multicellularity under the light of functional genomics.
- Untangling information, noise, and phylogenetic reconstruction in genome scale data.
- Within- and between-host viral evolution.

A few meeting highlights:

- All posters will be on display throughout the entire meeting.

- 27 symposia on cutting edge topics suggested by SMBE members and one Open Symposium for which 5 featured speakers will be selected though 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)

Early bird registration by March 1 will also benefit from up to 30% reduced registration fee and full consideration of submitted abstracts.

All details about registration, accommodation options

and travel discounts are available at the conference website: [www.smb2015.at](http://www.smb2015.at) The Local Organising Committee is looking forward to welcome you to Vienna next summer!

julia.hosp@gmail.com

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## Vienna SMBE MicroEvoDevo Jul12-16

SMBE SYMPOSIUM ON MICRO-EVO-DEVO - VIENNA JULY 12-16TH 2015.

Title: 'Micro-evo-devo: using natural variation to explain the how and why of phenotypic evolution'

Invited Speaker: Marie Anne-Felix (Institute of Biology of the Ecole Normale Supérieure, Paris)

Dear colleagues,

we would like to welcome you to submit your abstract to our symposium on Micro- Evo- Devo.

Micro-evo-devo synthesises population genetics and evolutionary developmental biology to take advantage of natural variation to explain the genetic and developmental bases, and fitness consequence of phenotypic change, as well as the evolutionary forces that have shaped it. Therefore, this symposium will highlight how the integrative framework of micro-evo-devo has great potential to explain how and why phenotypic diversity among populations has evolved. This symposium will provide a platform for the most recent advances using established models and attract researchers using recent advances in sequencing and genome editing technologies to investigate phenotypic evolution in emerging models. We expect that our proposed symposium will serve to consolidate this growing community and help the field to realise its full potential to enhance our understanding of the evolution of biological diversity.

Registration and abstract submission deadline is Feb 8, 2015 (<http://smb2015.univie.ac.at/registration/-registration-portal/>).

Please feel free to contact us directly in case you have any question.

Looking forward to seeing you in Vienna!

Luisa Pallares ([pallares@evolbio.mpg.de](mailto:pallares@evolbio.mpg.de)) Daniela Nunes ([msantos-nunes@brookes.ac.uk](mailto:msantos-nunes@brookes.ac.uk)) Alistair McGregor ([amcgregor@brookes.ac.uk](mailto:amcgregor@brookes.ac.uk))

Daniela Santos Nunes <[msantos-nunes@brookes.ac.uk](mailto:msantos-nunes@brookes.ac.uk)>

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## Vienna SMBE MolecularInnovation Jul12-16

Dear colleagues, it is our pleasure to invite you to submit abstracts to our symposium about **\*\*Origins and Evolution of Molecular Innovation\*\*** !

Our guest invited speaker is Prof. M. Mar Albà from the UPF in Barcelona.

This symposium will be a part of the 2015 Society for Molecular Biology and Evolution Meeting (<http://smb2015.at/>). The meeting will be held in the Hofburg Palace in Vienna, Austria. More details about the destination can be found here: <http://smb2015.univie.ac.at/destination/> The deadline for registration is Feb. 8, 2015. You may find registration information and a link to the registration portal here: <http://smb2015.univie.ac.at/registration/> Symposium description: Generally, the field of molecular evolution is dominated by studies of descent with accumulation of slight modifications. However, larger changes are also possible, in which entirely new molecular features originate for the first time.

We will consider rapid or spontaneous molecular innovations of diverse kinds (structures, functions, interactions, networks), with a preference for the most dramatic leaps between the absence and the presence of the molecular traits or features in question.

Timely examples of great interest in the community include (i) de novo emergence of new genes, protein domains, regulatory regions and (ii) neo-functionalization, e.g. via the acquisition of new and adaptive binding activities.

The symposium will not only address well-documented examples of spontaneous emergence of novel molecular traits, but also cover findings relevant to the processes of innovation and its aftermath. These include (but are not limited to) the roles of promiscuity (e.g. in the emergence of novel enzymatic functions) and stochasticity across different organization levels.

We look forward to seeing you in Vienna!

Joanna Masel ([masel@u.arizona.edu](mailto:masel@u.arizona.edu)) Rafik Neme ([rneme@evolbio.mpg.de](mailto:rneme@evolbio.mpg.de)) Erich Bornberg-Bauer ([ebb@wwu.de](mailto:ebb@wwu.de))

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## Vienna SMBE NetworkEvolution Jul12-16

SMBE 2015 Symposium on Evolution of Molecular Pathways and Networks, July 12-16, Vienna

We are pleased to invite you to participate in the symposium “Evolution of molecular pathways and networks: Molecular evolution meets systems biology”, which will take place at the annual meeting of the Society for Molecular Biology and Evolution (Vienna, July 12-16, 2015; <http://smbe2015.at/>).

Symposium summary: Proteins rarely work in isolation. On the contrary, they often operate as pieces of complex systems, including cells and organisms. As such, their function is mediated, and/or regulated, through interactions with other proteins. The complexity of intermolecular interactions within a cell can be represented in the form of various networks (including protein-protein interaction networks, metabolic networks, signaling networks, genetic networks, and transcriptional regulatory networks). In the last years, draft versions of such large-scale maps have started to become available, allowing a systems-level exploration of the cell. Understanding how proteins operate and evolve as a system is not only an exciting endeavor, but also one that can aid applications such as drug discovery and metabolic engineering. From the point of view of molecular evolution, understanding proteins’ patterns of evolution may benefit from considering their position in the networks of which they are part. For instance, it is known that proteins acting at the center of molecular networks (i.e., those that interact with many other proteins) are more selectively constrained (and thus more evolutionarily conserved) than those acting at the periphery. In this symposium we will explore how networks of interacting proteins have generated (grown) over evolutionary time, how a network approach can help understand gene’s patterns of evolution, and, in general, how networks evolve at the systems level.

Invited speakers: - Prof. David Robertson, Manchester University. - Dr. Ryan Gutenkunst, University of Arizona.

Important deadlines: - Early bird registration: March 1, 2015 - Abstract submission for oral presentations: February 8, 2015 - Abstract submission for poster presentations: March 29, 2015

We are looking forward to seeing you in Vienna!

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## Vienna SMBE RapidAdaptation Jul12-16

Dear Colleagues,

We are writing to announce our symposium on “Population genomics of rapid adaptation”, which will be held as part of the Society for Molecular Biology and Evolution (SMBE) meeting, July 12-16 in Vienna, Austria. Applications to give a talk as part of this symposium will be accepted through February 8; for details concerning how to submit an abstract, see the conference website (<http://smbe2015.at/>).

Symposium description:

One of the most puzzling observations in evolutionary biology is that organisms can often adapt surprisingly quickly to environmental challenges. Classical examples of such rapid adaptations include the domestication of plants and animals and the evolution of pesticide or drug resistance. It is now becoming increasingly clear that the potential for rapid adaptation is a ubiquitous feature of evolution across a wide spectrum of systems, ranging from experimental evolution in microbes, to the progression of cancer cells in the human body, to the rapid responses of species under climate change. The growing number of systems where rapid adaptations are directly observable presents us with the fascinating opportunity to study evolution in real time and to make progress in understanding what limits the rate of evolution and determines its likely outcome. In this symposium, we will focus on (i) novel approaches to detect and study rapid adaptation using population genomic data, (ii) case studies of rapid adaptation in natural populations, and (iii) experimental studies of rapid adaptation in model systems. Although rapid adaptation has long been associated primarily with the

evolution of polygenic traits that can adapt quickly by using standing genetic variation, we will also highlight recent work showing that adaptation at times can be rapid despite relying on de novo mutations.

Invited speakers: Graham Coop and Sasha Levy

Please do not hesitate to contact us with any questions.

We hope to see you this summer!

Philipp Messer (messer@cornell.edu) and Dmitri Petrov (dpetrov@stanford.edu)

Philipp W. Messer Assistant Professor Department of Biological Statistics and Computational Biology Cornell University 102J Weill Hall, Ithaca, NY 14853  
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Philipp Messer <philipp.messer@gmail.com>

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## Vienna SMBE SexChromosomeEvolution Jul12-16

SMBE 2015 Symposium on Sex Chromosome Evolution, July 12-16, Vienna <http://smbe2015.univie.ac.at/-registration/> Dear Colleagues:

We are pleased to invite you to attend a symposium on sex chromosome evolution titled 'Genomic and Epigenomic Evolution of Sex Chromosomes: Broad Patterns and Intriguing Cases', to be held on the SMBE conference of 2015 in Vienna on July 12th-16th. The intention of this symposium, is trying to bring together diverse types of research (for example, broad genomic analyses vs. experimental case studies) across different organisms with interesting sex chromosome systems, and hope to spark new ideas or discussions on the next important questions to be addressed in this exciting field of evolutionary biology. We really look forward to see your excellent work on various topics of sex chromosome evolution including recombination suppression between sex chromosomes, sex-determination evolution, sex-linked chromatin evolution, dosage compensation and so on.

Our confirmed invited speaker is Professor Ray Ming at University of Illinois at Urbana-Champaign. And there is a chance that the conference committee would allocate another featured speaker slot given the number of abstract submissions that we have received. Please note Feb. 8th is the deadline of the abstract submission for oral submission. After you register for the conference, you could submit the abstract here: [http://smbe2015.univie.ac.at/Abstract\\_Submission](http://smbe2015.univie.ac.at/Abstract_Submission) We look

forward to meet you in the Hofburg Palace of Vienna this summer!

Dr. Qi Zhou University of California, Berkeley  
zhouqi@berkeley.edu

Dr. John Wang Biodiversity Research Center, Academia Sinica johnwang@gate.sinica.edu.tw

Zhou Qi <zhouqi@berkeley.edu>

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## Vienna SMBE-Spatial-Population-Genetics Jul12-16

SMBE SYMPOSIUM ON SPATIAL POPULATION GENETICS - VIENNA

JULY 12-16TH 2015

Dear colleagues,

We are pleased to invite you to submit abstracts for a symposium at the SMBE 2015 meeting entitled: 'Pop-Gen in space! Theory and inference in spatial population genetics.'

Spatial processes are a key component of evolution as they play a crucial role in determining patterns of genetic variation within a species. The importance of spatial processes has been clear since the earliest days of evolutionary genetics and has continued to be an area of intense interest because of the potential to shed light on the history of populations, the nature of adaptive evolution, and speciation. Recently there have been multiple advances in theoretical models and statistical methodology that are transforming our ability to study spatial population genomics, and large datasets are making many new analyses possible. The purpose of our symposium is to provide a forum for a presentation of recent advances, as well as future challenges and prospects for spatial population genetics. Our confirmed headline speakers are Laurent Excoffier (Bern) and Nick Barton (IST Austria).

We encourage abstract submissions from any researchers in this area, particularly students and postdocs, and we aim to present an excellent set of talks from a diverse background of speakers. \*The DEADLINE for abstract submission is: February 8, 2015. \* Check submission details on SMBE's annual meeting webpage <http://smbe2015.at/> . Please feel free to contact us with any questions.

John Novembre (jnovembre@uchicago.edu)  
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## Vienna SMBE SpeciationGenomics Jul12-16

SMBE Speciation genomics - Vienna, July 12-16th 2015

Dear colleagues

We would like to invite you to join a symposium on Speciation genomics at the next SMBE meeting in Vienna. PLEASE NOTE: Abstracts for oral presentations can still be submitted until 8th of February. Deadline for abstracts for poster presentations 29th March.

Speciation is a fundamental evolutionary process: this process involves every living organism and its rates mirror atmospheric and geological changes on Earth, but its mechanisms are still largely a mystery. Usually, speciation is defined by mating barriers, which can arise either slowly, due to growing divergence between geographically or ecologically separated groups, or immediately, due to ploidy change.

Speciation research covers a broad array of scientific fields, starting from molecular and cellular biology to evolutionary biology. A rapidly growing amount of assembled genomes and transcriptomes make possible to study speciation in much more detail than before. Looking at patterns of genomic divergence, identifying footprints of selection, or mapping genes that are involved in reproductive isolation are just a few of the powerful genomic approaches that recently become available to study speciation. Today it is not rare that speciation research pushes the existing knowledge to frontiers of technologies and advanced algorithms.

This symposium will welcome research in model and non-model species integrating emerging themes and novel approaches, together with a reassessment of more traditional methodologies in order to understand why and how organisms diversify.

The invited speakers that will open the symposium are Luca Comai (UC Davis) and Christian Lexer (University of Fribourg). We encourage submissions from researchers active in this area working on any system. Students and postdocs are particularly welcome. Check submission details on the SMBE 2015 webpage <http://smbe2015.at/> Please contact us with any questions.

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## Vienna SMBE ViolationsKingmanCoalescent Jul12-16

SMBE 2015: Symposium on “Inference of demography and selection under violations of the Kingman coalescent assumptions”

Dear Colleagues, We are pleased to invite you to attend our symposium on Inference of demography and selection under violations of the Kingman coalescent assumptions to be held during the annual conference of the society for molecular biology and evolution (SMBE) in Vienna, July 12th-16th 2015.

\* Symposium description: Most of the population genetics theory and statistical tests for selection in genomic data have been developed following the Kingman’s coalescent model. However, these theoretical premises rely on biological and life-history assumptions which are often violated in many prokaryote, fungal, animal or plant species. In this symposium we highlight recent developments in population genetics theory taking into account previously ignored pervasive ecological and biological characteristics such as the skew in offspring production, fast adapting microparasites (virus, bacteria and fungi), long term resting stages or dormancy, and life cycles with alternating sexual and asexual cycles. We welcome theoretical and empirical studies investigating how these new assumptions affect nucleotide polymorphism, and the inference of adaptation and speciation processes compared to the Kingman model. We focus specifically on pioneering applications in 1) Darwinian medicine to understand the evolution of parasites, 2) disease management in agriculture to predict pathogen response to selective pressures, 3) the management of marine genetic resources to deploy sustainable fisheries, 4) the control of emergent diseases, and 5) the genomics of crop and animal domestication.\*\*

\* Invited speaker: Francois BALLOUX (University College London, UK) [www.ucl.ac.uk/ugi/research/francoisballoux](http://www.ucl.ac.uk/ugi/research/francoisballoux) SMBE 2015 website: <http://smbe2015.univie.ac.at/> \* The abstract submission deadline for oral presentations is February 8, 2015.



\* Abstracts for poster presentations should be sent by March 29, 2015.

\* Early bird registration fees are charged until March 1, 2015.

Looking forward to meeting you in Vienna this summer!

Do not hesitate to contact us with any questions.

Symposium organizers:

Tatiana GIRAUD University of Orsay - Paris, France  
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**WesternConnecticutStateU EvolBiol  
Apr18**

Dear Friends,

Western Connecticut State University is proud to announce that it will host the 2015 Sigma Xi Northeastern Regional Research Conference on Saturday, April 18th. This conference provides valuable opportunity for undergraduate and graduate students to showcase their research/scholarly work. We anticipate student and faculty participation from universities and community colleges throughout the New England states, New Jersey and New York. The conference is run in the same manner as a professional science conference. Student posters will be judged and each will be eligible to win

the Sigma Xi Award. Participation also promotes student interaction with peers from other institutions, as well as interaction with faculty mentors from other universities, and scientists and engineers from the private sector. The event will support a life sciences competition which includes evolutionary biology. Projects focusing on evolution education can contribute to the science education panel. Additionally, one of the key note talks is exclusively devoted to the analysis of evolutionary processes. \*Kent Holsinger, Ph.D., Distinguished Professor, Department of Ecology and Evolutionary Biology, University of Connecticut - "People, proteas, and evolutionary process: Whats math got to do with it?"

The web site for the conference is now open. <http://www.wcsu.edu/sigma-xi/> Please contact me if you have questions.

Thank you,

Theodora Pinou

Professor of Biology and Event Chair

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Theodora Pinou <[PinouT@wcsu.edu](mailto:PinouT@wcsu.edu)>

AarhusU NutritionalAdaptation	34	UCalgary AdaptationGenomics	49
CharlesU NightingaleSpeciation	35	UEastAnglia SexualSelectionNetworks	50
CharlesU Prague LepidopteraPollinationCameroon	36	UGlasgow EngineeringAdaptation	50
DeakinU MultivariateEvolution	36	UGreifswald 12 Adaptation	51
DurhamU EvolutionBiol	37	UHamburg BehaviouralEvolution	52
EastCarolinaU EvolutinaryBiol	38	UHelsinki EvolutionStressTolerance	52
GhentU Bioinformatics	39	UHull 3 Biodiversity	53
GhentU Bioinformatics PlantRegulatoryGenomics	39	UIdaho CoevolutionBiol	54
HeidelbergU 6 EvolutionaryAdaptation	40	UJerusalem Evolution microRNAs	54
ImperialCollege London BeeAdaptation	40	ULEeds 2 Genomics	55
ImperialCollege London HumanEvolGenetics	41	ULEicester HumanSTRDiversity	55
KansasStateU FishAdaptation	42	ULiverpool HostParasiteEvol	55
Leicester GenomicImprinting 2	42	UPotsdam Evolutionary Biology	56
McGillU PlantEvolution	43	UppsalaU 2 AmphibianEvolution	57
NewcastleU EvolutionaryGenetics	43	UppsalaU 2 AmphibianEvolution 2	57
NorthCarolinaStateU EvolGenetics	44	USalford Coevolution	58
OklahomaStateU GrassTilleringGenetics	44	USheffield AvianGenomics	59
SoutheasternLouisianaU PlantSystematics	44	USouthampton NHM London PlantAdaptation	59
StockholmU EvolutionaryGenetics	46	UToledo FishEvolution	60
SwanseaU MicrobialGenomics	47	UTurkuFinland SalmonPopDynamics	60
TowsonU AntSystematics	47	WesternWashingtonU EvolutionaryBiol	61
TrentU AmphibianPopGenetics	48		
UBerne HumanGenomics	48		

## AarhusU NutritionalAdaptation

Nutritional stress and thermal adaptation Applications are invited for a PhD fellowship/scholarship at Graduate School of Science and Technology, Aarhus University, Denmark, within the Bioscience programme. The position is available from 1 May 2015 or later.

Title: Nutritional stress and thermal adaptation

Research area and project description: Evolutionary genetics, ecophysiology and molecular biology. The PhD student should study effects of variable nutritional regimes and interactions between nutrition, temperature and genotype on stress resistance and life history traits using *Drosophila* as a model organism. It is intended to use rearing and test conditions that are ecological relevant making the studies of strong interest from ecological and evolutionary perspectives. Relevant molecular work should complement organismal phenotypic analyses, possibly followed up by the application of relevant “omics” techniques. The work will be done under the supervision of Prof. Volker Loeschcke (AU) in collaboration with Prof. MSO Torsten N. Kristensen from Aalborg University and in interaction with PhD students/post-docs Mads F. Schou and Tommaso Manenti and supported

by grants from the Danish Natural Research Council (the project will be funded by grants of Natural Science Research Council to Volker Loeschcke (2/3) and Torsten Nygaard Kristensen (1/3).

Qualifications and specific competences: A Master’s degree in Bioscience, Biotechnology or similar or a bachelor’s degree in a relevant subject are possible backgrounds. A strong interest in experimental as well as analytical work is required, and experience with the model organism *Drosophila* is an advantage.

Place of Employment and Place of Work: The place of employment is Department of Bioscience, Aarhus University, Denmark, and the place of work is the section for Genetics, Ecology and Evolution, Ny Munkegade 114-116, 8000 Aarhus C, or for part of the time at Department of Biotechnology, Chemistry and Environmental Engineering, Section of Biology and Environmental Science, Aalborg University, Fredrik Bajers Vej 7H, DK-9220 Aalborg East, Denmark

Contacts: Applicants seeking further information are invited to visit <http://talent.au.dk/phd/-scienceandtechnology/opencalls/specific-projects/-nutritional-stress-and-thermal-adaptation/> or contact: Volker Loeschcke, phone: +45 2899 2368, e-mail: volker@bios.au.dk, or Torsten Nygaard Kristensen, phone: +45 61463375, email: tnk@bio.aau.dk, for further information about the position.

Torsten Nygård Kristensen <tnk@bio.aau.dk>

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## CharlesU NightingaleSpeciation

Two PhD positions on nightingale speciation available from October 2015!

(<http://web.natur.cuni.cz/~radkas/index.php?page==opportunities>)

We are looking for motivated PhD students for the following projects:

### 1. Genomics of reproductive isolation in nightingales

Understanding the mechanisms of speciation is a major goal of evolutionary biology. Population genomics becomes an increasingly important tool for this research field and allows to investigate mechanisms and genetic basis of species formation even in non-model organisms that are not amenable to classical laboratory crosses. The aim of this PhD project is to elucidate the genetic architecture of reproductive isolation between two closely related song bird species, the Common Nightingale (*Luscinia megarhynchos*) and the Thrush Nightingale (*L. luscinia*). Using novel genotyping approaches based on next generation sequencing and previously developed species-specific SNP markers, the student will genotype several hundreds of DNA samples from naturally occurring hybrid populations between the two nightingale species, already collected during our previous research. The obtained data will allow us to investigate genome-wide patterns of interspecific gene flow and identify genomic regions responsible for nightingale speciation. Furthermore, we will use admixture mapping to examine genetic basis of several traits that are likely to contribute to prezygotic as well as postzygotic reproductive isolation in nightingales. Combination of admixture mapping with genome-wide patterns of introgression will enable us to infer the importance of different reproductive barriers in nightingale speciation. The student will be mainly responsible for the laboratory part of the project. We expect a motivated student interested in population genetics and evolutionary biology with at least basic training in molecular genetic techniques.

### 2. Interspecific competition and ecological differentiation in nightingales

Ecological character displacement, i.e. morphological divergence of species caused by interspecific competition, is an important process contributing to the origin of biological diversity. In hybridizing taxa, it can facilitate

the process of speciation by adding an additional degree of reproductive isolation between incipient species. In our previous study, we revealed that secondary contact between two closely related nightingale species, the Common Nightingale (*Luscinia megarhynchos*) and the Thrush Nightingale (*L. luscinia*), resulted in divergence in the beak size in sympatry suggesting partitioning of food resources between species. Such divergence should be maintained by strong selection not to be erased by interspecific gene flow. At the same time, local composition of nightingale food remains unknown. To better understand selective forces responsible for the morphological divergence in beak size, the PhD student should perform a detail survey of food supply and habitat composition in territories of both species in sympatry and allopatry. Moreover, we will study nightingale diet directly using neck collars and emetics on trapped birds, together with blood sampling and taking morphological measurements. Combination of morphological and ecological data with simultaneously gathered genomic data will allow us to examine genetic basis of bill size divergence and to infer the importance of bill size divergence in reproductive isolation. We are looking for a motivated student with good experience in field ornithology, able (after some training) to work independently in harsh field conditions.

Eligibility: Candidates must have finished the MSc. (or equivalent) by September 2015 at the latest.

Time and place: Student will work in a young multidisciplinary team based at the Faculty of Science, Charles University in Prague, Czech Republic. Fieldwork will be conducted in Poland. The position is available for up to four years, starting in October 2015.

Supervisor: Radka Reifová (Department of Zoology, Charles University, Prague) Co-supervisor: Jiří Reif (Institute for Environmental Studies, Charles University, Prague)

Salary: The PhD candidate's net monthly income will start at 11.500 CZK (ca 410 EUR) in the first year, and may progressively increase with experience and achievements during the study. (Note that living expenses in the Czech Republic are generally lower than in Western European countries.)

Funding: Projects will be funded by grant of the Grant Agency of the Czech Republic (Evolution of reproductive isolation in two songbird species, the Common Nightingale and the Thrush Nightingale: genomic and ecological perspective) awarded to the supervisor.

How to apply: If interested, please, send a CV, motivation letter and contact details of 2-3 senior scientists that can provide references on you in a single PDF



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>

## CharlesU Prague LepidopteraPollinationCameroon

A Ph.D. studentship

\*Butterflies and moths as pollinators along an Afrotropical altitudinal gradient\*

We are seeking a highly motivated Ph.D. student to join a project assessing studies of plant-pollinator relationships between butterflies and moths (Lepidoptera) with selected groups of flowering plants (Rubiaceae and Acanthaceae) on Mt. Cameroon. The student will process already collected material, as well as actively participate on field sampling (at least two times during the study) of data and their subsequent processing in collaboration with international specialists. The length of the study is 4 years.

The successful applicant will be supervised by Dr. Robert Tropek and Dr. Stepan Janecek as a part of the multidisciplinary team at the Faculty of Science, Charles University of Prague with a close collaboration with the Institute of Entomology and Institute of Botany, Czech Academy of Sciences.

\*Offered\*

- attractive scientific topic in an established international team
- standard university scholarship (up to 114,000 CZK annually according to discharging of the study responsibilities) together with the support of the STARS project (120,000 CZK annually; <http://www.stars-natur.cz>) for four years, it sufficiently covers living expenses in the Czech Republic

\*Required\*

- enthusiasm in nature and ecological science
- ability to lead a field research in challenging conditions of tropical environments
- fluency in English
- a MSc degree in biology or related fields

Desirable (but not necessary)

- previous experience of collaboration in scientific projects evidenced by a (co)authorship of research papers or conference contributions

- previous experience with insects and/or plants

- basic knowledge of French

All applicants will apply for the position online through <http://www.stars-natur.cz/>. The deadline for application is the 28th February 2015, the successful candidate will be selected till early April. The position is available from the beginning of 2015/2016 academic year.

All questions should be sent directly to Robert Tropek ([robert.tropek@gmail.com](mailto:robert.tropek@gmail.com)).

Robert Tropek <[robert.tropek@gmail.com](mailto:robert.tropek@gmail.com)>

## DeakinU MultivariateEvolution

Ph.D. Scholarship in Multivariate Evolution: Experimental evolution of multiple trait interactions under changed environments

I have a Ph.D. scholarship available for a first class student starting in 2015 or 2016 at the Waurn Ponds (Centre for Integrative Ecology) campus of Deakin University, Australia. The research takes advantage of my long term experimental evolution project which investigates multivariate evolution of male colour pattern components, female colour preferences and colour vision in 12 guppy mesocosms under three different light environments.

General topic: Quantitative genetics of experimental evolution of colour patterns and behaviour in guppies and its relationship to trait functions and functional interactions.

General aims: To examine the pattern, processes and causes of evolution of the G-matrix (genetic variance-covariance matrix) of multiple colour pattern components and their links to mate choice behaviour in populations which are actively evolving under different visual conditions. We are explicitly interested in the pattern and process of multivariate evolution under divergent environmental conditions. Questions include: What are the effects of correlational selection on the G-matrix? Does the form of the G-matrix influence multivariate evolution in the predicted ways? You can also investigate the causes of correlational selection, for example: Does correlational selection of colour pattern components result from their interacting effects on chromatic

and luminance contrast and hence on their efficacy as visual signals? There are a lot of different possible avenues of research so long as they investigate the patterns and process of multivariate evolution; I encourage all my students to follow the lines most interesting to them provided it is practical in the 3 years of research. If you are interested in any aspect of this, please email me (John A. Endler): [John.Endler@deakin.edu.au](mailto:John.Endler@deakin.edu.au)

Eligibility requirements: In addition to the general PhD requirements at Deakin (see the website <http://www.deakin.edu.au/students/research-degrees-doctoral-and-masters>) you will need some experience with quantitative genetics techniques and some multivariate statistics. Experience with MATLAB or R analysis is particularly welcome. First preference will be given to Australian citizens or permanent residents (the rules here) but if no appropriate candidates apply, I will give the fellowship to the best non-Australian who applies. You should be able to provide a very strong undergraduate record and letters of recommendation. Unlike other Australian scholarships, I do not expect you to have published any papers, in fact I'm highly suspicious of publication of work done as an undergraduate. However, you should definitely show your merit in your undergraduate record and letters of recommendation. These documents should also show that you are creative, original, innovative, and analytic rather than just a technician or a paper mill.

Stipend: Standard APA rate (AU \$25,849 in 2015) with standard conditions in regards to extensions and other allowances.

Dates and details: The closing date for applications is 1 July 2015; and the successful applicant should start no later than February or March 2016, sooner if possible. For more information on any aspect of the scholarship, please email me: [John.Endler@deakin.edu.au](mailto:John.Endler@deakin.edu.au). For information about the Centre for Integrative ecology, see <http://cie-deakin.com/> Important Notice: The contents of this email are intended solely for the named addressee and are confidential; any unauthorised use, reproduction or storage of the contents is expressly prohibited. If you have received this email in error, please delete it and any attachments immediately and advise the sender by return email or telephone.

Deakin University does not warrant that this email and any attachments are error or virus free.

Prof. John A. Endler. FAA, FAAAS Alfred Deakin Professor Editor-in-Chief, Evolutionary Ecology Centre for Integrative Ecology School of Life & Environmental Sciences Deakin University, Waurn Ponds Campus 75 Pigdons Road Waurn Ponds, VIC 3216, Australia email: [John.Endler@deakin.edu.au](mailto:John.Endler@deakin.edu.au) tel: 03 5227 1313, or

+61 3 5227 1313 mob: 0488 255 712 Deakin University  
CRICOS Provider Code 00113B

“John A. Endler” <[John.Endler@deakin.edu.au](mailto:John.Endler@deakin.edu.au)>

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## DurhamU EvolutionBiol

Molecular Ecology Group, Durham University, UK

Studentship opportunities still available:

Project 1: Evolution of habitat specialisation in the Arctic char

The evolution of multiple divergent phenotypes in post-glacial lakes has occurred repeatedly and independently in many fish taxa including salmonids (e.g. *Salmo*, *Oncorhynchus*, & *Salvelinus* species), the three-spined stickleback (*Gasterosteus aculeatus*), and smelt (*Osmerus* species). In this study next generation sequencing methodologies will be applied to understanding the evolution of char (*Salvelinus alpinus*) ecotypes in British lakes, comparing multiple sympatric morphs in separate lake systems. This studentship is open to all nationalities (funded by the Durham University DDS program). Selection of candidates begins January 14th 2015 and applications must be in by that date.

Project 2: The relative contribution of genetic drift and natural selection on founder populations of deer

Population bottlenecks and founder events are an important part of evolutionary process, generating stochastic variation among populations and potentially changing evolutionary trajectories. Natural selection is a weak force compared to genetic drift when population size is very small, yet strong selection could overcome this. In this study founder populations of reindeer (*Rangifer tarandus*) on South Georgia and roe deer (*Capreolus capreolus*) in the UK will be investigated using next generation sequencing methodologies to better understand the relative importance of drift and selection following founder events. This studentship is open to EU and UK nationals (funded by the Whitehead Trust). Selection of candidates begins January 14th 2015 and applications must be in by that date.

Project 3: Role of habitat boundaries in the evolution of population genetic structure in marine systems

A long-standing objective in evolutionary biology is to understand the mechanisms and drivers that determine the patterns and rate of differentiation, and eventual speciation among populations. Connectivity (the real-

ized potential for gene flow among populations) is key, but there are various interacting factors that determine the spatial and temporal pattern of movement. In this study the student will take advantage of a well-studied system where there is suspected to be an important interaction between prey choice and gene flow for the bottlenose dolphin (*Tursiops truncatus*). While based in Durham, this project will be co-supervised by Oscar Gaggiotti in St. Andrews and Per Berggren in Newcastle. This studentship is open to UK nationals only (NERC funding). The application deadline is February 2nd 2015.

For further information please contact Rus Hoelzel (a.r.hoelzel@dur.ac.uk).

To submit an application, please send a copy of your c.v., transcripts and a cover letter, and have two letters of reference sent to a.r.hoelzel@dur.ac.uk. Please also apply online at [https://banss.dur.ac.uk/blive\\_ssb/bwskalog.P\\_DisplLoginNon](https://banss.dur.ac.uk/blive_ssb/bwskalog.P_DisplLoginNon) "HOELZEL A.R." <a.r.hoelzel@durham.ac.uk>

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## EastCarolinaU EvoluitonaryBiol

### GRADUATE STUDIES IN ECOLOGY AND EVOLUTION AT EAST CAROLINA UNIVERSITY

The graduate program in the Department of Biology at East Carolina University invites applications from prospective PhD and MS students for fall 2015. East Carolina University is the third largest campus in the University of NC system and has an active and well-supported group of faculty working in the areas of ecology and evolution. Currently, we have >70 MS students and >20 doctoral students enrolled in our graduate programs. Students accepted into the Interdisciplinary Doctoral Program in Biological Sciences will receive two years of support with no teaching obligations and at least five years of support total, at a very competitive level. TA-ships are readily available in our two MS programs and Biology faculty members also supervise students in ECU's Coastal Resource Management PhD program. Our faculty members (see below) conduct research across the globe and excellent opportunities exist to work in terrestrial, freshwater, wetland and marine systems.

Our students enjoy living in the affordable community of Greenville, NC and having access to several natural areas, universities and research centers located in central and eastern NC. The Center for Biodiversity

at East Carolina University also provides graduate students with opportunities to participate in journal clubs, workshops, and outreach events and access to high performance desktop computers. In addition to resources within faculty labs, students also have access to a Central Environmental lab, a core genomics facility, and a high performance computing core.

Application deadlines vary with particular programs but students applying early will have a greater chance of receiving financial support. Please visit <http://www.ecu.edu/biology/> to find out more about our department, faculty and graduate programs. In addition to visiting departmental and faculty websites, please contact prospective mentors directly to our director of graduate studies, Terry West (westt@ecu.edu), for more information. We are happy to arrange visits for competitive prospective students and additional scholarship support may be available for the strongest applicants.

Departmental faculty with expertise in ecology and evolution include:

Marcelo Ardon: Aquatic ecosystem ecology and biogeochemistry. Chris Balakrishnan: Avian evolutionary and behavioral genomics. Seth Barribeau: Evolutionary ecology of hosts, parasites, and symbionts in pollinator and pest insects. Michael Brewer: Evolutionary genomics, systematics, and bioinformatics. David Chalcraft: Population and community ecology; ecological aspects of biodiversity. Robert Christian: Coastal ecosystem ecology and network ecology. Carol Goodwillie: Plant mating system evolution, plant population ecology and genetics. Pat Harris: Fish ecology and life history, fisheries management. Jinling Huang: Evolutionary genomics and bioinformatics. Fadi Issa: Neurobiology & Behavior, neurodegeneration. Claudia Jolls: Plant evolutionary ecology and conservation. Dave Kimmel: Plankton ecology. Trip Lamb: Systematics and phylogeography. Joe Luczkovich: Food web ecology and fish bioacoustics. Krista McCoy: Ecological development and physiology. Mike McCoy: Quantitative population and community ecology. Jeff McKinnon: Sexual selection, speciation, mainly in fish. Sue McRae: Behavioral ecology and social evolution in birds. Ariane Peralta: Microbial ecology, wetland ecology, agroecology Enrique Reyes: Landscape ecology, ecological modeling, coastal management. Roger Rulifson: Fish ecology and fisheries. Ed Stellwag: Vertebrate evo-devo and cis-regulatory network evolution. John Stiller: Molecular evolution and comparative genomics. Kyle Summers: Evolution of color, behavior in poison frogs; evolutionary medicine. Heather Vance-Chalcraft: Community ecology. Terry West: Human impacts on coastal ecosystems. Baohong Zhang: MicroRNA evolution, comparative genomics, and molecular genetics. Yong Zhu: Comparative evolu-

tion and molecular functions of hormones and receptors.

David R. Chalcraft Assoc. Professor of Biology Director of the Center for Biodiversity East Carolina University Greenville, NC 27858

252-328-2797

“Chalcraft, David” <CHALCRAFTD@ecu.edu>

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## GhentU Bioinformatics

Dear colleague,

The Comparative & Integrative Genomics lab < <http://bioinformatics.psb.ugent.be/cig/> > (Ghent University - VIB, Belgium) is currently looking for a \*PhD student in Bioinformatics\* to work on a research project focusing on Plant Regulatory Genomics.

Our mission: Our objective is to extract biological knowledge from large-scale experimental data sets using data integration, comparative sequence and expression analysis, and network exploration. We try to identify new aspects of genome biology, especially in the area of gene function prediction, gene regulation and evolutionary biology.

Job description

\* tackle specific research questions about gene regulation through the integration of experimental -omics data types (e.g. RNA-Seq and ChIP-Seq) and computational biology methods \* develop and apply automatic data processing routines as well as comparative genomics methods to infer regulatory networks across different plant species \* scientific research towards a PhD degree (4 year period) in the framework of a FWO funded research project \* work in close collaboration with colleague PhD students \* requirement of attending and presenting your work at international scientific meetings \* publish in peer-reviewed international journals

Your profile

\* you have a master in Bioinformatics, Computer Science, or a degree of Bioscience engineering \* you are enthusiastic about scientific research and have a strong interest in computer science, genomics and biology \* you are familiar with Linux/Unix and have knowledge of Python, Perl or Java \* you have good communication & writing skills \* you are proficient in English \* you are a pro-active team player

More info here: <http://bioinformatics.psb.ugent.be/>

[cig/RegulGenomics.jobdescription2015.pdf](#) Thanks to forward this message to potential candidates in your network.

Prof. Dr. Klaas Vandepoele Tel. 32 (0)9 33 13822 VIB Department of Plant Systems Biology, Ghent University Technologiepark 927, 9052 Gent, Belgium

Lab website:<http://bioinformatics.psb.ugent.be/cig/-N2N> MRP:<http://www.nucleotides2networks.be/> Twitter:[http://twitter.com/plaza\\_genomics](http://twitter.com/plaza_genomics) Klaas Vandepoele <klaas.vandepoele@psb.vib-ugent.be>

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## GhentU Bioinformatics PlantRegulatoryGenomics

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\* you have a master in Bioinformatics, Computer Science, or a degree of Bioscience engineering \* you are enthusiastic about scientific research and have a strong interest in computer science, genomics and biology \* you are familiar with Linux/Unix and have knowledge

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Prof. Dr. Klaas Vandepoele Tel. 32 (0)9 33 13822 VIB Department of Plant Systems Biology, Ghent University Technologiepark 927, 9052 Gent, Belgium

Lab website:<http://bioinformatics.psb.ugent.be/cig/N2N> MRP:<http://www.nucleotides2networks.be/> Twitter:[http://twitter.com/plaza\\_genomics](http://twitter.com/plaza_genomics) Klaas Vandepoele <klaas.vandepoele@psb.vib-ugent.be>

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## HeidelbergU 6 Evolutionary Adaptation

Heidelberg University, Centre for Organismal Studies  
Karlsruhe Institute of Technology

6 PhD scholarships within the research training group “Evolutionary novelty and adaptation - from molecules to organisms”

Application deadline: 15.02.2015

The research training group is located at the Centre for Organismal Studies (COS), Heidelberg University. It unites nine international research groups with complementary expertise in evolutionary biology, developmental biology, and ecology employing state-of-the-art molecular tools and imaging technology as well as field research in diverse habitats such as desert caves, coral reefs, and alpine systems.

Research Program: The fellows will be educated and trained beyond existing boundaries and model organisms at ecological, genetic, and mechanistic levels of evolutionary biology. This broad education will allow the fellows to develop novel views that encompass contemporary concepts and future opportunities of the field. All projects offered represent a unique patch from the evolutionary past, which together unite different time scales of evolutionary research into one coherent education program. Outlines of available projects and participating groups are available on the webpage [http://www.cos.uni-heidelberg.de/index.php/graduate\\_school](http://www.cos.uni-heidelberg.de/index.php/graduate_school)  
Teaching Concept: Fellows will be trained in the collab-

orative research environment at COS, with a focus on organismal biology. All fellows will be integrated into the established PhD program under the umbrella of the prestigious Hoffmann-Berling International Graduate School (HBIGS) of the Heidelberg Life Sciences.

Requirements: We invite applications from highly motivated candidates with above-average qualifications, passion for and experience in research, and the willingness to actively participate in the graduate school. Successful applicants will have (1) an Masters degree (or equivalent) in Biology or another relevant discipline, (2) a solid background in ecology / development and/or evolution, (3) an excellent command of the English language, and (4) a strong motivation to join an interdisciplinary and international research training environment.

Applications: Written applications, in English, should be submitted via HBIGS; applications for up to three projects are possible. They should include a CV including copies of all degrees, documentation of English proficiency, a motivation letter, and two letters of recommendation. Please refer to the HBIGS website for additional details (<http://www.hbigs.uni-heidelberg.de/>). The motivation letter should include your statement-of-purpose why you would like to become a member of our graduate school and a short explanation for your project choice. Applicants are asked to submit the above-mentioned documents before February, 15th 2015. Interviews will take place in March, 2015 in Heidelberg. For questions regarding the graduate school please contact the spokesperson, Dr. Steffen Lemke ([steffen.lemke@cos.uni-heidelberg.de](mailto:steffen.lemke@cos.uni-heidelberg.de))

Steffen Lemke Group Leader Centre for Organismal Studies (COS) Universität Heidelberg Im Neuenheimer Feld 230 69120 Heidelberg Germany

phone +49 6221 54 5553 fax +49 6221 54 5639 email [steffen.lemke@cos.uni-heidelberg.de](mailto:steffen.lemke@cos.uni-heidelberg.de)

Steffen Lemke <[steffen.lemke@cos.uni-heidelberg.de](mailto:steffen.lemke@cos.uni-heidelberg.de)>

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## ImperialCollege London BeeAdaptation

PhD Studentship advertised at Imperial College London, Silwood Park campus, UK (full funding to UK residents only)

Title: Bee foraging in fragmented landscapes

Supervisors: Dr Richard Gill ([r.gill@imperial.ac.uk](mailto:r.gill@imperial.ac.uk)), Dr



Samraat Pawar Department: Life Sciences

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

Alongside the habitat fragmentation issue, agricultural practices present a 'pesticide exposure landscape' to foraging insects. Pesticide exposure is known to decrease foraging performance whereby foraging bout duration is prolonged in combination with less food being brought back per unit foraging time<sup>1-2</sup>, yet we still understand little about what specific behavioural mechanisms are being affected and the knock-on effect to colony functioning<sup>3</sup>.

This project will investigate how specific stressors set limits on bee foraging performance. The results gained from such experiments will then be used to inform and develop spatial model(s)<sup>4</sup> to look at the probability of foraging success under given levels of habitat fragmentation.

The research project will provide the PhD student with a number of benefits: i) it will integrate a number of critical interdisciplinary skills including controlled experiments and modelling; ii) it crosses a number of scientific fields such as behavioural ecology, applied ecology and theoretical biology; iii) the research is of high impact and will result in quality publications as well as results that can inform end users and policy makers; and iv) the student will join a productive, diverse and social research group.

Imperial College London is a world leading university; the Times Higher Education placed it as the leading university in the Life Sciences REF2014 for research intensity (<http://www.timeshighereducation.co.uk/features/ref-2014-rerun-who-are-the-game-players/-2017670.article>). The QS annual world university rankings 2014/2015 placed Imperial College as 2nd best in the world. The student will be based at the Silwood Park campus which currently has a growing and internationally renowned community of researchers and excellent facilities for the project to be carried out. The Grand Challenges in Ecosystems and the Environment (GCEE) initiative has invested significantly into ensuring a world leading group of scientists addressing important global issues.

1. Gill et al. 2012 Nature (doi:10.1038/nature11585)
2. Gill & Raine 2014 Functional Ecology (doi:10.1111/1365-2435.12292)
3. Bryden, Gill et al. 2013 Ecology Letters (doi:10.1111/ele.12188)
4. Pawar et al. 2012 Nature (doi:10.1038/nature11131)

For more information on how to apply visit us at [www.imperial.ac.uk/changingplanet](http://www.imperial.ac.uk/changingplanet) Deadline for application is 25th January 2015.

Dr Richard Gill Lecturer Department of Life Sciences Imperial College London Silwood Park campus Buckhurst Road, Ascot Berkshire, SL5 7PY UK Phone: +44 (0)20 759 42215 Webpage: <http://www.imperial.ac.uk/AP/faces/pages/read/Home.jsp?person=r.gill> Grand Challenges in Ecosystems and the Environment Initiative Theme leader: Managing target species in complex ecosystems

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

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## Imperial College London HumanEvolGenetics

NERC-funded PhD studentship available for anthropological genetics at Imperial College London.

Attention students looking to do a PhD in human evolutionary genetics. We are currently accepting applications for a PhD student to be co-supervised by Dr. Jason Hodgson and Prof. Miguel Araujo. The title of the project is "Understanding the relationship between tsetse flies, trypanosomiasis, and humans in rural Africa using population genomics and ecological niche modelling." Details can be found at: [https://workspace.imperial.ac.uk/grantham/Public/SSCP%20DTP/DTP%20projects%202015/-LS\\_Hodgson\\_2015.pdf](https://workspace.imperial.ac.uk/grantham/Public/SSCP%20DTP/DTP%20projects%202015/-LS_Hodgson_2015.pdf) The project will require a fun mix of fieldwork, lab work, and an integrated analytical approach employing population genomics and ecological niche modelling.

Applications need to be received by January 25th, 2015. Directions for how to apply can be found at: <http://www.imperial.ac.uk/grantham/postgraduate-training/science-and-solutions-for-a-changing-planet/-studentship-opportunities/> Please contact me with any queries: j.hodgson@imperial.ac.uk

Eligibility for the studentship is limited to those with 'settled status' in the UK (i.e. no restrictions on how long you can stay in the UK, you have been ordinarily resident in the UK for three years prior to the start of

the studentship, for non EU-nationals you have not been residing in the UK wholly for educational purposes).

jason.a.hodgson@gmail.com

## KansasStateU FishAdaptation

### Research focus

We are seeking a highly motivated doctoral student to conduct research on the physiological adaptation of prairie stream fishes. The primary objective is to utilize natural thermal gradients in spring-fed prairie streams to study the effects of temperature variation and variability both on individual and population level responses. The project includes field components and analysis of long-term data sets to test how thermal regimes affect population dynamics of grazing minnows. In addition, laboratory experiments will be used to quantify variation in eco-physiological traits within and among species. The ultimate goal is to establish how individual traits can be used to predict population level responses. There is flexibility for the student to develop independent research within the broad scope of the project. This research is a collaborative effort between different labs at KSU. It will be conducted primarily at the Konza Prairie Biological Station and is part of the Konza Prairie Long-Term Ecological Research (LTER). Preferred applicants will have earned a M.S. degree and exhibit equal enthusiasm for field-based work and experimentation in the laboratory. For more information, check <http://www.sulfide-life.info/mtobler/news2/news2-2/142-ph-d-research-assistantship-in-physiological-ecology-of-prairie-stream>. Salary The stipend is \$20,826 plus tuition per calendar year. A health insurance plan is available.

Application deadline January 31 2015

Application materials Please send a brief cover letter, resume, transcripts, GRE scores, and contact information for two references to [tobler@ksu.edu](mailto:tobler@ksu.edu) by the deadline to be considered for this position.

Michael Tobler Division of Biology Kansas State University 116 Ackert Hall Manhattan, KS 66506

Phone: 785-532-6652 (office); 785-532-0617 (lab)

Website: <http://www.sulfide-life.info/mtobler> Humans are not the pinnacle of evolutionary progress but only an aberrant side branch of fish evolution. - Moyle

[michi.tobler@gmail.com](mailto:michi.tobler@gmail.com)

## Leicester GenomicImprinting 2

This is a readvertisement as an additional funding stream has come online. Can we ask previous applicants to also apply to the CENTA stream.

Dear evoldir

A PhD studentship starting October 2015 is available by competition to study the role of genomic imprinting in social insect biology, jointly supervised by me (Dr Eamonn Mallon [ebm3@le.ac.uk](mailto:ebm3@le.ac.uk)) and Dr. Ezio Rosato at the University of Leicester. Further details at <http://bit.ly/1bRFqnL> Project outline: This project will attempt to establish the role of genomic imprinting in the important pollinator species, the bumblebee *Bombus terrestris*. Genomic imprinting is the differential expression of alleles in diploid individuals, with the expression being dependent upon the sex of the parent from which it was inherited. Genomic imprinting is an important area of research in plant breeding and in evolutionary biology and has relevance to some human cancers and developmental syndromes. Bees are potentially a model for genomic imprinting because they have a small, sparsely methylated genome. The PhD student will carry out all experiments and bioinformatic analysis under the guidance of the supervisory team. They will be provided with training in R, a powerful and increasing popular statistical programming language, Python, a general-purpose, high-level programming language widely used in bioinformatics, molecular biology, RNA-seq, anatomical dissection and neuroanatomy, in situ hybridisation, confocal microscopy and bee husbandry as required.

\*References\* Amarasinghe, H. E., Clayton, C. I. & Mallon, E. B. (2014) Methylation and worker reproduction in the bumble-bee (*Bombus terrestris*). *Proc. R. Soc. B Biol. Sci.* 281, 20132502

Yan et al (2014) Eusocial insects as emerging models for behavioural epigenetics. *Nat Rev Genet* advance online publication.

This project is available for a PhD studentship is available as part of the Midlands Integrative Biosciences Training Partnership, <http://bit.ly/1C9m94x> Eligibility: British nationals who have lived in the UK all their lives are eligible. Also eligible are non-British nationals who have settled status AND have been resident in the UK for 3 years immediately prior to the date of the start of the course. EU nationals who have been ordi-

narly resident in the UK and Islands for three years immediately prior to the date of start of the course; \*EU nationals not resident in the UK are eligible\* \*for matched funding studentships.\*

To apply formally please see <http://bit.ly/1rsnR6V>. Application deadline the 31/1/2015 Please contact me (ebm3@le.ac.uk) if you would like to discuss the project informally Dr Eamonn Mallon

There are two competitions please apply to both

MITBP <https://www2.le.ac.uk/colleges/medbiopsych/-research/Postgraduate%20Opportunities/mitbp-at-the-university-of-leicester/application> and CENTA <http://www2.le.ac.uk/study/research/funding/centa/-how-to-apply-for-a-centa-project> Application deadline the 31/1/2015

Dr Eamonn Mallon Lecturer in Evolutionary Biology  
Room 220 Department of Biology University of Leicester  
LE1 7RH UK

Tel 01162523488 Email ebm3@le.ac.uk

“Mallon, Eamonn B. (Dr.)” <ebm3@leicester.ac.uk>

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## McGillU PlantEvolution

Graduate student positions in Plant Evolution at McGill University, Montreal.

Position 1. Self-incompatibility is the most effective method by which flowering plants enforce outcrossing and maintain a system of mating that the negative consequences of inbreeding depression in progeny. The self-incompatibility system in the Brassicaceae is perhaps the best characterized one. We have recently found exciting evidence suggesting that this system has evolved more than once within the family (<http://www.plosbiology.org/article/info%3Adoi%2F10.1371%2Fjournal.pbio.1001560>). We are looking to recruit a graduate student (M.Sc. or Ph.D. level) to assist us in furthering this investigation.

Position 2. Climate change is producing new ecological challenges for plants in this century (e.g., temperature, water stress conditions). When phenotypic plasticity is insufficient for plants to cope with such challenges, they must either adapt evolutionarily or face local extinction. We are exploring how next generation sequencing approaches can help us to better understand the underlying genetics and evolutionary genomics of this process. We would like to recruit a graduate student (Ph.D. level)

to work on this problem in our lab.

Please send me your CV and a brief statement detailing: (1) which position you are interested in applying for; (2) why you are interested in the position and any relevant experience you may have; and (3) the names of 3 people we may write to for letters of reference. This information should be sent to Prof. Daniel Schoen: [schoenlab@gmail.com](mailto:schoenlab@gmail.com) by 15 February 2015 (for Canadian students) and 30 December 2014 (for non-Canadian students).

[dan.schoen@mcgill.ca](mailto:dan.schoen@mcgill.ca)

“Daniel Schoen, Prof.” <[dan.schoen@mcgill.ca](mailto:dan.schoen@mcgill.ca)>

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## NewcastleU EvolutionaryGenetics

Newcastle University is looking for excellent applicants for PhD projects funded through the NERC funded Doctoral Training Partnership IAPETUS. Two Evolutionary Genetics projects are available:

Living on the edge: can adaptation at the edge of a species range accommodate rapid climatic change in a long-lived species? [http://www.iapetus.ac.uk/wp-content/uploads/2014/11/IAP\\_14\\_44-NEW-Wolff.pdf](http://www.iapetus.ac.uk/wp-content/uploads/2014/11/IAP_14_44-NEW-Wolff.pdf) Mating system evolution in a grassland species: self-compatibility and male sterility [http://www.iapetus.ac.uk/wp-content/uploads/2014/11/IAP\\_14\\_43-NEW-Wolff.pdf](http://www.iapetus.ac.uk/wp-content/uploads/2014/11/IAP_14_43-NEW-Wolff.pdf) These two studentships are part of the NERC funded Doctoral Training Partnership IAPETUS. This has 12-16 PhD studentships available, with competition between a large number of projects. For full details of requirements and details how to apply: <http://www.iapetus.ac.uk/aboutstudentships/> Please note that IAPETUS is only able to consider applications from Home/European Union candidates. International (non-EU) candidates are not eligible to be considered. Also, a candidate from another EU country who has not been resident in the UK for 3 years or more prior to the commencement of their studies with IAPETUS, will only be eligible for a fees-only studentship

Interested students are advised to apply early, the ultimate application deadline is 2nd February 2015.

For further information on the two projects mentioned above: Dr Kirsten Wolff Reader in Evolutionary Genetics Newcastle University, School of Biology Devonshire Building 5th floor Newcastle NE1 7RU, UK Phone: 0191 208 4852

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/) [kirsten.wolff@newcastle.ac.uk](mailto:kirsten.wolff@newcastle.ac.uk)

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## NorthCarolinaStateU EvolGenetics

Genetics Graduate Program Now Accepting Applications for Fall 2015!

The Graduate Program in Genetics is \*still\* currently accepting applications (until February 1, 2015) for M.S. and Ph.D. students for the Fall 2015 semester. This program was established in 1952, and is one of the longest running genetics graduate programs in the USA.

The graduate training faculty are a highly interactive group performing research in all aspects of genetics from molecules to populations. Our research encompasses behavioral genetics, biomedical genetics, computational genetics and bioinformatics, evolutionary, population and quantitative genetics, and molecular, cellular and developmental genetics.

Our faculty utilize a wide range of traditional and non-traditional model systems in their research. We consider graduate students to be professionals in training, and provide a well-rounded program of academic, research and professional training. Students are intimately involved in program activities have a strong voice in shaping the program. We provide broad and comprehensive graduate training in genetics and also flexible academic programs tailored to meet the background and career goals of the individual student.

For more information go to [\\*genetics.sciences.ncsu.edu\\*](http://*genetics.sciences.ncsu.edu) or email Trudy Mackay ([trudy\\_mackay@ncsu.edu](mailto:trudy_mackay@ncsu.edu)) or Melissa Robbins ([melissa\\_robbins@ncsu.edu](mailto:melissa_robbins@ncsu.edu)).

You may also contact us by phone at 919-515-2292.

[merobbi3@ncsu.edu](mailto:merobbi3@ncsu.edu)

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## OklahomaStateU GrassTilleringGenetics

Research focus: We are seeking a highly motivated student to conduct research on evolutionary and quantitative genetics of branching in grasses, as part of an NSF Plant Genome grant focused on tillering in pani-

coid grasses (in collaboration with researchers at West Virginia University, Brigham Young University, and the University of California at Berkeley). The primary objective of this research is to use three panicoid grasses, maize, sorghum, and Setaria, to identify components of the gene regulatory network controlling branching. Our lab is focused on Setaria, combining traditional QTL mapping with expression QTL studies, mutant analysis, and modeling to understand the genetic components of branching and their responses to environmental stimuli such as shading. There is considerable flexibility for graduate projects within this broad theme.

Essential qualifications include successfully completed masters degree in genetics and/or molecular biology, experience in molecular lab techniques including working with RNA, experience in growing plants, and excellent writing skills. Desirable qualifications include experience with quantitative and phylogenetic analysis software, next generation sequence library construction and data analysis, and programming in R and/or Python.

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

Application deadline: February 13th, 2015; but applications will be reviewed as they arrive.

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

Andrew Doust Botany Department Oklahoma State University Physical Sciences 301 Stillwater, OK 74078

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

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

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## SoutheasternLouisianaU PlantSystematics

MASTERS POSITIONS IN PLANT EVOLUTION AND SYSTEMATICS Fall 2015 with Rick Miller, Southeastern Louisiana University

RESEARCH PROGRAM: We are seeking highly motivated master's students to conduct research in plant

evolution and systematics. One of our current research areas is the biology of the crop wild relatives of sweetpotato, a small clade of morning glories, the Batatas group. We are developing an understanding of the evolutionary relationships and population genetic structure of this hybridizing complex. The potential master's projects (listed below) will complement our molecular systematic investigations. The ultimate goal is to understand the evolutionary relationships of the crop wild relatives and traits of potential importance that can be used for improvement of sweetpotato. This research is being carried out in collaboration with an international team of systematists, evolutionary biologists, and crop scientists studying the genomics, systematics of the crop wild relatives, as well as breeding sweetpotato to meet challenges from pathogens and climate change.

We have a broad understanding of the evolution and systematics of morning glories. Our lab is equipped for both molecular studies and field research. We have a large collection of morning glory germplasm, an excellent greenhouse, and experimental gardens at LSU agriculture station in Hammond.

**RESEARCH PROJECTS:** (1) Taxonomy of the Batatas complex: The current taxonomy of the sweetpotato crop wild relatives is provisional and could benefit from a revision using an expanded sample, as well as being informed by recent molecular systematic results. This project would include a geomorphometric analysis of corolla and sepal shape to aid in species delineation.

(2) Crossing studies among members of the Batatas group: The fourteen species of the Batatas group exhibit varying levels of interfertility. We want to document levels of interfertility among populations within the complex to help explain the observed genetic structure. We also want to determine those crosses that may allow traits to be bred into the cultivated sweetpotato, which is a hexaploid.

(3) Studies of drought resistance among the sweetpotato crop wild relatives: Sweetpotato is commonly grown on small farms that are often challenged by changing weather. Drought is one of the main conditions reducing sweetpotato production. We will use greenhouse studies and field experiments to examine levels of drought resistance in the crop wild relatives to identify populations that could provide important characteristics for crop improvement. This research area also allows for studies of the ecophysiology of morning glories, which are widespread weedy species found throughout the Americas.

**ADDITIONAL PROJECTS IN OUR LAB:** (1) Systematics of morning glories: We have an ongoing research effort to study the systematics of morning glories. We

have an excellent understanding of the broad groups within morning glories (tribe Ipomoeae) and are poised to develop more focused studies of particular clades.

(2) Coevolution of the morning glory/fungal symbiosis that results in the production of ergot alkaloids: It has long been known that morning glory seeds contain ergot alkaloids. Recently it was determined that these alkaloids are produced through the symbiotic interaction between morning glories as hosts and *Periglandula*, an epibiotic fungi. We are interested in the evolution of the symbiont at both the intraspecific level and among morning glories and *Periglandula* in general.

**SUPPORT:** Teaching assistantships will be available on a competitive basis. You will teach introductory biology labs and have a great opportunity to have gain important teaching experience.

**QUALIFICATIONS:** Bachelor's degree and qualifying GPA and GRE scores. It is useful to have prior research experience. Most important is identifying your own research interests that are consistent with the ongoing research in our lab. Useful information regarding our graduate program can be found at [http://www.southeastern.edu/acad\\_research/depts/-biol/grad\\_degree/index.html](http://www.southeastern.edu/acad_research/depts/-biol/grad_degree/index.html). **APPLICATION MATERIALS:** A cover letter identifying your research interests, resume, transcripts, GRE scores and arrange for two letters of recommendation. Please contact Rick Miller ([rickmiller@selu.edu](mailto:rickmiller@selu.edu)) to discuss your interest in our lab and the details of the application process (one to the Biology department and a separate application to the Graduate School).

**DEADLINE OF APPLICATION:** Fall 2015 application deadline is 1 February.

**FACULTY:** The graduate faculty has strengths in organismal biology including such areas as fish and snake systematics, turtle physiology, butterfly ecology, environmental microbiology, and amphibian ecology.

**LOCATION:** Hammond is located north of New Orleans and east of Baton Rouge. It is a

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## StockholmU EvolutionaryGenetics

A PhD student position is currently available at Stockholm University and Science for Life Laboratory in the research group of Dr. Tanja Slotte.

The complete ad for this position is available on the Stockholm University webpage: <http://www.su.se/english/about/vacancies/phd-studies/phd-student-position-in-evolutionary-plant-ecology-1.217840> Project description We are recruiting a PhD student to work within the project “Evolutionary consequences of dominance at a locus under long-term balancing selection”, which is funded by the Swedish Research Council. The aim of this project is to investigate evolutionary processes at the self-incompatibility locus (S-locus) in Brassicaceae plants. In particular, we wish to characterize the genetic basis of recurrent losses of self-incompatibility and the evolutionary consequences of S-locus dominance, both at the sequence and phenotypic level. The project will entail sequencing and evolutionary genetic analysis of S-locus alleles, phenotypic characterization of progeny from controlled crosses, and analyses of large-scale expression and methylation data. We will mainly focus on the crucifer genus *Capsella* (Brassicaceae), an emerging model for the study of mating system evolution.

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

Qualifications To be accepted for the PhD program, the applicant must have a University degree in Biology at the advanced level (e.g. Masters) of at least 240 credits, including at least 60 credits at the advanced level, or equivalent knowledge. Previous degrees should also

include a thesis of at least 30 credits at advanced level in a relevant subject.

Terms of employment The PhD study should be completed within four years of full time study. Besides studies, the PhD-student may be involved in teaching and other duties to a maximum of 20 %, in which case the study time will be extended correspondingly.

Selection criteria The selection is based on the applicant’s ability to successfully pursue the research education. Special emphasis is put on the applicant’s knowledge and skills within the subject area, ability to express her/himself verbally and in writing, analytical aptitude, creativity, initiative and independence, and a capacity for working together with other researchers. Previous experience of evolutionary genomic analyses and basic molecular genetic lab work is desirable. Experience of experimental plant work is beneficial. The evaluation will be made based on the relevance of past education and experience, grades from previous university courses (in particular at the advanced level), the quality and ambition of the independent project work, references, the cover letter motivating the candidate’s interest, and interviews.

Information For further information, please contact the project leader Tanja Slotte, [tanja.slotte@su.se](mailto:tanja.slotte@su.se), at the Department of Ecology, Environment and Plant Sciences. Personal webpage: <http://tanjaslottelab.se> University webpage: <http://www.su.se/emb/english/about-us/staff/r-s/tanja-slotte-1.174088> Science for Life Laboratory: <http://www.scilifelab.se> Union representatives Anqi Lindblom-Ahlm (Saco-S) and Lisbeth Häggberg (Fackförbundet ST), tel. 08-16 2000 (exchange), and Gunnar Stenberg (SEKO), tel. 070-316 43 41.

Application The application should contain a letter of intent (one to two pages that explain why you are interested in working on this project, why you are interested in studying for a PhD, what you hope to accomplish during your PhD studies, and what skills you can bring to this project), CV, transcripts of all university courses with grades, a copy of your university degree, degree project thesis (or, if not yet completely finished, a draft version or related writing), name and contact information of two references, and any other documents you would like

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## SwanseaU MicrobialGenomics

PhD studentship in Immunology and Evolutionary Microbial Genomics (Swansea University, UK)

General description: Research will be conducted under the direct supervision of Dr. Thomas Wilkinson and Professor Samuel K. Sheppard, and based in the Department of Medical Microbiology and Infectious Diseases at the College of Medicine of Swansea University (United Kingdom). The successful student will join a team of multi-disciplinary scientists working in the MRC Cloud Infrastructure for Microbial Bioinformatics (CLIMB) Centre and the BBSRC-funded medical mass spectrometry team. More information on the research group can be found on <http://www.sheppardlab.com/>. Project details: Early and rapid detection of infection is a major goal of Clinical Microbiology. In particular an ability to differentiate between sepsis and other non-infectious causes of systemic inflammation such as Systemic Inflammatory Response Syndrome (SIRS) is particularly pertinent as it will determine antibiotic administration. Recently, we and others have identified 25-hydroxycholesterol as an important inflammatory mediator regulating the production of pro-inflammatory IL-1 driven responses. To date these studies have linked inflammation with the antiviral interferon response. In this context less is known about 25-hydroxycholesterol and bacterial infection. This project will investigate whether major bacterial pathogens, including *Staphylococcus aureus*, *Campylobacter* and *Escherichia coli* generate unique metabolic signatures of 25-hydroxycholesterol and its degradation products. We will use the whole genome data of over 5,000 bacterial isolates organised in our online databases to select the major disease causing clones for host / pathogen whole blood modelling prior to Mass Spectrometry analysis of isolated sera.

The project will focus on two major areas of host pathogen interactions: i) the cellular response of the organism and host; ii) the population genomics of microbes so that host responses specific to a species or evolutionary conserved lineages of pathogens can be identified.

Requirements: Enthusiasm and practical experience in immunology, microbiology, molecular techniques and computer-based genetic analysis is necessary but training and support will be provided to strengthen these

areas. The successful candidate will be highly motivated, creative, independent and have a good degree in immunology, molecular biology, microbiology, bioinformatics, genetics or ecology (BSc or MSc, 2:1 or 1st only). Previous experience in a molecular biology/immunology laboratory or in bioinformatics research is also strongly desirable. Good English writing and oral skills are essential.

Details: - The duration of the studentship is 3 years (2015-2018). - The position is open until filled, but a preferred deadline for application is 31st July 2015, to allow for registration to start in the Fall semester. - The position is fully open for UK and EU students. - Salary will be commensurate with regular UK postgraduate stipends, i.e. £13,863/year (~ euro 18,425/year), tax-free. - Tuition fees are fully covered by the studentship. - Students will also have opportunities to attend national and international conferences during their candidature and a chance to compete for internal College of Medicine travel bursaries.

Application: Please contact us (sheppardlab@gmail.com) for applications (please attach CV and describe motivation). More details: <http://www.sheppardlab.com/> Dr. Guillaume Méric NISCHR Health Research Fellow Medical Microbiology and Infectious Diseases Swansea University, College of Medicine ILS1 Building Room 531 (Floor 5) Singleton Park, Swansea SA2 8PP United Kingdom ~ E-mail: g.meric@swan.ac.uk Phone: +44(0)1792-606672 ~ Sheppard Laboratory: <http://www.sheppardlab.com/> MRC CLIMB Consortium: <http://www.climb.ac.uk/> Guillaume Méric <g.meric@swansea.ac.uk>

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## TowsonU AntSystematics

Towson University V Ant Systematics, Evolution and Biodiversity

Seeking masters-level graduate students to participate in on-going studies of ant systematics, evolution, and biodiversity. The LaPolla Lab at Towson University is involved in several ant research projects ranging from revisionary systematics to biotic inventories and is actively looking to add additional graduate students to conduct independent thesis projects. Students would be expected to conduct both lab and field work in a variety of settings. Interested students should contact Dr. John LaPolla at [jlapolla@towson.edu](mailto:jlapolla@towson.edu). Deadline for submission of application materials (Fall 2015 admission) is

March 15, 2015.

For further information about the Towson University Biology Graduate Program see: [http://wwwnew.towson.edu/biologicalsciences/-graduate\\_program.html](http://wwwnew.towson.edu/biologicalsciences/-graduate_program.html) John S. LaPolla, Ph.D. Associate Professor of Biology Co-Director, Biology Graduate Program Dept. of Biological Sciences 8000 York Road Towson University Towson, MD 21252 USA phone: 410-704-3121 fax: 410-704-2405

“Lapolla, John S.” <JLapolla@towson.edu>

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### TrentU AmphibianPopGenetics

MSc, PhD, and PDF positions available V Amphibian occupancy patterns, population genetics, and disease dynamics

Funded by a Strategic NSERC grant (2014), we are building a team of 4 PhD students, 2 MSc students, and 2 post-doctoral fellows, to work on research related to the detection and monitoring of amphibians and their pathogens (chytrid fungus, ranavirus) in Canada.

Using environmental DNA as a basis for the research, the team will conduct: 1) Habitat occupancy modeling for amphibians and their pathogens; 2) Analysis of the evolutionary dynamics of pathogens and amphibian hosts; 3) Assessment of potential synergistic interactions between pathogens and aquatic contaminants; and 4) Modeling the drivers of amphibian population decline. We may also include a component assessing host and pathogen epigenetics and gene expression.

Students will develop research projects that fit within the context of the broader program, such as: Validation of eDNA for detecting amphibians; Assessment of ranavirus pathogenicity; Chytrid fungus evolutionary dynamics; and Modeling drivers of amphibian occupancy and pathogen-induced gene expression. We are seeking students to initiate their research in Spring or Fall 2015, with the research to be conducted across southern Ontario. At least 2 PhD students are needed by May 1, 2015.

Interested applicants should submit a letter of interest, CV, unofficial transcripts and names of 3 references to: Dennis Murray, Trent University, [dennismurray@trentu.ca](mailto:dennismurray@trentu.ca) ([www.dennismurray@trentu.ca](http://www.dennismurray@trentu.ca)). Because several positions must be filled urgently, postings will be closed as soon as qualified applicants are found. There-

fore, interested applicants should apply early.

Individual research team members also can be contacted and include: Craig Brunetti, Trent University [craigbrunetti@trentu.ca](mailto:craigbrunetti@trentu.ca) ([www.brunettilab.com](http://www.brunettilab.com)); Chris Kyle, Trent University [christopherkyle@trentu.ca](mailto:christopherkyle@trentu.ca) (<http://kylelab.nrdpfc.ca>); David Green, McGill University [david.m.green@mcgill.ca](mailto:david.m.green@mcgill.ca) (<http://redpath-staff.mcgill.ca/green/-David%20Green's%20Home%20Page%20frames.htm>); David Lesbarreres, Laurentian University [dlesbarreres@laurentian.ca](mailto:dlesbarreres@laurentian.ca) (<http://gearg.jimdo.com/people/head/>); Marie-Josée Fortin, University of Toronto [mariejosee.fortin@utoronto.ca](mailto:mariejosee.fortin@utoronto.ca) (<http://labs.eeb.utoronto.ca/fortin>); Chris Wilson, Ontario Ministry of Natural Resources and Forestry [chris.wilson@ontario.ca](mailto:chris.wilson@ontario.ca) (<http://web.nrdpfc.ca/cwilson.htm>); Christine Bishop, Environment Canada [cb.bishop@ec.gc.ca](mailto:cb.bishop@ec.gc.ca) (<http://christinebishop.blogspot.ca>)

dennis murray <[dennismurray@trentu.ca](mailto:dennismurray@trentu.ca)>

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### UBerne HumanGenomics

A PhD position is available for 3 years at the University of Berne to detect patterns of selection in the human genome. The exact subject of the PhD will depend on the qualifications of the candidate but he/she could work on the detection of selection in gene networks (1, 2) based on levels of genomic and expression diversity, the effect of past range expansions on functional genomic diversity (3, 4) of various human groups, or the detection and the measure of levels of background selection in the human genome.

We are looking for a highly motivated individual with a good background in population genomics or bioinformatics and good written and oral communication skills. Computational, programming and statistical skills are a plus for the position. The PhD candidate will be mainly supervised by L. Excoffier, but the PhD student should also interact with Prof. Marc Robinson-Rechavi in Lausanne, with Dr. Anna-Sapfo Malaspinas, a new group leader at IEE, and with other senior members of the CMPG lab.

The CMPG lab is hosted by the Institute of Ecology and Evolution at the University of Berne, and it offers a very international and stimulating research environment. It is also affiliated to the Swiss Institute of Bioinformatics (SIB) and the successful PhD candidate will join its PhD



training network to further his/her education. Berne is ideally located in the middle of Switzerland and Europe, and provides rich cultural and outdoor activities. The gross salary starts at around 32,000 CHF per year and will follow the University of Berne progression scale.

Please send an application letter stating your motivation for the position, a CV, and contact information of two references to [laurent.excoffier@iee.unibe.ch](mailto:laurent.excoffier@iee.unibe.ch). The position remains open until filled, and the successful candidate could start as early as February 2015. See the web page <http://www.cmpg.iew.unibe.ch/content/jobs> for a copy of this information and links with more details on this position.

References:

1. J. T. Daub et al., *Mol Biol Evol* 30, 1544 (Jul, 2013).
2. M. Foll, O. E. Gaggiotti, J. T. Daub, A. Vatsiou, L. Excoffier, *Am J Hum Genet* 95, 394 (Oct 2, 2014).
3. S. Peischl, I. Dupanloup, M. Kirkpatrick, L. Excoffier, *Mol Ecol*, (Sep 18, 2013).
4. V. Sousa, S. Peischl, L. Excoffier, *Curr Opin Genet Dev* 29C, 22 (Aug 23, 2014).

– Laurent Excoffier

Computational and Molecular Population Genetics (CMPG) Institute of Ecology and Evolution, University of Bern 6, Baltzerstrasse, CH-3012 Bern, Switzerland Tel: +41 31 631 30 31 Fax: +41 31 631 48 88 Email:[laurent.excoffier@iee.unibe.ch](mailto:laurent.excoffier@iee.unibe.ch) <http://cmpg.iew.unibe.ch> Computational Population Genetics Swiss Institute of Bioinformatics (SIB) [http://www.isb-sib.ch/groups/Computational\\_Population\\_Genetics.htm](http://www.isb-sib.ch/groups/Computational_Population_Genetics.htm) Laurent Excoffier <[laurent.excoffier@iee.unibe.ch](mailto:laurent.excoffier@iee.unibe.ch)>

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## UCalgary AdaptationGenomics

GRADUATE STUDENT POSITIONS at the UNIVERSITY of CALGARY

Local adaptation and the architecture of complex traits: theory and comparative genomics Sam Yeaman AIHS CAIP Chair in computational evolutionary biology

I'd like to take this opportunity to invite prospective graduate students to apply for positions in the lab that I will be starting in the Department of Biological Sciences at the University of Calgary in September 2015. In particular, I am looking for candidates that are interested in working on de novo genome assembly, mapping, and comparative genomics or analytical and simulation-based population genetic theory. I have received full

funding from AIHS and U of C to cover two research projects (see descriptions below):

- 1) Theoretical exploration of the effect of demography and environment on genomic signatures of local adaptation
- 2) Comparative genomics of rearrangements involving genes associated with local adaptation

Graduate student positions will include full funding (\$21K/year) is available through a combination of lab-supported stipends and TA-ships offered through the University of Calgary. Of course, I encourage students to find their own funding (e.g., NSERC, Eyes High and AIHS), and will offer additional support to students that come with partial or full funding of their own. While I have several ideas for graduate student projects, I will encourage students to explore their own ideas, as long as they align with my broad interests.

TO APPLY: Please send a CV and a short description of your interest in the position to [yeaman@zoology.ubc.ca](mailto:yeaman@zoology.ubc.ca), along with the names and emails of three people I could contact for reference letters. Please be sure to clearly highlight any skills and experience related to genome assembly, NGS library prep, statistics, bioinformatics, or programming. I will begin reviewing applications on February 1st, 2015, but please contact me to check in if you need to make a quick decision.

POTENTIAL RESEARCH PROJECTS:

- 1) Theoretical exploration of the effect of demography and environment on genomic signatures of local adaptation

Theory has shown that migration-selection balance can shape the architecture of local adaptation, but testing this theory using genomic data remains a major challenge. The aim of this project is to extend existing theory to make explicit predictions about the effect of realistic demographies and environments on genomic signatures of local adaptation. In particular, I am planning to focus on recurrent conditionally-deleterious mutation as a source of load and on haplotype-level signatures of local adaptation. This work will use individual based simulations to explore these ideas and the development of new statistical tools to describe the patterns we find. I am also keen on exploring the effect of spatial + temporal heterogeneity on the evolution of genome architecture through small rearrangements. I typically use Nemo (written in C++) but am open to other ideas and approaches.

- 2) Comparative genomics of rearrangements involving genes associated with local adaptation

Theory shows that migration-selection balance favours the fixation of rearrangements that build clusters

of genes involved in local adaptation (Yeaman 2013, PNAS). Recent empirical work has shown that loci with signatures resembling local adaptation in the threespine stickleback tend to be clustered together (Jones et al. 2012, Nature; Miller et al. 2014, Genetics). To test whether these putative clusters have evolved through rearrangements, this project will undertake de novo assembly of the genomes of several close and distant relatives of the threespine stickleback. In combination with existing and emerging genomic resources, we will reconstruct the long-term patterns of genome rearrangement in this group and test hypotheses about the involvement of selection and local adaptation. This study has full funding for 7 years, and will employ a combination of Illumina short reads, PacBio long reads, and potentially some physical and linkage mapping, or other innovative methods. I also plan to undertake comparative genomic studies in other taxa where more genomes have already been assembled (Arabidopsis, Helianthus, Solanaceae, Cichlids, etc.).

Beyond these projects my interests tend to be quite broad, so if you have a cool idea and want to work with me, I'd love to hear about it!

yeaman@zoology.ubc.ca

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### UEastAnglia SexualSelectionNetworks

Responses to sexual environments modelled as neural networks. Norwich Research Park Doctoral Training Partnership PI: T Chapman (<https://www.uea.ac.uk/-biological-sciences/people/profile/tracey-chapman>) Co-Is: Tamas Dalmay, Irina Mohorianu.

The ability to respond appropriately to the environment (e.g. temperature, day length, presence of females or same-sex rivals) is crucially important. Therefore the detection of environmental cues, and integration of information from them, are vital. Recently, there has been much interest in modelling the underlying biological mechanisms responsible, using 'neural networks'. Our recent work suggests that the response of male fruitflies to conspecific mating rivals can be modelled via this type of network. The aim is to test this idea and identify the alternative pathways involved. This will be done via the analysis of RNA sequencing data of the transcriptomes of males with manipulated sensory systems.

<http://biodtp.norwichresearchpark.ac.uk/projects/>

[project-detail/project/88](#) Contact for more information: tracey.chapman@uea.ac.uk Application Deadline: 06/03/2015

“Tracey Chapman (BIO)”  
<Tracey.Chapman@uea.ac.uk>

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### UGlasgow EngineeringAdaptation

The engineering of adaptation: Exploring the genetic basis of biomechanics and function in an exemplar adaptive radiation

Project summary:

Adaptive radiations provide a fascinating framework for evolutionary investigations. In many cases such radiations are characterized by substantial variation in craniofacial anatomy which relates to ecological function. African cichlids provide what is considered by many to be the most dramatic example of an adaptive radiation, especially with regards to craniofacial variation where species have adopted an incredible degree of specialization. However, despite possessing such a wide range of phenotypes African cichlids can share a largely similar genetic background. This makes for highly tractable investigations into the genetic basis of craniofacial biomechanics and function. For this project we aim to leverage the wide range of craniofacial phenotypes available in African cichlids as well as their recently derived genomic resources. Specifically, we aim to determine 1) the genetic basis of adaptive craniofacial shape and bone structure, 2) verify candidate genes by testing their function, and 3) identify the mechanisms underlying jaw joint formation and its biomechanical properties. This project will take advantage of an interdisciplinary supervisory team which spans basic evolutionary biology, development, genetics, anatomy, and engineering. Therefore, this project will involve a broad range of training and interdisciplinary skills. We are seeking an enthusiastic student with knowledge in only some of these areas, and a willingness to learn from different fields. A prior degree in engineering is not necessary as this is a biologically driven project, although applications from a range of academic backgrounds is welcomed.

If this project is of interest please make all initial contact with Dr. Kevin Parsons (Kevin.Parsons@glasgow.ac.uk). <http://www.gla.ac.uk/researchinstitutes/bahcm/staff/-kevinparsons/> Stipend: pounds 13,863 per annum (2014/15 rate) Start date: 1 October 2015

Visit our website for more information: <http://www.gla.ac.uk/colleges/mvls/graduateschool/-researchopportunities/researchopportunities/-mvlseprcstudentships/> Applicant Instructions These are 3.5-year PhD studentships. The financial package will include a 3.5-year stipend, approved University of Glasgow fees, Research Training Support Grant (RTSG) and a conference allowance. Please read the details outlined below before commencing the online application process, which is available here: <http://www.gla.ac.uk/research/opportunities/howtoapplyforaresearchdegree/> Students will also participate in our outstanding skills training programme throughout their studies.

**Residence criteria** The MVLS/EPSRC grant provides funding for tuition fees and stipend for UK and \*EU nationals that meet all the required eligibility criteria. \*Note that EU nationals must be able to demonstrate that they have resided in the UK for three years prior to commencing the studentship. If not, EU nationals are still able to apply to the programme, but would be eligible to receive a 'fees only' award.

**How to Apply** You can apply here: <http://www.gla.ac.uk/research/opportunities/-howtoapplyforaresearchdegree/> Within the application, at the programme of study search field option, please select 'MVLS/EPSRC Studentship'.

As much as is possible please provide the following supporting documents during upload of application: - CV/Resume - Degree certificate - Language test (if relevant) - Passport - Personal statement - Reference 1 - Reference 2 - Transcript

Kevin.Parsons@glasgow.ac.uk

## UGreifswald 12 Adaptation

University of Greifswald, Germany

12 PhD positions: Research Training Group RESPONSE

Application deadline approaching: 17th January 2015

The Research Training Group "Biological responses to novel and changing environments - RESPONSE" (RTG 2010), funded by the Deutsche Forschungsgemeinschaft (DFG), invites applications for

12 Ph.D. positions.

The RTG is based at the University of Greifswald, Ger-

many ([www.uni-greifswald.de](http://www.uni-greifswald.de) [1]).

Starting date: April 1st 2015. Duration: 3 years. Salary: German salary scale (TV-L 13, 65%).

**Research Program**

The ability to respond to novel and changing environmental conditions, either by phenotypic plasticity, genetic adaptation, or range shifts, is pivotal to the longer-term survival of all organisms. Owing to increasing concerns about the consequences of human-induced global change, such responses have attracted increasing interest in recent years. RESPONSE focuses on the plastic and genetic capacities for in situ responses (cluster A) and on the factors limiting or facilitating dispersal to new habitats (cluster B). The RTG aims at deepening our understanding of the limits to population persistence, enabling more accurate predictions regarding the fate of populations under changing conditions. Our research program spans different levels of biological organization, ranging from molecular and physiological mechanisms to ecological population-level responses, and a wide variety of organisms including myxomycetes, plants (trees), and animals (snails, crustaceans, insects, spiders, bats). Please refer to [www.uni-greifswald.de/-RESPONSE](http://www.uni-greifswald.de/-RESPONSE) [2] for further information, especially on the available individual research (= Ph.D.) projects and specific requirements. Note that all projects involve field work at least to some extent.

**Teaching Concept**

A teaching program accompanies the interdisciplinary research strategy. It covers different scientific topics and techniques relevant to the RTG as well as soft skills relevant to career development, and includes summer schools, journal clubs, practical courses, lectures, and individualized educational as well as mentoring programs. Each Ph.D. project involves visiting stays at different laboratories, partly abroad. The participation in the teaching program is mandatory.

**Requirements**

We invite applications from highly motivated candidates with above-average qualifications, passion for and experience in research, and the willingness to actively participate in the RTG. Successful applicants will (1) hold a M.Sc. degree (or equivalent) in Biology or another relevant discipline, (2) have a solid background in ecology and evolution, (3) experience with methods and / or organisms relevant to the RTG, (4) an excellent command of the English language, which will be the official language of the RTG, and (5) will be motivated to join an interdisciplinary research training environment.

**Applications**

To apply please submit an application form, a CV including copies of all degrees, a motivation letter, and two letters of recommendation. Forms (application form, recommendation letter) are available at [www.uni-greifswald.de/RESPONSE](http://www.uni-greifswald.de/RESPONSE) [2]. The motivation letter should include your motivation to become a member of RESPONSE, your preferred projects (list three), and a short explanation for your project choice. Applicants should submit the above mentioned documents, except the recommendation letters, as PDF files attached to a single email to the speaker of the RTG, Prof.Dr. Klaus Fischer (klaus.fischer@uni-greifswald.de), before January, 17th 2015. Recommendation letters should be sent by the referees directly to klaus.fischer@uni-greifswald.de. The most promising candidates will be invited to Greifswald, and interviews will take place between February 16th and 19th, 2015. The University of Greifswald is an equal opportunity employer, and the RTG strongly encourages qualified disabled persons, women, and candidates with children to apply. Application expenses cannot be refunded by the state of Mecklenburg-Western Pomerania. The official version of the advertisement is published at the university's homepage.

Prof. Dr. Klaus Fischer e-mail: klaus.fischer@uni-greifswald.de

For any enquiries please contact Klaus Fischer via e-mail.

Links:

[1] <http://www.uni-greifswald.de/> [2] <http://www.uni-greifswald.de/RESPONSE> "kfischer@uni-greifswald.de" <kfischer@uni-greifswald.de>

## UHamburg BehaviouralEvolution

\*PhD position on "information use in an unpredictable environment - a case study on wild zebra finches"\*

We offer a PhD position on information use in the opportunistically breeding zebra finch, \**Taeniopygia guttata*\*. In a combination of field and lab experiments in Australia, we will address unresolved key issues in information ecology linked to unpredictable environmental conditions. We seek a motivated PhD student with a strong background in Behavioural Ecology, Field Ecology, Information Ecology and/or Experimental Ecology. Some experience with hormonal analyses is advantageous.

The 3-year position is funded by a grant of the German Science Foundation to Wiebke Schuett (PI) and Simon Griffith (Co-I). The PhD student will spend in total at least one year each in Germany (University of Hamburg) and Australia (Macquarie University & field). We also offer the PhD candidate the opportunity to apply for a PhD jointly awarded between the University of Hamburg and Macquarie University. Salary level is TV-L 13 (65%, ca. 1400-1600 EURO/m after deductions).

The full ad can be found on:

[http://www.uni-hamburg.de/uhh/stellenangebote/-wissenschaftliches-personal/Biologie\\_16-02-15.pdf](http://www.uni-hamburg.de/uhh/stellenangebote/-wissenschaftliches-personal/Biologie_16-02-15.pdf)

Please apply by 16.2.2015.

For further information please contact Wiebke Schuett (wiebke.schuett@uni-hamburg.de).

Dr. Wiebke Schuett (PhD) Zoological Institute University of Hamburg Martin-Luther-King-Platz 3 20146 Hamburg Germany [http://www.uni-hamburg.de/-biologie/BioZ/zis/vb/mitarbeiter/schuett\\_e.html](http://www.uni-hamburg.de/-biologie/BioZ/zis/vb/mitarbeiter/schuett_e.html)  
wiebkesch@googlemail.com

## UHelsinki EvolutionStressTolerance

PHD STUDENT POSITION IN ECOLOGY AND EVOLUTION OF STRESS TOLERANCE IN A BUTTERFLY METAPOPOPULATION

Applications are invited for a four-year PhD fellowship in the research group of Marjo Saastamoinen as part of the ERC funded META-STRESS project (Starting Grant scheme). The successful applicant will join the Centre of Excellence in Metapopulation Research at the University of Helsinki.

The PhD project aims to understand the life-history responses and underlying mechanisms that allow organisms to cope with environmental stress in the wild. The large metapopulation of the Glanville fritillary (*Melitaea cinxia*) butterfly gives a unique opportunity to study processes operating from genes within individuals all the way to metapopulation-level dynamics (> 20 years of data). The PhD project will focus on individual variation in stress tolerance within and among local populations and the role of local adaptation. In addition you will assess the impact of stress tolerance on other key-life-history traits. There is also potential to use recently developed genomic tools to identify mechanisms involved in stress tolerance.

In practice, you will carry out field work in the Åland Islands archipelago (SW Finland) and conduct experimental work in the laboratory and under semi natural field conditions. You are expected to present your findings in scientific meetings and workshops, as well as prepare publications for international scientific journals.

Motivated students with a MSc degree in ecology, evolutionary biology or molecular biology (or other related fields) are encouraged to apply. Prior expertise in experimental design, statistical analysis or laboratory work are a bonus but your most important assets are enthusiasm for research, motivation to learn new things, and ability to work independently while being an active member of a research team.

Please send your application to [biotiede-mrg@helsinki.fi](mailto:biotiede-mrg@helsinki.fi) by 16 February 2015 with title PhD META-STRESS. Attach a CV (with possible publications included), a copy of your transcript records (printout of the courses you've completed during your MSc), contact details of two references (e.g. MSc thesis supervisor), and a letter (MAX 1 page) with a description of your researcher interests and why you would be a suitable candidate for the project.

The salary will be based on level 2 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal performance. All standard pension benefits and occupational health care are provided for university employees.

The work is scheduled to start in the spring/early summer 2015. For more information, please contact Dr Marjo Saastamoinen ([marjo.saastamoinen@helsinki.fi](mailto:marjo.saastamoinen@helsinki.fi)) and visit the website at <http://www.mv.helsinki.fi/home/msaastam/index.html> For information on the University of Helsinki, please visit: <http://www.helsinki.fi/university/index.html> Dr Marjo Saastamoinen

Academy Research Fellow

Center-of-Excellence in Metapopulation Biology

Department of Biosciences

PO Box 65 (Viikinkaari 1)

FI-00014 University of Helsinki

FINLAND

tel. + 358 (0)50 448 4471

<http://www.mv.helsinki.fi/home/msaastam/> Marjo Saastamoinen <[marjo.saastamoinen@helsinki.fi](mailto:marjo.saastamoinen@helsinki.fi)>

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## UHull 3 Biodiversity

Dear Evoldir members,

I am pleased to announce that three fully-funded PhD studentships are available in the Evolutionary Biology Group at the University of Hull, UK, starting September 2015.

The studentships are as follows (please follow the links for more information or contact the first supervisors for informal enquiries):

1. Untangling molecular food webs to investigate the impact of invasive predators on whole communities and ecosystem services < <http://www2.hull.ac.uk/student/scholarships/science/untanglingmolecularfoodwebs.aspx> > Supervisors: Dr Lori Lawson Handley ([l.lawson-handley@hull.ac.uk](mailto:l.lawson-handley@hull.ac.uk)), Dr Bernd Haenfling, Dr Darren Evans (Hull), Dr Helen Roy (Centre for Ecology & Hydrology), Prof Neil Boonham (FERA)
2. Rapid biodiversity monitoring of freshwater pond diversity using environmental DNA: Supervisors: Developing state-of-the-art tools to inform wetland management < <http://www2.hull.ac.uk/student/scholarships/science/rapidbiodiversitymonitoring.aspx> > Dr Bernd Hänfling ([b.haenfling@hull.ac.uk](mailto:b.haenfling@hull.ac.uk)), Dr Lori Lawson Handley, Dr Phil Wheeler (Hull), Prof Neil Boonham (FERA)
3. Discovering and monitoring endangered Triops cancriformis populations in ephemeral ponds < <http://www2.hull.ac.uk/student/scholarships/scienceandengineering/-discoveringandmonitoringtriops.aspx> > Supervisors: Dr Africa Gómez ([a.gomez@hull.ac.uk](mailto:a.gomez@hull.ac.uk)), Dr Bernd Hänfling, (Hull) Dr Larry Griffin (Wildfowl & Wetlands Trust), Prof Neil Boonham (FERA)

Please note the closing date is \*\*\*2nd February\*\*\*, so please forward this advert to anyone you think might be interested or contact us and apply as soon as possible

Many thanks and best wishes for the new year

Lori

Dr Lori Lawson Handley School of Biological, Biomedical and Environmental Sciences University of Hull Cottingham Rd, Hull, HU6 7RX U.K.

Tel 0044 1482 462061

Email [l.lawson-handley@hull.ac.uk](mailto:l.lawson-handley@hull.ac.uk)

<http://www2.hull.ac.uk/science/biology/-research/evolutionary%20biology/-lori%20handleys%20research.aspx> Twitter: @Calvia14

L.Lawson-Handley@hull.ac.uk

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## UIdaho CoevolutionBiol

Ph.D. position in coevolutionary biology at the University of Idaho

The Nuismer and Joyce labs at the University of Idaho are actively recruiting a Ph.D. student interested in developing novel statistical approaches for estimating the strength of coevolutionary selection within natural populations. Our overall goal is to develop Bayesian statistical tools that allow key parameters of existing coevolutionary models to be estimated using widely available data drawn from studies of phenotype matching and local adaptation. Through collaboration with Dr. Butch Brodie (University of Virginia), opportunities exist for developing and testing these new statistical tools using data on the well-studied interactions between toxic newts and their garter snake predators. Substantial scope exists for student driven innovation and extension to other types of data.

Applicants with a strong background in mathematics, statistics, and computation are encouraged to apply. However, applications from students with a strong background in evolutionary biology or ecology who have a keen interest in learning to develop mathematical, statistical, and computational tools are also encouraged. Depending on the successful applicant's background and primary interests, graduate work will take place in the Department of Biology (<http://www.uidaho.edu/-sci/biology>), the Graduate Program in Bioinformatics and Computational Biology (<http://www.uidaho.edu/-cogs/bcb>), the Department of Mathematics (<http://www.uidaho.edu/sci/math>), or the Department of Statistics (<http://www.uidaho.edu/sci/stat>). We anticipate that funding will be primarily through a research assistantship, beginning in fall, 2015.

To apply, please send an email describing your background and interests to Dr. Scott Nuismer ([snuismer@uidaho.edu](mailto:snuismer@uidaho.edu)) or Dr. Paul Joyce ([joyce@uidaho.edu](mailto:joyce@uidaho.edu)).

[snuismer@uidaho.edu](mailto:snuismer@uidaho.edu)

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## UJerusalem Evolution microRNAs

A postdoc position (funded up to 4 years) and a PhD student position (funded up to 5 years) are available in the Moran lab at Department of Ecology, Evolution and Behavior at the Hebrew University of Jerusalem, Israel (HUJI). These positions will be funded by a new European Research Council (ERC) project aimed to shed new light on the evolution of post-transcriptional regulation by microRNAs. In our lab we use the sea anemone \**Nematostella vectensis*\* as a model and employ various biochemical, genetic, microscopic and computational approaches to answer our questions. The fellowships associated with the project are at the very high end of Israeli standards and the successful candidates will also receive funds for attending relevant international workshops and conferences.

The Hebrew University of Jerusalem (HUJI) is Israel's premier university. HUJI has been ranked among the top universities in the world in two comprehensive surveys conducted by The Times Higher Education Supplement of London and Shanghai University. The host lab is located at the Natural Sciences campus, where a wide range of available technical services and facilities enable the cutting-edge research in various fields of Life Sciences. Our department is highly international and the lab working language is English.

The suitable candidate should have experience in standard biochemical and molecular biology techniques. Having prior experience in microscopy and/or computational analysis of HiSeq data is an advantage.

More details about our research group can be found online at [yehumoran.com](http://yehumoran.com). Interested candidates are welcome to contact Yehu Moran ([yehu.moran@mail.huji.ac.il](mailto:yehu.moran@mail.huji.ac.il)). Please send a CV, list of publications and contact details of 2-3 referees.

Yehu Moran <[yehu.moran@mail.huji.ac.il](mailto:yehu.moran@mail.huji.ac.il)>

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## ULeeds 2 Genomics

Two separate PhD projects are available with my group in the School Biology, University of Leeds, UK, for UK and EU students.

1. Ecological Genomics of UK and European Bats. NERC-DTP funded project, closing date 2nd Feb 2015. More details here: <http://www.nercdtp.leeds.ac.uk/projects/index.php?id=178>
2. Emerging infectious diseases (flexible topic disease ecology/evolutionary genomics of disease vectors). University of Leeds 110 Anniversary Research Scholarships. Closing date 29th January 2015. More details here: <http://www.fbs.leeds.ac.uk/gradschool/keywords/documents/FBS110infoandprojects.pdf>

Dr Simon Goodman

Dr Simon Goodman School of Biology Manton Building University of Leeds Clarendon Way Leeds, LS2 9JT, UK

Tel: +44-(0)113-3432561, Fax: +44-(0)113-3432835 Email: [s.j.goodman@leeds.ac.uk](mailto:s.j.goodman@leeds.ac.uk) Skype: [simon.j.goodman](https://www.skype.com/user/simon.j.goodman) Twitter: @DrSimon\_Goodman

[S.J.Goodman@leeds.ac.uk](mailto:S.J.Goodman@leeds.ac.uk)

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## ULeicester HumanSTRDiversity

PhD studentship: Next-generation sequencing approaches to short-tandem repeat sequence variation: mutation processes, haplotype evolution and forensic application

A fully funded four-year BBSRC CASE PhD Studentship is available with Prof Mark Jobling and Dr Jon Wetton to use next-generation sequencing (NGS) to study the internal structure of human short-tandem repeats. These markers are universally used in forensic analysis, but genotyping considers only allele length, and not allele sequence. The next decade promises to bring the power of NGS to bear on forensic identification, yet little is known about what new opportunities and problems sequence data will bring. The project will address the following questions: i) What is the internal sequence variability of autosomal and Y-STRs

in human populations? ii) How are sequence variants (e.g. variant repeats, microdeletions) related to linked SNP variation? iii) What does the information from (i) and (ii) add to our understanding of microgeographic variation? iv) What can we learn about STR mutation processes from an appreciation of sequence variability? v) How can information from (iii) and (iv) be used in a forensic context?

Close collaboration with Key Forensic Services Ltd. (<http://www.keyforensic.co.uk>) is an essential part of the project, and the student will spend 3-6 months in their laboratories on the University of Warwick campus.

For further details and how to apply, see: <http://www.findaphd.com/search/ProjectDetails.aspx?PJID=1164> Prof Mark A. Jobling Wellcome Trust Senior Research Fellow in Basic Biomedical Science Department of Genetics Room G5, Adrian Building University of Leicester University Road Leicester LE1 7RH UK

tel.: +44 (0)116 252 3427 mob.: +44 (0)7955 882334 fax: +44 (0)116 252 3378 email: [maj4@le.ac.uk](mailto:maj4@le.ac.uk) web: <http://www2.le.ac.uk/departments/genetics/people/jobling> Mark Jobling <[maj4@leicester.ac.uk](mailto:maj4@leicester.ac.uk)>

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## ULiverpool HostParasiteEvol

PhD Studentship at the University of Liverpool, UK: The spatial ecology of host-parasite communities

Supervisors:

Profs Andy Fenton and Mike Begon (University of Liverpool)

Dr Amy Pedersen (University of Edinburgh)

Prof Owen Petchey (University of Zurich)

With on-going concerns about zoonotic diseases and increasing cases of emerging infectious diseases, it has never been more important to understand disease dynamics in natural populations. Parasites exist within hierarchies of biological organisation (infecting individual hosts, within populations, within communities, across landscapes). Infection therefore depends on multiple factors (parasite transmission mode, host characteristics, host location, environmental characteristics etc). Separating these factors is a major challenge. Metacommunity theory may provide the tools to understand how these factors interact to determine parasite community structure. To develop and test these approaches we need high resolution, spatially structured host and parasite

datasets, which are very rare.

We have 6 years' worth of longitudinal data of wild rodents and their parasites (nematodes, cestodes, protozoa, viruses, bacteria) at fine temporal scales (every 2-4 weeks) under spatially-hierarchical sampling (traps within grids within woodlands). These data provide a unique resource to explore the spatial ecology of parasites.

This studentship will explore how environmental and individual-level factors interact to determine infection risk and parasite community structure. The student will explore: (1) the extent to which parasite communities vary across space, (2) whether there are 'hotspots' of infection by different parasites, and (3) the roles of individual and environmental factors in driving infections. This work will primarily use our existing data, although the student could conduct their own experiments as needed.

This project will suit students with interests in community and/or disease ecology, and particularly those with strength in statistical analyses. The student will work with ecologists with considerable experience in natural disease systems, and will receive training in conceptual, quantitative and empirical aspects of host-parasite ecology.

The studentship is part of the NERC 'ACCE' Doctoral Training Partnership, and will be based at the University of Liverpool, where the student will be a member of the highly-active research groups of Professors Fenton and Begon, and part of a wide-ranging research environment, spanning the Universities of Liverpool, Edinburgh and Zurich.

This studentship is fully funded for UK residents, but fees only for EU and International citizens. For informal enquiries please contact Professor Andy Fenton (a.fenton@liverpool.ac.uk). Applicants should send a CV, cover letter and contact details of two academic referees to Mrs Linda Marsh (biolres@liverpool.ac.uk). Deadline: Sunday 11th Jan 2015.

Professor Andy Fenton Institute of Integrative Biology Biosciences Building Crown Street University of Liverpool Liverpool L69 7ZB Tel: 0151 795 4473 Fax: 0151 795 4408 <http://www.liv.ac.uk/integrative-biology/staff/andrew-fenton> "Fenton, Andy" <A.Fenton@liverpool.ac.uk>

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## UPotsdam Evolutionary Biology

Graduate position: UPotsdam\_Evolutionary\_Biology

A 3-year PhD position (TVEL 13/2) is available at the Unit of Evolutionary Biology/Systematic Zoology at the University of Potsdam, starting April 1st 2015.

The Unit of Evolutionary Biology/Systematic Biology has a strong focus on population genetic and speciation research, involving various taxonomic groups and a suite of molecular, morphological, and behavioural approaches (see <http://www.uni-potsdam.de/ibb/arbeitsgruppen/ordentliche-professuren/evolutionsbiologie-spez-zoologie.html> for recent work).

The successful applicant will work on the genomic basis of adaptation in one of the vertebrate models studied in the group. The project will have a strong bioinformatics component and may involve field work.

The position includes a teaching duty of 2 hours/week in Zoology/Evolutionary Biology for undergraduates.

Applicants must hold a university degree (Diplom or Master of Science in Biology, Bioinformatics, or a related discipline). Familiarity with modern molecular genetic techniques (PCR etc.), genomic data analysis, and/or multivariate statistics is preferable.

The University of Potsdam is an equal opportunity employer. If equally qualified, disabled applicants will be preferably considered. The University of Potsdam aims at increasing the number of female researchers and encourages qualified women to apply.

Potsdam is a beautiful city in close vicinity to the German capital of Berlin. Potsdam University takes an effort to assist its members in family-related issues and has repeatedly been awarded the total e-quality award.

Please send your application by email (preferably in a single pdf) before January 31st 2015 to: Prof. Dr. Ralph Tiedemann, University of Potsdam, Institute of Biochemistry and Biology, Evolutionary Biology/Systematic Zoology, Karl-Liebknecht-Str. 24-25, Haus 26, D-14476 Potsdam, Germany, Email: tiedeman@uni-potsdam.de

ljlal@uni-potsdam.de



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## UppsalaU 2 AmphibianEvolution

Two PhD positions in amphibian evolutionary ecology at Department of Ecology and Genetics, Evolutionary Biology Center, Uppsala University, Sweden from March 2015

**Position 1** The fungus *Batrachochytrium dendrobatidis* (Bd) causes the disease Chytridiomycosis and is believed to be one of the major causes for recent global declines of amphibians. Bd was first found in Sweden in 2011. This position is aimed at elucidating the relationship between Bd infection and fitness in natural populations of Swedish amphibians. The main objective is to determine the extent of Bd infection in Swedish amphibians and experimentally study how resistance differs among amphibian species and populations. The position is jointly funded by the research council Formas and Uppsala University.

**Position 2** The project focuses on local adaptation at different spatial scales, the role of a key candidate gene in adaptation and how different selective agents and trade-offs between these agents shape the phenotypic variation in natural populations using the moor frog *Rana arvalis* as study system. The PhD student will investigate the genetic basis of larval growth and development rates along a latitudinal gradient and in a network of local wetlands using a recently discovered candidate gene and genomic approaches, and estimate experimentally ecological tradeoffs associated high growth and development rates. The position is jointly funded by the Swedish Research Council and Uppsala University.

**Qualifications:** We are looking for bright and highly motivated individuals with MSc Degree within ecology, evolutionary biology or equivalent. Experience on molecular genetic and genomic techniques (especially in position 2) and amphibian ecology/evolutionary biology are assets. The ideal candidate will be able to work both independently and as part of a team. A high standard of spoken and written English is required. The projects are supervised by professors Anssi Laurila and Jacob Höglund. For further information please see

<http://www.ebc.uu.se/Research/IEG/zoeko/People/-Anssi.Laurila/> and <http://www.ebc.uu.se/Research/IEG/zoeko/People/Jacob.Hoglund/> or contact Anssi Laurila via email ([anssi.laurila@ebc.uu.se](mailto:anssi.laurila@ebc.uu.se)) for any informal inquiries.

Uppsala University (<http://www.uu.se>) is an international research university focused on the development of science and education. It has 41.000 students from all over the world, 6,500 employees and a turnover of SEK 5,900 million, creating an international and stimulating research environment. The Evolutionary Biology Centre (EBC, <http://www.ebc.uu.se/>) is one of the world's leading research institutions in evolutionary biology. The city of Uppsala is a vibrant university town with easy access to surrounding nature. It offers a high standard of living and is well connected to the Swedish capital Stockholm and Stockholm-Arlanda international airport.

**Application procedure:** The application should include a description of research interests and past experience, a CV, copy of degrees and official transcripts, a copy of the Master thesis, and other relevant documents. The application should also include contact information to two reference persons who can provide confidential letters of recommendation.

Rules governing Ph.D. candidates are set out in the Higher Education Ordinance Chapter 5, §1-7, and in the Uppsala University's rules and guidelines, at <http://regler.uu.se/>. Please submit your application no later than 31th of January 2015. UFV-PA 2014/3803. The link to apply can be found at:

<http://www.uu.se/en/about-uu/join-us/details/?positionId=3D49758>

Anssi Laurila Animal Ecology/ Department of Ecology and Genetics Evolutionary Biology Center Uppsala University Norbyvägen 18D 75236 Uppsala Sweden

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## UppsalaU 2 AmphibianEvolution 2

Apologies for double-posting but the link in the original ad sent last week appears broken. Please use this link to find the original ad <http://www.uu.se/en/about-uu/join-us/details/?positionIdI758> to find the original ad and the link for application.

Best wishes,

Anssi

Two PhD positions in amphibian evolutionary ecology at Department of Ecology and Genetics, Evolutionary Biology Center, Uppsala University, Sweden from March 2015

**Position 1** The fungus *Batrachochytrium dendrobatidis*

(Bd) causes the disease Chytridiomycosis and is believed to be one of the major causes for recent global declines of amphibians. Bd was first found in Sweden in 2011. This position is aimed at elucidating the relationship between Bd infection and fitness in natural populations of Swedish amphibians. The main objective is to determine the extent of Bd infection in Swedish amphibians and experimentally study how resistance differs among amphibian species and populations. The position is jointly funded by the research council Formas and Uppsala University.

**Position 2** The project focuses on local adaptation at different spatial scales, the role of a key candidate gene in adaptation and how different selective agents and trade-offs between these agents shape the phenotypic variation in natural populations using the moor frog *Rana arvalis* as study system. The PhD student will investigate the genetic basis of larval growth and development rates along a latitudinal gradient and in a network of local wetlands using a recently discovered candidate gene and genomic approaches, and estimate experimentally ecological tradeoffs associated high growth and development rates. The position is jointly funded by the Swedish Research Council and Uppsala University.

**Qualifications:** We are looking for bright and highly motivated individuals with MSc Degree within ecology, evolutionary biology or equivalent. Experience on molecular genetic and genomic techniques (especially in position 2) and amphibian ecology/evolutionary biology are assets. The ideal candidate will be able to work both independently and as part of a team. A high standard of spoken and written English is required. The projects are supervised by professors Anssi Laurila and Jacob Höglund. For further information please see

[http://www.ebc.uu.se/Research/IEG/zoeko/People/-Anssi\\_Laurila/](http://www.ebc.uu.se/Research/IEG/zoeko/People/-Anssi_Laurila/) and [http://www.ebc.uu.se/Research/IEG/zoeko/People/Jacob\\_Hoglund/](http://www.ebc.uu.se/Research/IEG/zoeko/People/Jacob_Hoglund/) or contact Anssi Laurila via email ([anssi.laurila@ebc.uu.se](mailto:anssi.laurila@ebc.uu.se)) for any informal inquiries.

Uppsala University (<http://www.uu.se>) is an international research university focused on the development of science and education. It has 41.000 students from all over the world, 6,500 employees and a turnover of SEK 5,900 million, creating an international and stimulating research environment. The Evolutionary Biology Centre (EBC, <http://www.ebc.uu.se/>) is one of the world's leading research institutions in evolutionary biology. The city of Uppsala is a vibrant university town with easy access to surrounding nature. It offers a high standard of living and is well connected to the Swedish capital Stockholm and Stockholm-Arlanda international airport.

**Application procedure:** The application should include a description of research interests and past experience, a CV, copy of degrees and official transcripts, a copy of the Master thesis, and other relevant documents. The application should also include contact information to two reference persons who can provide confidential letters of recommendation.

Rules governing Ph.D. candidates are set out in the Higher Education Ordinance Chapter 5, §1-7, and in the Uppsala University's rules and guidelines, at <http://regler.uu.se/>. Please submit your application no later than 31th of January 2015. UFV-PA 2014/3803. The link to apply can be found at:

<http://www.uu.se/en/about-uu/join-us/details/-?positionId=49758> Anssi Laurila

Animal Ecology/ Department of Ecology and Genetics  
Evolutionary Biology Center  
Uppsala University  
Norbyvägen 18D  
75236 Uppsala  
Sweden

[anssi.laurila@ebc.uu.se](mailto:anssi.laurila@ebc.uu.se)

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## USalford Coevolution

Two weeks left to apply for a funded PhD position on the coevolution of parasitic crustacean and their fish hosts. Please follow the online application procedure, here: <http://www.findaphd.com/search/ProjectDetails.aspx?PJID=60849&LID=1725>

Professor Stefano Mariani Chair in Conservation Genetics Associate Head, Research & Innovation | School of Environment & Life Sciences Room 316, Peel Building, University of Salford, Salford M5 4WT, UK t: +44 (0)161-295-6913 | m: +44 (0)7712-689-871 | [s.mariani@salford.ac.uk](mailto:s.mariani@salford.ac.uk) <http://www.salford.ac.uk/environment-life-sciences/els-academics/stefano-mariani> ResearchID: A-2964-2012; ORCID: <http://orcid.org/0000-0002-5329-0553> LABELFISH Atlantic Network: <http://www.labelfish.eu/> the new Stock Identification Methods book is out: <http://www.elsevier.com/books/stock-identification-methods/cadrin/978-0-12-397003-9> Mariani Stefano <[S.Mariani@salford.ac.uk](mailto:S.Mariani@salford.ac.uk)>

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## USheffield AvianGenomics

PhD Studentship: Genomics and genetic architecture in a wild bird

Supervisor: Jon Slate (University of Sheffield); collaborators: Ben Sheldon (Oxford), Marcel Visser (Netherlands Institute of Ecology), Martien Groenen (Wageningen).

This project is part of the recently funded Centre for Advanced Modelling (see below) at the University of Sheffield. The student will utilise a recently collected dataset of 600,000 SNP genetic markers, typed in approximately 2000 great tits, making it one of the largest genetic datasets for any natural population. The aim of the project is to understand the genetic architecture of quantitative traits in a population of great tits that has been the focus of a long-term individual-based study, running since 1947. One of the aims of the project will be to determine whether an individual's genome can predict its phenotype. So-called genomic prediction or genomic selection underpins modern animal and plant breeding, as well as personalised medicine, but it has never been attempted in the context of environmental or ecological research. The project builds on an ERC grant previously held by JS and will run alongside a recently funded NERC grant on genomic prediction. There will be opportunities for the student to collaborate with great tit ecologists in Oxford and with ecologists and genome biologists at NIOO-KNAW and Wageningen University in the Netherlands. The laboratory and phenotypic data are already collected so the project is risk-free in terms of data collection. The project is ideally suited to a mathematics, physics or computer science graduate, or to a biological sciences graduate with evidence of strong quantitative skills (e.g. MSc in genomics or bioinformatics related discipline). Enquiries to Jon Slate ([j.slate@sheffield.ac.uk](mailto:j.slate@sheffield.ac.uk)).

Centre for Advanced Biological Modelling

This PhD project is funded by Leverhulme Trust-Centre for Advanced Biological Modelling at the University of Sheffield.

The Centre for Advanced Biological Modelling (CABM) will harness cutting edge mathematical and computing skills to address major problems in biology. Biology at the University of Sheffield is defined by its strength in combining approaches across time-scales from ecological to evolutionary, and has been the subject of significant

recent investment. Exploiting this breadth of research excellence, the areas of focus for the CABM will extend our cutting edge research in basic biology by harnessing the latest mathematical and computational techniques. The recruitment process of the CABM will focus on attracting outstanding students from the physical and mathematical sciences, and training them to address leading biological problems. This multi-disciplinary initiative will transform our research excellence in organismal biology and fill a chronic training gap in the biology. Its legacy will be a cohort of research scientists at the cutting edge of biological modelling with the skills to tackle major societal problems.

Selection process: Short listing will take place as soon as possible after the closing date and the successful applicants will be notified promptly. Short listed applicants will be invited for an interview to take place at the University of Sheffield on the 27th February 2015. More details at <http://www.findaphd.com/-search/ProjectDetails.aspx?PJID=60931&LID=1381>  
Jon Slate <[j.slate@sheffield.ac.uk](mailto:j.slate@sheffield.ac.uk)>

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## USouthampton NHM London PlantAdaptation

Graduate position: U. Southampton/NHM London Adaptation (note the deadline for receipt of applications is 8th January)

Mark Chapman (Centre for Biological Sciences, University of Southampton) and Mark Carine (Department of Life Sciences, Natural History Museum) are looking for a PhD student to study how gene expression variation relates to plant adaptation.

Summary: With climate change likely to lead to major changes in the world's biota and to impact on our ability to grow crops, it is pertinent to understand how plants adapt to different ecological regimes, in particular those differing in temperature. A thorough investigation of groups of species which have adapted in parallel to differences in altitude would shed light on the genes and pathways that are involved in adaptation to temperature.

This project focuses on the Canary Islands flora, an ideal model for such a study since recent speciation in the flora has been governed in part by altitudinal (and thus temperature) shifts.

The project will characterize phylogenetic relationships

of endemic lineages in diverse taxa to identify altitudinally differentiated sister taxa. Divergence in gene expression between these taxon pairs will be characterised, and loci exhibiting a signature of divergent selection will be identified. By using study taxa drawn from diverse angiosperm families we can address the question: are parallel genetic changes responsible for evolutionary changes underlying temperature adaptation?

If you are interested in this studentship and would like more information (note the nationality requirements, funding situation and other requirements) please take a look at:

<http://noc.ac.uk/gsnocs/project/genomics-parallel-adaptation-temperature-divergent-niches> Best wishes,

Dr. Mark A. Chapman M.Chapman@soton.ac.uk +44 (0)2380 594396

Co-ordinator - Centre for Underutilised Crops [@CUCsoton](http://www.southampton.ac.uk/cuc/=0Atweet)

Centre for Biological Sciences University of Southampton Life Sciences Building 85 Highfield Campus Southampton SO17 1BJ

M.Chapman@soton.ac.uk

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## UToledo FishEvolution

Ph.D. Student Research Assistantship in Fish Genetics and Ecology Dept. Environmental Sciences and Lake Erie Center, University of Toledo Toledo, OH Closing Date: Feb. 1, 2015 for priority consideration, late applications accepted

Web Address: <http://www.utoledo.edu/nsm/lec/-research/glg/index.html> Description

PhD research assistantship for new project on Yellow Perch population genomics/genetics, Next-generation Sequencing, environmental DNA, kin selection, and chemical cues that may regulate homing. Ph.D. in Biology-Ecology Track through The Department of Environmental Sciences at the University of Toledo <http://www.utoledo.edu/nsm/envsciences/-grad/index.htm>. State of the art project in Dr. Carol Stepien's Great Lakes Genetics/Genomics Lab <http://www.utoledo.edu/nsm/lec/research/-glgl/index.html>, < <http://www.utoledo.edu/nsm/lec/research/glg/index.html,%20which> > which < <http://www.utoledo.edu/nsm/lec/research/glg/index.html,%20which> > is nationally and internationally

well-known, well-published, and well-funded, with excellent placement of graduate students as federal agency researchers, postdocs, and university professors. Project work will be at the University of Toledo's Lake Erie Center (<http://www.utoledo.edu/nsm/lec/>). Apply now to begin the Fall 2015 semester. Ok to start in summer 2015 too. RAship: \$23,000-\$25,000 annual stipend, tuition, general fees, and student medical insurance paid.

### Qualifications

Excellent, hard-working Ph.D. graduate student to begin fall or summer 2015 (get your application in now) for dissertation research on yellow perch population genetics and genomics, next-generation DNAsequencing, environmental DNA, and kin selection and chemical cues that may regulate homing. Accomplished in writing, PCR, statistics, and field and laboratory skills. Preference to MS degree in hand and publication(s) in molecular ecology, fisheries, population genetics, or a related field. Required: GPA 3.0+, GRE (verbal+quantitative) of 1100 (303 on the new GRE grading scale) and 4.5 analytical writing, respectively. Foreign students: minimum TOEFL of 250 (computer-based, or 600 paper-based) and 450 (150 on the new GRE grading scale) on the verbal GRE are required.

### How to Apply

Send CV, cover letter, unofficial transcripts, GRE scores, TOEFL if foreign applicant to Dr. Carol Stepien via [carol.stepien@utoledo.edu](mailto:carol.stepien@utoledo.edu). Must meet minimum scores above. Apply to PhD in Biology-Ecology track in Dept. Environmental Sciences: [http://www.utoledo.edu/-nsm/envsciences/grad/degreereq/phd\\_bio.html](http://www.utoledo.edu/-nsm/envsciences/grad/degreereq/phd_bio.html) 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.

Contact Dr. Carol Stepien University of Toledo Lake Erie Center and Dept. Environmental Sciences 6200 Bayshore Rd. Toledo OH 43616 Phone: 4195308362 Fax: 4195308399 [carol.stepien@utoledo.edu](mailto:carol.stepien@utoledo.edu)

[Katy.Klymus@utoledo.edu](mailto:Katy.Klymus@utoledo.edu)

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## UTurkuFinland SalmonPopDynamics

PhD Position, Finland: Population dynamics and evolutionary genetics of life history variation in Atlantic salmon

We are seeking a highly motivated PhD student who is enthusiastic about working in an inter-disciplinary environment. The studentship is a part of a research consortium that aims at integrating evolutionary genetics, ecological modelling and environmental sociology to understand the external drivers of life history changes in a heavily fished Atlantic salmon population complex and to advance sustainable use of these aquatic natural resources. This project has been recently funded as a part of the Finnish Academy Arctic Research program.

The Teno River, located in northernmost Europe, supports one of the largest and most biodiverse naturally reproducing stocks of Atlantic salmon in the world. The Teno salmon monitoring programme, that has been running for 40+ years and involves close co-operation between scientific research and local fishers, provides multiple sources of data for this project. In addition to long-term catch data, it includes an archive of over 100,000 scale samples, containing information on, for example, life history strategies and growth rates of the Teno salmon across four decades. These samples also provide a source of DNA for genetic monitoring and linking genotype and phenotype. Statistical inference in the project will focus on several particularly intensively monitored populations within the Teno population complex, and aim at broadening the understanding of the overall population dynamics of Teno salmon. Genomic research will focus on understanding the genetic basis of life history traits studied in the ecological modelling component e.g. age-at-maturity and repeat spawning.

The PhD student is expected to contribute both to the genomic and ecological data analyses, and therefore enthusiasm for, and experience with, population genetics and/or ecological modelling is desired. A strong background in mathematics, (Bayesian) statistics, bioinformatics or genomics is an advantage. Depending on the interests of the student, there are possibilities to work in the genetics lab and/or participate in fieldwork on the Teno River. Informal inquiries and applications (as a single pdf file) should be addressed to Prof. Craig Primmer ([craig.primmer@utu.fi](mailto:craig.primmer@utu.fi)). Applications should include a CV (with names and contact details of at least two referees), and a max. 2 page letter of motivation. Undergraduate students who are yet to graduate should also include a letter from a faculty member indicating an estimated graduation date. Review of applications will commence on Feb 28 with the preferred starting date being June 2015. The position is available until (and therefore expected graduation date is) the end of 2018. The starting salary is 2171 EUR per month.

The supervisors of the project are Craig Primmer, University of Turku, Finland (<http://users.utu.fi/primmer/>), Jaakko Erkinaro and Henni Pulkkinen, Natural Re-

sources Institute Finland ([www.luke.fi](http://www.luke.fi)). The student can be based at either of the supervisors departments in Turku or Oulu, but will be required to spend extended periods in both locations.

Relevant publications on the research topic Johnston et al. (2014) Genome-wide SNP analysis reveals a genetic basis for sea-age variation in a wild population of Atlantic salmon (*Salmo salar*). *Molecular Ecology* 23: 3452-3468 Kuikka et al. (2014) Experiences in Bayesian inference in Baltic salmon management. *Statistical Science* 29: 42-49. Niemelä et al.. (2006). Temporal variation in abundance, return rate and life histories of previously spawned Atlantic salmon in a large subarctic river. *Journal of Fish Biology* 68: 1222-1240.

– Craig Primmer, Academy Professor Division of Genetics and Physiology Department of Biology, University of Turku, FINLAND

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[craig.primmer@utu.fi](mailto:craig.primmer@utu.fi)

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## Western Washington University Evolutionary Biology

The Biology Department at Western Washington University has openings for graduate students starting Fall 2015. Faculty members in the department offer a wide range of expertise, from molecular biology to ecology. Graduate students are eligible for teaching assistantships, which fund the majority of tuition and provide a stipend of \$12,116 per year. WWU is located in Bellingham, WA, a coastal city north of Seattle at the base of Mt. Baker in the northwestern part of the state.

Potential advisors

Marion Brodhagen: Microbiology, molecular biology, and chemical ecology. Our lab studies the plant pathogenic fungus *Aspergillus* and aflatoxin, a potent toxin produced by this fungus. Our current projects involve the ability of certain plant secondary metabolites to stop growth and/or toxin production by *Aspergillus*. Future research directions will include investigations of the molecular mechanisms by which these

plant compounds alter fungal metabolism. We also are interested in the role of *Aspergillus* in colonization of plastics labeled biodegradable, in agricultural settings. *Aspergillus* is a key colonizer of such plastics but its ability to break down polymers is unclear, as is the extent of toxin formation during plastic colonization.

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

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

Ben Miner: Students in my laboratory focus on how marine organisms alter their morphology and behavior in response to different environmental conditions, typically biotic conditions. Current projects in my lab include research on wasting disease in sea stars, predator-induced hatching plasticity in marine animals, context-dependent inducible offenses and defenses in marine organisms.

Craig Moyer: My interests are marine microbiology and geomicrobiology focusing on molecular approaches for exploring microbial diversity, community structure and ecological interactions. Presently, my lab and I are focused on the study of iron-oxidizing Zetaproteobacteria acting as the ecosystem engineers in microbial mats found at strong redox boundaries, including seep,

spring and vent habitats. We are also examining the evolutionary divergence of surface and deep subsurface Zetaproteobacteria in hydrothermal systems.

Merrill Peterson: Ecology and Evolution of Insects. The primary focus of our lab is on insect diversification and diversity. Potential graduate student projects include: 1) experimental investigation of the mechanistic basis of sperm precedence in hybridizing *Chrysochus* beetles, 2) analyses of the factors influencing insect species richness in rapidly-declining natural habitats in the region (e.g., lowland prairies, coastal dunes), and 3) using a database of the regions moth collections to document community-wide responses to climate change.

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

Dietmar Schwarz: Ecological and Evolutionary Genetics and Genomics, Evolutionary Ecology. Schwarz's lab offers opportunities to study speciation, hybridization, and adaptation in host specific insects (apple maggot flies and relatives) on a USDA supported project. Students may also have the opportunity to collaborate with Alejandro Acevedo-Gutierrez on non-invasive molecular studies of seal foraging ecology.

Anu Singh-Cundy: Plant Physiology. We study plant reproduction at the physiological, cellular, and molecular levels. Current projects are focused on understanding the role of HD-AGPs, which are proteins that promote pollen tube growth, in members of the Solanaceae and also in *Arabidopsis*.

More information can be found at: [http://www.biol.wvu.edu/biology/gradprog\\_brochure.shtml](http://www.biol.wvu.edu/biology/gradprog_brochure.shtml) or by contacting Dr. Ben Miner, Graduate Program Advisor, at benjamin.miner at wvu.edu

Benjamin Miner <Benjamin.Miner@wvu.edu>

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## Jobs

23andMe Computational Biologist ..... 63	RBG Kew 29 Science Positions ..... 76
AarhusU Bioinformatics ..... 64	RBG Kew ManyPositions Conservation ..... 76
ArizonaStateU Scientist or Postdoc SequenceAnalysis 64	RoyalOntarioMuseum Toronto Ornithologist ..... 77
CentralMichiganU UndergradSummerPosition ..... 65	StockholmU EvolutionaryZoology ..... 78
DukeU FieldAssistant PlantEvolution ..... 66	TempleU Evolution Comp Sci ..... 78
EasternKentuckyU CommunityEcologist ..... 66	TempleU Phylogenomics Phylomedicine ..... 79
Germany 2 FieldAssistants BehavEvol ..... 67	UAlabama Staff ComputationalEvolution ..... 79
GoetheU Frankfurt Bioinformatics ..... 67	UCalgary Bioinformatics ..... 80
INRA France 30 EvolutionaryBiol ..... 68	UCambridge 2 EvolutionaryGenetics ..... 81
KentStateU PlantEvolution ..... 68	UMainz EvolutionaryGenomics ..... 82
MichiganStateU MuseumDirector ..... 69	UMissouri Columbia BioinformaticsCompBiol ..... 83
Minnesota SummerResearch PlantEvolution ..... 70	UMontana ResAssist AlgalEvolution ..... 84
MortonArboretum DirectorTreeScience ..... 70	UNewMexico FieldLabTech PlantAnimalInteractions 84
MortonArboretum Illinois TreeConservation ..... 72	UOtago 2 EvolutionaryEcol ..... 85
NorthCarolinaMuseum CrustaceanTechnician ..... 72	USvalbard SpeciesAdaptation ..... 85
NSF Virginia SystematicsBiodiversityDirector ..... 73	UWashington MarineConservation ..... 86
Okinawa ComputingTech BiodiversityEvolution ... 74	Vienna 2 FieldAssist AvianBehaviour ..... 86
OmahaZoo ResAssist Bioinformatics ..... 75	WestChesterU PlantMolecularGeneticist ..... 87
Ottawa InvertebrateCurator ..... 76	

### 23andMe Computational Biologist

Computational Biologist - Research & Development  
23andMe Mountain View, CA, United States

Do you wish that your work had a more direct impact on people? Are you excited about the potential of human genetics to make a real difference in the world? At 23andMe, we believe that genetics is on the cusp of huge advances, and that our unique database of hundreds of thousands of genotypes and almost two hundred million phenotype data points gives us an incredible opportunity to advance not only biomedical research, but our understanding of ourselves.

We are looking for a colleague with extensive training and experience in computational biology to join our highly productive, world-class research team. This person will be involved in the analysis of human genetic data and the development of product features that depend on a mix of computational skills, statistical knowledge, creativity, and biological insight. The scope and breadth of our vision means that most of the necessary techniques have yet to be developed anywhere in the world.

We are looking for someone excited to work with our Product Managers in a cross-functional collaboration

to define and design features that help 23andMe deliver a quality experience to our customers. This includes improving existing ancestry features and tools, as well as developing and expanding in novel directions. This person is also expected to participate in the communication and public relations efforts of the company, including giving scientific talks, presenting at genealogy conferences, and disseminating research findings to a non-scientific audience.

#### QUALIFICATIONS:

- PhD in Computational Biology or related field (eg, Genetics, Computer Science, Engineering, Physics, Math, Bioinformatics) - Strong bioinformatics and biostatistics background - Background in algorithm development - Proficiency with scripting languages (eg, Python, R, bash) - Enthusiasm for working in a highly collaborative environment

#### ALSO VALUABLE:

- Evolutionary or population genetics research experience
- Demonstrated record of developing and distributing tools for the analysis and visualization of genomics data
- Experience with C/C++

Experience mentoring other scientists and familiarity with epidemiological principles are highly desirable.

Apply online: [23andme.com/careers/ob790fwb/](http://23andme.com/careers/ob790fwb/)

ABOUT US

23andMe is the leading personal genetics company. We are dedicated to helping individuals understand their own genetic information through DNA analysis technologies and web-based interactive tools. Our mission is to personalize health care by making and supporting meaningful discoveries through genetic research. Combining web development, computer science, genetics, social media, and informatics, 23andMe is at the forefront of a new era in personal genetics.

kbryc@23andme.com

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## AarhusU Bioinformatics

Associate professor in bioinformatics (ID 705456)

A position as associate professor in bioinformatics is available starting September 1, 2015 at the Bioinformatics Research Center (BiRC), Aarhus University, Denmark.

BiRC is an interdisciplinary research center that employs about 40 researchers and PhD students. The research at BiRC spans major areas of bioinformatics, and BiRC is involved in teaching and supervision of students on all levels from BSc to PhD.

The successful candidate is expected to establish his or her own research group and profile, participate actively in collaborations with other researchers at BiRC and Aarhus University, and contribute to teaching and supervision of students.

Applicants are expected to have research experience from several years as assistant professor or similar. They must document a strong record of original research and have teaching experience at undergraduate/graduate level. Applicants within all areas of bioinformatics are welcome.

For more information please contact the director of BiRC, Christian Nørgaard Storm Pedersen, e-mail [cstorm@birc.au.dk](mailto:cstorm@birc.au.dk), phone +45 8715 5559.

For information about BiRC in general, see <http://www.birc.au.dk>. Formalities and salary range

Science and Technology refers to the Ministerial Order on the Appointment of Academic Staff at Danish Universities under the Danish Ministry of Science, Technology and Innovation. The application must be in English and include a curriculum vitae, degree certificate, a complete list of publications, a statement of future research plans and information about research activities,

teaching portfolio and verified information on previous teaching experience (if any). Guidelines for applicants can be found here.

Appointment shall be in accordance with the collective labour agreement between the Danish Ministry of Finance and the Danish Confederation of Professional Associations. Further information on qualification requirements and job content may be found in the Memorandum on Job Structure for Academic Staff at Danish Universities.

Salary depends on seniority as agreed between the Danish Ministry of Finance and the Confederation of Professional Associations.

Deadline

All applications must be made online and received by: 01.03.2015. Use the following link [http://birc.au.dk/fileadmin/www.birc.au.dk/-Associate\\_professor\\_in\\_bioinformatics.705456.pdf](http://birc.au.dk/fileadmin/www.birc.au.dk/-Associate_professor_in_bioinformatics.705456.pdf)

Mikkel H. Schierup Bioinformatics Research Center, Aarhus University, CF Mollers Alle Building 1110, 8000 Aarhus C Denmark Ph: +45 8715 6535 Email: [mheide@birc.au.dk](mailto:mheide@birc.au.dk) <http://www.birc.au.dk/~mheide> Mikkel Heide Schierup <[mheide@birc.au.dk](mailto:mheide@birc.au.dk)>

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## ArizonaStateU Scientist or Postdoc SequenceAnalysis

The Biodesign Institute at Arizona State University and the Center for Evolution and Cancer is searching for a Staff Scientist or Postdoctoral Research Associate to perform analysis of high throughput sequencing data on multi-region samples to measure genetic diversity within breast cancers, AML, and potentially other types of cancer. They will be responsible for setting up and maintaining a state-of-the art pipeline for high throughput sequencing data, as well as the development of new algorithms to mine that data.

The Center for Evolution and Cancer was the first of its kind to apply evolutionary biology to cancer biology both at the cell level, studying the evolutionary dynamics of carcinogenesis and therapeutic resistance, and at the organismal level, studying the evolution of cancer suppression in whales, elephants and other species. Scholars will be part of a highly interdisciplinary research team led by Dr. Carlo Maley and also be part of a larger community of interdisciplinary researchers at Arizona State University in the Center for Evolution and



Medicine and the Centre for Evolution and Cancer at the Institute for Cancer Research in London, bringing together evolutionary biologists, ecologists, computational biologists, mathematical modelers, cancer biologists and oncologists to make fundamental discoveries in understanding cancer and improving cancer prevention and management.

Interactions among faculty, Postdocs and students across the Institute and the University are central to a variety of ongoing research and educational programs. These interactions allow our Postdoctoral Research Associates to develop their expertise in research and build towards an independent research program. Alternatively, this position could develop into a longterm collaboration as a staff scientist in the Maley lab. Faculty, Postdocs and students are actively involved with a number of other centers, institutes, and research groups on campus that promote transdisciplinary approaches to issues of local and national significance, affording outstanding research and training experiences that extend beyond traditional disciplinary boundaries. The Biodesign Institute is a research hub that makes an important contribution to the advancement of ASU as a leader of knowledge generation and utilization.

#### Qualifications:

Ph.D. or extensive expertise in computational biology, bioinformatics, systems biology, biostatistics, or related field. The ideal candidate would have expertise in both evolutionary biology and high throughput sequence analysis of neoplasms. Background in single cell sequencing and/or the human microbiota would be favored. Relevant publications in high quality peer review journals is desired.

To apply, please submit to [maley@asu.edu](mailto:maley@asu.edu) as a single pdf document the following materials: 1) a cover letter specifying relevant qualifications and training, 2) curriculum vitae, 3) statement of current research interests and expertise (2 page maximum), 4) two letters of reference, and 5) one peer-reviewed publication. Please include 'Application for Postdoc- Sequencing' in the email subject line. Initial review of applications will begin on February 1, 2015; if not filled, review will continue every week thereafter until the search is closed. A background check is required for employment.

Arizona State University is a new model for American higher education, an unprecedented combination of academic excellence, energy and broad access. This New American University is a single, unified institution comprising four differentiated campuses positively impacting the economic, social, cultural and environmental health of the communities it serves. Its research is inspired by real world application blurring the boundaries that

traditionally separate academic disciplines. ASU serves more than 80,000 students in metropolitan Phoenix, Arizona, the nation's fifth largest city. ASU champions intellectual and cultural diversity, and welcomes students from all fifty states and more than one hundred nations across the globe.

Arizona State University is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will be considered without regard to race, color, sex, religion, national origin, disability, protected veteran status, or any other basis protected by law.

– Carlo C. Maley, Ph.D. Associate Professor Director, Center for Evolution and Cancer at UCSF School of Life Sciences Arizona State University

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

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## CentralMichiganU UndergradSummerPosition

Central Michigan University is seeking undergraduate students to participate in a 10-week research experience at its Biological Station (CMUBS) on Beaver Island, Michigan. This program will provide funding for 5-7 undergraduates to work with CMU faculty on research projects related to the chemical, physical and biological aspects of the Lake Michigan nearshore shunt and its influence on nearshore-offshore coupling. Students will live and work on Beaver Island from June 1 V August 7, 2015, receiving a \$4,000 stipend, together with free room and board and up to \$500 for travel to Beaver Island and the CMU Biological Station. More information on the program and the online application are available at: [https://www.cmich.edu/colleges/cst/cmubs/students/summer\\_research/Pages/default.aspx](https://www.cmich.edu/colleges/cst/cmubs/students/summer_research/Pages/default.aspx). Applications, along with supporting materials, are due by Friday, February 27, 2015, with the final selection of participants expected by March 27, 2015.

Questions can be directed to Jessica Lapp, coordinator of the Institute for Great Lakes Research, via email to [jessica.lapp@cmich.edu](mailto:jessica.lapp@cmich.edu) or by phone to 989-774-4401.

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Dr. Andrew R. Mahon, Ph.D. Assistant Professor Department of Biology, Institute for Great Lakes Research Brooks Hall 188 Central Michigan University Mt. Pleasant, MI 48859 USA

Lab Website: <http://people.cst.cmich.edu/mahon2a>

Now on Twitter @CMU\_Antarctica

The Mahon Lab in Antarctica 2013 Blog: <http://-cst.cmich.edu/antarctica> Phone: Office: (989) 774-1177 Lab: (989) 774-1187

email: mahon2a@cmich.edu

Office: Brooks Hall 190 Lab: Brooks Hall 214

“Mahon, Andrew R” <mahon2a@cmich.edu>

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### DukeU FieldAssistant PlantEvolution

The Mitchell-Olds lab at Duke University seeks a highly motivated, detail-oriented assistant for field research in the northern Rocky Mountains, summer 2015. We are studying *Boechera*, a perennial herb that offers genetic tractability and ecological context. Current field experiments focus on questions related to local adaptation, plant defense against herbivory, and breeding systems.

Our research sites are located in east-central Idaho. Base camp is a set of trailers located near the beautiful town of Salmon. Trailers include heat, hot water, a landline, and wireless internet access. Travel distances between sites are long, which necessitates many hours in the car. Our team usually returns to the trailers to sleep but applicants should be familiar with (and enjoy!) camping for the times when this is not feasible. Weather conditions in the Rockies can be severe, and assistants should expect to work in snow and rain as well as 90 degree temperatures. Regular (approximately monthly) trips are made to Missoula, Montana for groceries and other supplies.

Successful applicants are expected to assist in data collection and data entry, plant care, transplanting, seed collection, and driving research vehicles. Applicants must be able to stoop/kneel for extended periods of time; hike up to 1 mile while carrying heavy loads; hike up and down steep hills; and dig or dibble holes in hard ground. The work can be physically demanding and tiring, and the research team usually collects data 5-6 days per week. A good sense of humor and a positive attitude are necessities!

Qualifications: 1) some undergraduate education in biology, ecology, or related field, or equivalent experience; 2) experience camping and working outdoors and/or previous field research experience; 3) ability to perform repetitive tasks with a cheerful attitude and with atten-

tion to detail; 4) willingness to live and work in close proximity with other researchers in a trailer; 5) a current driver's license. Previous experience working with plants is preferable but not required. Transportation, room with internet access, and salary will be provided. Applicants must be available throughout the field season from approximately June 1st through mid-August, but exact start and end dates are flexible.

The deadline for applications is February 27th, 2015. Interested applicants should submit: 1) a short cover letter describing their qualifications as well as future academic and professional goals; 2) a résumé outlining previous work experience, relevant courses (completed or in progress), extracurricular activities; and 3) contact information of two character references.

Email to:

Rose Keith, rak24@duke.edu Program in Genetics and Genomics, Duke University

rose.keith@duke.edu

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### EasternKentuckyU CommunityEcologist

We are hoping to attract Community Ecologists of all sorts. Including those that may be interested in phylogenetic community ecology or other aspects of evolution and community ecology.

-Brad

Community Ecologist Position

The Department of Biological Sciences at Eastern Kentucky University is accepting applications for a Community Ecologist at the rank of Assistant Professor. This is a 9-month, tenure-track position to begin August 15, 2014. Teaching responsibilities will include courses in the department's undergraduate biology and graduate degree (MS) programs and participation in introductory non-majors courses. Primary courses to be taught include the introductory course in ecology and evolution and other courses within the candidate's areas of expertise. The successful candidate will be expected to establish an active research program in area of specialty that includes mentoring undergraduate and master's level students. Requirements include a Ph.D. from a regionally accredited or internationally recognized institution. Candidates must have a strong record of research accomplishments and must provide evidence of

excellent teaching and communication skills. Review of applications will begin March 2 and will continue until position is filled. All interested applicants must apply via [jobs.eku.edu](http://jobs.eku.edu) (search requisition number 0616576). See also: <http://biology.eku.edu/insideloook/community-ecologist-position> . -Brad

Brad R. Ruhfel Assistant Professor & Curator Dept. Biological Sciences Eastern Kentucky University <http://people.eku.edu/ruhfelb> Brad Ruhfel <Brad.Ruhfel@eku.edu>

arriving in Seewiesen. Applicants should also be aware that Lyme disease (carried by ticks) is prevalent in the area and should inform themselves about this disease beforehand.

Applications: Review of the applications will begin February and continue until the position is filled. To apply, please send (1) a statement of relevant experience, (2) a short resume or CV, and (3) contact information for two references to Dr. Petri Niemelä (eMail: [niemela@biologie.uni-muenchen.de](mailto:niemela@biologie.uni-muenchen.de)).

“Niemela, Petri” <[niemela@biologie.uni-muenchen.de](mailto:niemela@biologie.uni-muenchen.de)>

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## Germany 2 FieldAssistants BehavEvol

### EXPERIENCED FIELD ASSISTANT

Needed in full time for Field Cricket Project at the Ludwig Maximilians University of Munich (LMU) & Max Planck Institute for Ornithology.

Websites: <http://www.behavioural-ecology.bio.lmu.de/people/postdocs/niemela/index.html> <https://www.orn.mpg.de/159079/Research-Group-Dingemans>

Location: Munich (LMU) and Seewiesen, Bayern, Germany.

Job description: The field assistants will help to collect life-history data on Field Crickets (*Gryllus campestris*) in the wild from end of March to the end of June 2015. The research focuses primarily on identifying how the social environment (i.e. other individuals) generate and maintain individual differences in behavior and behavioral plasticity. Research is also concentrated on identifying how environmental conditions affect the expression of behavioral variation. Assistants will work closely with an international team consisting of one post-doc, two field assistants and various students. The research project is intense and will have typically only 1 day off per week. Duties include behavioral observations, cricket handling (marking, measuring), data entry and data management.

Qualifications/Experience: Candidates should have a BSc in Biology or a related field. Candidates must have experience with handling small insects and working as part of a research group. Ideal candidates are highly motivated, well organized and able to work independently, while at the same time able to function well in a group.

A small financial compensation and accommodation will be provided. Accepted assistants should be vaccinated against Tick Borne Encephalitis (TBE or FSME) before

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## GoetheU Frankfurt Bioinformatics

Evolutionary Bioinformatics A position in evolutionary bioinformatics is available in the lab of Prof. Imke Schmitt at the Senckenberg Biodiversity and Climate Research Centre and Goethe University Frankfurt. The successful candidate will support ongoing projects on the evolution and adaptation of lichen-forming fungi and fungal communities by assisting with next generation sequencing data analysis. Depending on the candidate's preferences, he/she can also develop his/her own projects. We are looking for applicants with a Bachelor (or similar degree) in biology or computational biology, and expertise in de novo genome assembly, genome annotation, or metabarcoding. Experiences with python, perl, bash, or R are necessary; knowledge of unix, parallelization on clusters and massive RAM computers is advantageous. Additional tasks will be supporting the lab members in computer administration, data archiving, and data organization. The ideal candidate works well in a team, is highly motivated to work independently, communicates well, and speaks fluent English. My lab and the entire institute provide a very supportive atmosphere. The broader research environment at Senckenberg and Goethe University offers chances for collaboration with experts in fields ranging from molecular ecology and evolution, phylogenetics, to macroecology and climate change biology (modeling and statistics). Attractive computing infrastructure is available (high-RAM computers, clouds, and clusters). Frankfurt, a vibrant city in the center of Germany, provides ample cultural and recreational opportunities and excellent infrastructure for travel. Salary will be TV-H E11, according to the German public service pay scale. We offer full benefits, and training opportunities. The position is available from April 1st 2015, with a flexible start date. The initial contract will be for two

years, but it can be extended indefinitely. To apply, please send a cover letter detailing research interests and experience, a C.V., a copy of your bachelor certificate, and a list of two professional references. Please email your application to Prof. Dr. Katrin Böhning-Gaese, c/o Senckenberg Gesellschaft für Naturforschung, Senckenberganlage 25, 60325 Frankfurt am Main, recruiting@senckenberg.de, indicating reference number #8.2 before February 28.2015. Informal inquiries to Imke Schmitt (imke.schmitt@senckenberg.de), before the application are welcome.

Dr. Imke Schmitt Goethe University Frankfurt and Biodiversity and Climate Research Centre BiK-F Senckenberganlage 25 60325 Frankfurt am Main Germany

Tel.: +49 6975421855 email: imke.schmitt@senckenberg.de website: [www.bik-f.de/root/index.php?page\\_idC4](http://www.bik-f.de/root/index.php?page_idC4) office: Mertonstr. 17-21, Jügelhaus 421C

Imke Schmitt <Imke.Schmitt@senckenberg.de>

## INRA France 30 EvolutionaryBiol

Ranked the number one agricultural institute in Europe and number two in the world, INRA (National Institute for Agricultural Research - France) carries out mission-oriented research for high-quality and healthy foods, competitive and sustainable agriculture and a preserved and valorised environment.

Every year, INRA seeks researchers from all disciplines to reinforce laboratory and fieldwork teams. Researchers will be heavily involved in scientific networks and tackle environmental, economic and social issues. They are expected to strive for excellence and come up with useful, concrete applications for the real world. Individual research projects will go hand in hand with group efforts in a bid to further knowledge and innovation, in order to produce sustainably, preserve the environment, and improve human nutrition.

INRA is recruiting 30 Research Scientists (PhD or equivalent) through open competitions and offering permanent positions.

Positions are open in a wide range of scientific disciplines such as animal quantitative genetics, quantitative genetics and plant development, agrifood sciences and techniques, metabolism and physiology, genetic mechanisms of adaptation, physico-chemistry of interfaces and biological processes for the environment, functional ecol-

ogy and modelling, evolutionary ecology and modelling, ecology, genetics, pathogens, veterinary and agrifood sciences (microbiology, molecular protozoology and immunology), applied mathematics and informatics, compromise and uncertainty in the evaluation and management of ecosystem services, economics and many more.

Applications are available until to March 2, 2015.

All useful information to apply is available on: [http://jobs.inra.fr/eng/offers/emploi\\_perm/open-competitions/cr2/?campagne=23129&intitule=-open+competitions&concours=24348](http://jobs.inra.fr/eng/offers/emploi_perm/open-competitions/cr2/?campagne=23129&intitule=-open+competitions&concours=24348) For further details: [concours.chercheurs@paris.inra.fr](mailto:concours.chercheurs@paris.inra.fr)

[INRA] < <http://www.inra.fr/> >

Corinne NICOLAS

Assistante RH en charge de la mobilité, des études et de la communication de recrutement

[corinne.nicolas@paris.inra.fr](mailto:corinne.nicolas@paris.inra.fr)

DRH - Service Recrutement et Mobilité

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147 rue de l'Université

75 338 Paris Cedex 07

France

[www.inra.fr](http://www.inra.fr) Corinne Nicolas  
<Corinne.Nicolas@paris.inra.fr>

## KentStateU PlantEvolution

ART & MARGARET HERRICK ENDOWED PROFESSORSHIP IN PLANT BIOLOGY

The Department of Biological Sciences at Kent State University invites applications and nominations for the Herrick Endowed Professorship of Plant Biology. The position is open rank; we encourage applications from highly successful individuals who are currently Assistant, Associate or Full Professors (or at equivalent rank at non-academic institutions).

The recipient of the Herrick Endowed Professorship is expected to contribute to research, education, and graduate training within the Ecology and Evolutionary Biology (EEB) program. Applicants working in terrestrial plant ecology or plant evolutionary biology

are particularly encouraged to apply. Candidates must have a Ph.D. or an equivalent degree and must demonstrate substantial research accomplishments, including but not limited to an established record of publication, sustained and substantial extramural research funding, and demonstrated success in training and mentoring.

The position includes significant on-going research support from the Herrick endowment, and a nationally competitive start-up package.

Kent State University ([www.kent.edu](http://www.kent.edu)), the second largest university in Ohio, is a state-supported, doctoral degree granting institution ranked as 'high research' by the Carnegie Foundation. Kent State's eight campus system has a total enrollment of nearly 42,000 students. The Kent campus population consists of 22,000 undergraduates and 5,000 graduate students and includes individuals from all 50 states and over 100 countries. The city of Kent combines the eclectic atmosphere of a small midwest college town with easy access to major metropolitan centers, including Cleveland, Akron, Columbus, and Pittsburgh.

The Department of Biological Sciences ([www.kent.edu/-biology](http://www.kent.edu/-biology)) is the largest in the College of Arts and Sciences, with over 80 MS and PhD students, approx. 1100 undergraduate majors across a broad spectrum of degree programs (including Botany, Ecology, and Conservation), and 41 faculty on the Kent campus. Facilities and resources include an active herbarium, plant conservatory, an interdisciplinary Center for Ecology and Resource Sustainability (CENRS), and 18 managed natural areas available for research and teaching. The Department has formal affiliations or active collaborations with non-academic organizations across northeast Ohio, including: the Holden Arboretum, the Cleveland Botanical Garden, Cuyahoga Valley National Park, Cleveland Metroparks, Cleveland Museum of Natural History, and the Nature Conservancy of Ohio. International opportunities for teaching, training, and research are supported by membership in OTS, and a formal agreement with the University of Costa Rica.

Application materials, nominations, and inquiries should be submitted electronically to [plantbiology-chair@kent.edu](mailto:plantbiology-chair@kent.edu). To apply, please submit:

- (1) a letter of interest in the position
- (2) a curriculum vita
- (3) a statement of accomplishments and future interests in research and training

References would be requested at a later date

NOTE - ROLLING DEADLINE: Review of applications will begin immediately and continue until the position is filled.

Kent State University is an Affirmative Action/Equal Opportunity Institution and requires compliance with the Immigration Reform and Control Act of 1986. We strongly encourage candidates that will enhance faculty diversity and inclusion across our campus.

“CASE, ANDREA” <[acase@kent.edu](mailto:acase@kent.edu)>

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## MichiganStateU MuseumDirector

### MSU Museum Director Position

Michigan State University seeks a dynamic leader with the ability to generate and execute a vision for the future to serve as director of its AAM-accredited science and culture museum. Founded in 1857 as part of the university's land-grant mission, the MSU Museum <[museum.msu.edu](http://museum.msu.edu)> serves university and worldwide academic communities, scholars, and public audiences through research, exhibitions, public programs, and services. MSU itself began as a bold experiment that democratized higher education and helped bring science and innovation into everyday life.

The director will advance the Museum's mission of scholarly research and public engagement, provide sound management and fiscal direction, and balance the needs and interests of multiple constituencies. The director will engage in fundraising as part of the University's Capital Campaign, and seek external support from public and private foundations that advance scholarship, technology, education, exhibitions, and distance learning activities at the Museum. The director will enhance partnerships between the MSU Museum and other academic units on campus as well as regional and national organizations where interests align in research, teaching, exhibits, and public programs.

The MSU Museum has significant science and culture collections that include approximately one million specimens and objects in Anthropology, Natural Science, Folk Arts and History. It is comprised of 30 full-time and part-time administrative, faculty, curatorial and support staff. The museum building contains exhibits, natural science collections, and office space. Additional science and culture collections are housed in three other campus buildings. The collections are accessible through multiple national and international electronic databases. Staff members are engaged in exhibition development, including a traveling exhibition service. They are involved locally, nationally and internationally in research, scholarship, development of collections, and electronic

access to collections data. Staff members also work with diverse communities on research and programming. The MSU Museum is a Smithsonian Affiliate, a CITES-registered scientific institution, and a partner with the Michigan Council of Arts and Cultural Affairs in select statewide programs.

The Office of the Provost administers the MSU Museum; the director reports to the Associate Provost for University Outreach and Engagement. MSU Colleges of Arts and Letters, Social Science, Natural Science, Education, and Agriculture and Natural Resources/Extension provide funding and staff to the Museum. The Museum cultivates and maintains interdisciplinary linkages across campus, particularly in college-based programs in the sciences, arts and humanities, and international studies. The MSU Museum Council includes members of the community and campus who facilitate public engagement and serve as an advisory group to the director.

The ideal candidate will have:

- a vision for an innovative trans-disciplinary university museum
- executive leadership experience, including experience with accreditation and/or best practices in professional museum standards
- a proven track record of sound fiscal management
- demonstrated success in fundraising and attracting new membership
- evidence of successful collaboration with diverse stakeholders
- a terminal degree in a discipline related to Museum collections or comparable work experience
- a record of scholarship and research.

Position is open until filled. Review of applications will begin on February 1, 2015. To apply, please submit a cover letter of interest, a full curriculum vitae, contact information for three references, and three representative scholarly publications through the MSU COMPASS application system <https://jobs.msu.edu> for job posting #0659.

For inquiries and additional information, contact the chair of the search committee, Professor Margaret Crocco ([croccom@msu.edu](mailto:croccom@msu.edu)).

Michigan State University is an Affirmative Action/Equal Opportunity Employer. Applications from women and members of minorities are strongly encouraged. Persons with disabilities have the right to request and receive reasonable accommodation.

“Cybil Nicole Cavalieri \” Nikki\” <[cavali13@msu.edu](mailto:cavali13@msu.edu)>

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## Minnesota SummerResearch PlantEvolution

Job: Summer research internships 2015

Are you interested in field research experience and learning about the ecology and evolution of plants and plant-animal interactions in fragmented prairies? We are looking for 3-6 summer researchers for an NSF-funded project investigating how habitat fragmentation influences inbreeding, pollination, herbivory, and demography in purple coneflower, *Echinacea angustifolia*, populations in western Minnesota. We anticipate hiring 2-3 REUs, 2-3 summer field assistants, and one or two 12-month research interns. This is a great opportunity for aspiring ecologists, conservation biologists, and evolutionary biologists to gain research experience and learn about the ecology and evolution of plants in fragmented prairies!

No experience is necessary, but you must be enthusiastic and hard-working. During the summer, you will monitor natural plant populations, measure plant traits in experimental plots, and assist in all aspects of research. Undergraduate students will have the opportunity to pursue an independent project as an REU participant. Potential projects could involve hand-pollinating plants, observing & collecting insects, monitoring flowering phenology, conducting statistical analyses, or computer programming.

If you would like more information or wish to apply, please visit this website <http://echinaceaProject.org/-opportunities/> or contact Stuart Wagenius. Applications will be reviewed starting 27 February 2014 for REU positions and 6 March for other positions.

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

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## MortonArboretum DirectorTreeScience

We are advertising for a permanent scientist position at The Morton Arboretum (Lisle, IL) under the title “Director of the Center for Tree Science.” The candidate will be expected to run their own research group in any

field related to tree science (e.g. molecular systematics, evolution, trait evolution, evo-devo, etc.) that complements the existing research groups at the Arboretum. Please can you share with the EvolDir group?

Thank you, Murphy Westwood

Director of the Center for Tree Science:

The Morton Arboretum invites nominations and applications for a Center for Tree Science Director, to lead and manage the Center at The Morton Arboretum to produce world-class scientific research with important practical applications to advance tree science. The Center for Tree Science brings together experts from botanical gardens, universities, government, industry, and other organizations to participate in collaborations that generate new knowledge and provide training to address key challenges facing trees in urban areas and in the wild.

The Director, in cooperation with the Vice President of Science and Conservation and the Center for Tree Science Steering Committee will lead the development and implementation of strategic objectives, set project priorities for the Center, and pursue opportunities for research, collaboration, funding, and enhanced relationships with appropriate agencies, people, and institutions. The goal of the Center for Tree Science is to energize and expand tree science by creating a nucleus of experts who regularly work together, exchange ideas, and use their collective achievements and strengths to increase research, training, and funding opportunities for tree science.

The Director will administer the program's personnel, budgets, grants and contracts, safety, and facilities; develop and support collaborative external relationships; lead fundraising for the program; write and speak to diverse audiences on behalf of the Center and the Arboretum as a whole; and foster integration with other program areas.

The Director will be expected to devote significant time to conducting her/his own research in a field complementing existing Arboretum research programs, publishing in scientific journals, obtaining extramural funding, contributing to the scientific and green-professional communities, and participating in Arboretum education and collections programs.

Qualifications: Ph.D. in botany, forest science, horticulture, ecology, or related field; at least seven years' experience conducting top-level research relating to woody plants; record of effective written and oral communication with academic, professional, and public audiences; knowledge and interest encompassing the Arboretum's disciplinary breadth; significant experience in adminis-

trative leadership in a public garden, government agency, academic institution, or similar organization; record of securing grant and/or philanthropic support for science; and effective interpersonal skills.

Review of applications will begin December 15, 2014, and continue until the position is filled. Applicants should send a letter of application including statements of research, curriculum vitae, and contact information for three references to The Morton Arboretum, Human Resources, 4100 Illinois Route 53, Lisle, IL 60532, or [jobs@mortonarb.org](mailto:jobs@mortonarb.org). For further information or to nominate candidates, please contact the Vice President of Science and Conservation, Dr. Nicole Cavender, at 630-725-2091 or [ncavender@mortonarb.org](mailto:ncavender@mortonarb.org).

The Morton Arboretum is a 1,700-acre public botanical garden, featuring one of the world's most diverse collections of woody plants, over 900 acres of natural areas, a comprehensive research library, modern laboratories and herbarium, and outreach education for professional and public audiences. Research at the Arboretum has focused throughout its 92-year history on finding practical solutions to the challenges of selecting and maintaining healthy trees in developed landscapes and natural woodlands, and on communicating results to practicing professionals and the general public as well as the research community. See [www.mortonarb.org](http://www.mortonarb.org). The Morton Arboretum is an equal opportunity employer, committed to achieving a diverse workforce.

\*Murphy Westwood, PhD\* Tree Conservation Specialist at The Morton Arboretum < <http://www.mortonarb.org/> > & Global Tree Conservation Officer for Botanic Gardens Conservation International < <http://www.bgci.org/> >

The Morton Arboretum | 4100 Illinois Route 53 | Lisle, Illinois 60532 T 630-719-7965 | [mwestwood@mortonarb.org](mailto:mwestwood@mortonarb.org) | @MurphyWestwood < <https://twitter.com/MurphyWestwood> >

Connect with us: Facebook < <http://fb.com/MortonArboretum> > | Twitter

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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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## Morton Arboretum Illinois Tree Conservation

The Morton Arboretum invites nominations and applications for a full-time Conservation Biologist with a strong interest in tree conservation. Applicants with a strong plant conservation biology background are encouraged to apply. Research topics may include conservation genetics, niche/distribution modeling, experimental approaches to restoration ecology, population viability analysis, community assembly, trait-based or phylogenetic ecology, leading edge evolutionary dynamics, dispersal biology, or other topics in conservation biology. The successful applicant will demonstrate a commitment to integrating basic research on why woody plants succeed or decline with application to plant conservation.

Research conducted in this position should be of broad, national or international interest and work toward the goals of the Arboretums Center for Tree Science (CTS) < <http://www.mortonarb.org/science-conservation/center-tree-science-securing-future-trees> >. The Tree Conservation Biologist will work collaboratively with other CTS researchers, the CTS Tree Conservation Specialist, and collaborators worldwide to impact tree conservation practices regionally and globally.

The Arboretum is well placed to facilitate interactions with students, graduate students, postdocs and faculty in the plant sciences throughout the Chicago region. Involvement in mentoring junior scientists at some level is expected. Additionally, a long history of collaboration with Forest Preserve Districts in the Chicago region provides a springboard for potential long-term experimental and observational research.

Expectations include establishing an internationally recognized research program; publishing in scientific, professional, and popular journals; obtaining extramural funding; interacting with conservation and scientific communities; and contributing to Arboretum educational and horticultural programs. There are opportunities for academic teaching and advising, with potential adjunct faculty status at area universities.

Qualifications: Ph.D. in conservation biology or related field; a strong background in sampling, analysis and experimental design; in-depth understanding of plant ecology and conservation; proficiency in ecological mod-

eling and statistical analysis of ecological data; demonstrated commitment to conservation research and its application to conservation practice; strong written and verbal communication skills.

Applicants should send a letter of application and curriculum vitae to: The Morton Arboretum, Human Resources, 4100 Illinois Route 53, Lisle, IL 60532 or [jobs@mortonarb.org](mailto:jobs@mortonarb.org). For further information or to nominate candidates, please contact Search Committee Chair, Dr. Andrew Hipp ([ahipp@mortonarb.org](mailto:ahipp@mortonarb.org); (630-725-2094). Applications will be accepted until the position is filled. For full consideration, submit application materials by February 28, 2015.

The Morton Arboretum is a 1,700-acre public botanical garden, featuring one of the worlds most diverse collections of woody plants, over 900 acres of natural areas, a comprehensive research library, modern laboratories and herbarium, and outreach education for professional and public audiences. Research at the Arboretum has focused throughout its 92-year history on finding practical solutions to the challenges of selecting and maintaining healthy trees in developed landscapes and natural woodlands, and on communicating results to practicing professionals and general public as well as the research community. See [www.mortonarb.org](http://www.mortonarb.org) The Morton Arboretum is an equal opportunity employer, committed to achieving a diverse workforce.

\*Colleen Emrick \* | Human Resources Specialist The Morton Arboretum | 4100 Illinois Route 53 | Lisle, Illinois 60532 T 630-719-7997 | F 630-725-2040 | [\\*cemrick@mortonarb.org](mailto:*cemrick@mortonarb.org) <[jgoodsmith@mortonarb.org](mailto:jgoodsmith@mortonarb.org)> \* | [mortonarb.org](http://mortonarb.org)

Colleen Emrick <[cemrick@mortonarb.org](mailto:cemrick@mortonarb.org)>

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## North Carolina Museum Crustacean Technician

### Part Time Crustacean Technician

The North Carolina Museum of Natural Sciences seeks a detailed individual to fill the position of Crustacean Technician. This position is for 20 hours per week.

Primary Job Responsibilities include: 50% Process Specimens and Data: Sort mixed lots of specimens to the appropriate taxonomic level. Record appropriate data from specimens (identifications, measurements, weights, morphology notes, stomach contents, sex, collectors, localities, dates, habitat, etc.); catalog specimens; file



data. Enter specimen data into ACCESS-based, relational database. Prepare specimens, including chemically preserved specimens, skeletal preparations, and other preparations, for research collections according to published professional guidelines and information provided by other curators. Acquire and maintain inventories of specimen containers and other equipment and supplies. Prepare appropriate labels and storage containers for specimens. Properly incorporate prepared specimens into research collections. Monitor research collections, maintaining proper ambient and fluid-level conditions, organization, and security, and protecting against damage. Assure proper care of specimens awaiting preparation. Help maintain order and cleanliness in preparation areas and other work areas, controlling odors and disposing of waste properly; maintain order, condition, and security of tools and equipment used; and safely use, store, and dispose of dangerous chemicals.

25% Build Collections: Conduct and assist with field work, including specific research projects; assist in the collection of data and specimens, and in the acquisition of associated materials (field data, catalogues, etc.). Assist other agencies and research institutions by providing information, assist with research and specimen loans.

15% Research and Special Projects Assistance: Provide support services (mapping, data entry, slide preparation, document preparation) for research projects and other museum-wide special projects. Train interns and volunteers for support in daily responsibilities and special projects. Respond to public requests in person or via written or telephone correspondence. Assist with educational programs such as public field trips and classes outside the museum.

10% Prepare, Review and resolve transaction requests/disseminate information: Properly receive, document, sort, and house incoming donations, loans, exchanges, etc., and properly invoice, pack and ship outgoing donations, loans, exchanges, etc. Review all donation and loan papers and review transactions for completeness. Communicate with Collections Manager to accession incoming materials.

**EDUCATION AND/OR EXPERIENCE** Bachelor's degree in Biology preferred Working knowledge of Microsoft Office and other basic computer programs. Excellent organizational, analytical and problem solving skills.

**QUALIFICATIONS** Ability to follow precise directions for safe and accurate curation/preservation of specimens. Ability to work with an interdisciplinary professional team. Ability to exercise initiative and good judgment in anticipating problems before they arise. Ability to effectively coordinate and track multiple projects simul-

taneously, prioritize, work well under pressure with a high degree of accuracy, and meet stringent and overlapping deadlines.

Ability to be an outstanding ambassador to the Museum. Excellent verbal and written communication skills.

**TO APPLY** Please send a cover letter, resume, and three professional references to: [Jamie.Smith@naturalsciences.org](mailto:Jamie.Smith@naturalsciences.org)

Jamie M. Smith Collections Manager, Invertebrates North Carolina State Museum of Natural Sciences Phone: (919)707-8869 Fax: (919)715-2294 <http://www.naturalsciences.org/research/index.html> Postal Mailing Address: NC Museum of Natural Sciences Research Laboratory Mail Service Center 1626 Raleigh, NC 27699-1626 USA

Shipping Address (FedEx, UPS, etc.): NC Museum of Natural Sciences Research Lab 1671 Gold Star Drive Raleigh, NC 27607 USA

[jamie.smith@naturalsciences.org](mailto:jamie.smith@naturalsciences.org)

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## NSF Virginia SystematicsBiodiversityDirector

We are currently seeking to fill one permanent Program Director position in the Systematics and Biodiversity Science cluster in the Division of Environmental Biology at the National Science Foundation in Arlington, Virginia. The deadline for submitting applications is February 9, 2015.

Additional details about the position and application process can be found below and on the following web page: <https://www.usajobs.gov/GetJob/ViewDetails/-390306500> Simon Malcomber, Ph.D. Program Director, Systematics and Biodiversity Science Division of Environmental Biology National Science Foundation 4201 Wilson Boulevard, Room 640.04 Arlington, VA 22230 Tel: 703-292-8227 Email: [smalcomb@nsf.gov](mailto:smalcomb@nsf.gov)

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The National Science Foundation < <http://www.nsf.gov/about/> > (NSF) is seeking candidates for Program Director in the Systematics and Biodiversity Science Cluster (SBS) within the Division of Environmental Biology (DEB), Directorate for Biological Sciences (BIO) in Arlington, VA.

The DEB supports fundamental research on popula-

tions, species, communities, and ecosystems. Scientific emphases range across many evolutionary and ecological patterns and processes at all spatial and temporal scales. Areas of research include biodiversity, phylogenetic systematics, molecular evolution, life history evolution, natural selection, ecology, biogeography, ecosystem services, conservation biology, global change, and biogeochemical cycles. Research on origins, functions, relationships, interactions, and evolutionary history may incorporate field, laboratory, or collection-based approaches; observational or manipulative experiments; synthesis activities; as well as theoretical approaches involving analytical, statistical, or simulation modeling.

The SBS cluster supports research that advances our understanding of the diversity, systematics, and evolutionary history of organisms in natural systems. This research addresses fundamental questions in biodiversity, taxonomy, and phylogenetics, such as: What kinds of organisms exist in the natural world? How are they related? How did evolution lead to patterns of global biodiversity in time and space? How can phylogenetic history shed light on evolutionary patterns and processes in nature? Example topics include: expeditionary biodiversity research and discovery; identification and classification of organisms; and phylogeny and comparative phylogenetic biology. The SBS Cluster seeks to fund projects that are transformative - that is, those that innovatively and fundamentally transform our approaches to analyzing and understanding global biodiversity, its origins, distribution, and evolutionary history. The Cluster places a high value on integrative and holistic approaches to systematics research and training - i.e., those approaches and projects that integrate across all the components within the cluster (biodiversity discovery, organismal biology, taxonomy, phylogenetics, and evolution) and that train highly integrative systematists who can conduct research across the entire spectrum of these activities.

The responsibilities of the Program Director include long-range planning and budget development for the areas of science represented by the program or program cluster, the administration of the peer review process and proposal recommendations, the preparation of press releases, feature articles and material describing advances in the research supported, and coordination and liaison with other programs in NSF, other Federal agencies and organizations. Additional duties and responsibilities include the following:

#### PROGRAM PLANNING AND MANAGEMENT

\* Maintains a healthy balance of support for all the needs of the research and education enterprise through program, division, directorate, Foundation, or interagency

activities. \* Manages program resources to provide optimal appropriate scientific judgment to insure integrity and consistency in the grant/declination process without conflicts of interest, and with balance among appropriate sub-fields and institutions, and participation of all qualified scientists. \* Manages an effective, timely merit review process, with attention to increasing the size and quality of the reviewer pools and insuring participation by women, minorities and disabled scientists. \* Provides scientific expertise, evaluation and advice for other programs in NSF, including international programs, and other research programs, and cross-directorate programs. \* Advises and assists in the development of short-and-long range plans, establishing goals and objectives for support of research programs. \* Plans the budget for the program considering past, present and future fiscal years, allocates resources within the budget by distributing scarce resources among competitive projects, and manages post-award evaluation.

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## Okinawa ComputingTech BiodiversityEvolution

Job: Research Computing Technician

The Economo Lab (<http://arilab.unit.oist.jp>) at the Okinawa Institute of Science and Technology (<http://www.oist.jp/>) is seeking qualified applicants for a Research Computing Technician position. The lab works at the interface of ecology, evolution, and natural history, with an empirical focus on ant biodiversity. We use a variety of approaches to understand the biodiversity of communities, including field expeditions, collections-based research, phylogenetics, 3D imaging and morphometrics, ecological genomics, computational modeling, biodiversity informatics, and quantitative theory.

Duties: The hired individual will be responsible for computational support of lab research including designing and maintaining research databases, maintaining lab websites, assist with design and maintenance of data analysis pipelines, application support for utilizing HPC resources, and performing phylogenetic/phylogenomic analyses.

Qualifications: A Bachelor's degree in science or technical fields, and experience with scientific research computing is required. The ideal candidate would have a good baseline of programming and scripting skills, including familiarity with both compiled (e.g. C/C++) and interpreted (R, Matlab, Python) languages, familiarity with computational phylogenetics and bioinformatics, and ability to learn independently. Proficiency with Linux, SQL-based database design and administration, and at least basic familiarity with server administration are required. Experience with one or more of the following would be highly desirable but is not required; GIS, ecoinformatics, web programming, parallel computing, and statistical computing.

Job Data: OIST is a newly established international graduate university located in the resort area of Onnason, Okinawa, Japan, and offers a high quality of life and good working conditions. Logistical and financial assistance with relocation will be provided, along with a competitive salary and benefits package. OIST is an English-language working environment and knowledge of English is required, knowledge of Japanese is helpful but not necessary.

To apply, please send a cover letter explaining your background and interest in the position, CV, and list of three references with contact information as a combined PDF to <arilab.oist@gmail.com> with 'Technician Application' in the subject line. Informal enquiries and questions are also welcome at <economio@oist.jp>. Application review will begin February 1, 2015 and continue until the position is filled.

Evan P. Economo Assistant Professor Biodiversity and Biocomplexity Unit Okinawa Institute of Science and Technology 1919-1 Tancha Onnason, Kunigamigun Okinawa, Japan 904-0495 <http://arilab.unit.oist.jp/>  
evaneconomo@gmail.com

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## OmahaZoo ResAssist Bioinformatics

Applications are invited for a Laboratory Technician in the Conservation Genetics Department at Omaha's Henry Doorly Zoo & Aquarium (<https://workforcenow.adp.com/jobs/apply/-posting.html?client=omahazoo>). The Laboratory Technician will participate in ongoing molecular and bioinformatics research. Importantly, the technician will utilize sophisticated computer programs during the analysis of datasets from next generation sequencing.

This technician will develop high-throughput solutions to improve scalability of in-house genetic interpretation tools. The technician will be responsible for developing a pipeline for genomic analyses and database monitoring and maintenance. Early-career technicians will have the opportunity to gain on-the-job training regarding bioinformatics.

Duties: The Laboratory Technician will confer with research staff to determine data needs and programming requirements and to provide assistance with database-related research activities. Importantly, the technician will utilize bioinformatics techniques to analyze or manipulate large datasets from next generation sequencing in a Unix/Linux environment. Sophisticated computer programs will be used to gather, analyze, and track data regarding biological functions or characteristics in order to gain a better understanding of computational evolutionary biology and comparative genomics. The technician will develop high throughput solutions to improve scalability of in-house genetic interpretation tools. Duties will involve writing or modifying existing computer code to perform analysis of high-throughput sequencing data including the analysis of whole genome sequencing data. The technician will need to develop a pipeline for genomic analyses as well as a system for monitoring database performance and perform any necessary maintenance, upgrades, or repairs. Ultimately the technician will complete statistical analyses and prepare reports on related findings. Additionally, the technician will assist multiple research projects as well as routine maintenance within the laboratory. Participation in group activities such as grant preparation and reporting, literature searches, and manuscript writing efforts will be expected. All laboratory staff will maintain cleanliness and sanitation while complying with safety procedures in their employed laboratories. Duties will include non-research activities such as facility maintenance and outside work.

Qualifications: Ideally, the Laboratory Technician will have a thorough knowledge of bioinformatics, molecular genetics and related techniques, and have a good understanding of biological sciences. Experience in bioinformatics and next-generation sequencing is highly preferred. A Bachelor's degree in the Genomics, Genetics, Bioinformatics or Computer Science or related field is required. Ideal candidates will have a proficiency in Linux, programming experience in at least one of the following programming languages: C, C++, Java, Perl, or Python. Knowledge of parallel processing and computing and the use of R statistic software would be beneficial. Early-career technicians will have the opportunity to gain on-the-job training regarding bioinformatics.

Start Date: immediate

Location: Omaha, Nebraska, USA.

Please visit the Omaha's Henry Doorly Zoo & Aquarium Job Listing webpage at [www.omahazoo.com/careers/](http://www.omahazoo.com/careers/) for full job description and to formally submit an application. Applicants should include a cover letter describing previous experience, a resume, and the names and contact information for two references. Please also send a copy of your application materials to Dr. Edward Louis Jr. at [genetics@omahazoo.com](mailto:genetics@omahazoo.com)

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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## Ottawa Invertebrate Curator

The Canadian National Collection of Insects, Arachnids, and Nematodes is seeking to fill Research Scientist positions to conduct taxonomic research on terrestrial arthropods, including one of the following: groups of importance as beneficial biocontrol agents against pests in Canada or against potential threats (invasive species) to Canadian agriculture (braconid wasps, soil mites or predatory mites); groups that may threaten Canadian agriculture (cutworm moths, leaf beetles, leaf hoppers or plant hoppers); or groups of importance to the health of soils in Canadian agricultural systems (soil mites). Preference will be given to Canadian citizens, but non-Canadians are encouraged to apply in the event that a qualified Canadian citizen cannot be found to fill a certain position.

For more info: <https://emploisfp-psjobs.cfp-psc.gc.ca/psrs-srfp/applicant/page1800poster=-256504&toggleLanguage=en&psrsMode=-1&noBackBtn=true> Research Scientist - Insect/Mite Taxonomist

Organization Name: Agriculture and Agri-Food Canada - Science and Technology Branch Location: Ottawa (Ontario) Classification: SE - RES - 01, SE - RES - 02, SE - RES - 03, SE - RES - 04 or SE - RES - 05 Salary: \$53,161 to \$133,410 (Salary is commensurate with qualifications) Closing Date: January 12, 2015 - 23:59, Pacific Time Useful Information <<http://jobs-emplois.gc.ca/centres/psrs-srfp/date-eng.htm>> Reference Number: AGR14J-010860-000024 Selection Process Number: 14-AGR-NCR-EA-ST-333 Vacancies: 5 Employment Tenure: Indeterminate and/or Term Web site: For further information on the department, please

visit Agriculture and Agri-Food Canada <[http://http://www.agr.gc.ca/index\\_e.php](http://http://www.agr.gc.ca/index_e.php)>

[Sophie.Cardinal@AGR.GC.CA](mailto:Sophie.Cardinal@AGR.GC.CA)

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## RBG Kew 29 Science Positions

Twenty nine positions in the Science Directorate at the Royal Botanic Gardens, Kew are now open for applications. Positions include:

- Ten early career research fellowships - Research leader posts in the fields of taxonomy, systematics, evolution, nomenclature, eTaxonomy, collections, conservation, natural capital and plant health - Informatics positions
- Technical, curatorial, policy and support roles

The positions are listed below - see <https://careers.kew.org/home.html> for more details. The deadline for applications is 15 February 2015.

Please circulate this information to interested colleagues.

Research positions: Early Career Research Fellowship (10 positions available) Senior Research Leader - Plant Health Research Leader - Conservation Genetics Research Leader - Crop Plants Research Leader - Digital Collections Research Leader - Identification and Naming (Americas) Research Leader - Integrated Monography Research Leader - Plant & Fungal Names & eTaxonomy Senior Biodiversity Informatician Biodiversity Informatician Lead Developer - Drupal

Technical positions: Senior Science Officer - Policy Imaging/EM Lab Technician Molecular Lab Technician Seed Germination Assistant Digital Collections Assistant Lab-based Collections Assistant

Support positions: Science Administrator - Communications Support Officer to the Millennium Seed Bank Support Officer to the Senior Science Team

[W.Baker@kew.org](mailto:W.Baker@kew.org)

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## RBG Kew Many Positions Conservation

A large number of jobs are currently being advertised at RBG Kew with a 1 Feb deadline for applications.

For example:

Early Career Research Fellowships (12) Research Leader - Conservation Genetics Research Leader - Crop Plants Research Leader - Digital Collections Senior Research Leader - Plant Health

<https://careers.kew.org/vacancies.html> Please refer to UK immigration policy to determine work visa eligibility for non-EU applicants: <https://www.gov.uk/government/organisations/uk-visas-and-immigration>  
B.Dentinger@kew.org

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## RoyalOntarioMuseum Toronto Ornithologist

Ornithologist - The Royal Ontario Museum

The Royal Ontario Museum (ROM) is Canada's pre-eminent international museum and houses some of Canada's most important collections in both Natural History and World Cultures. The Department of Natural History at the ROM (<http://www.rom.on.ca/en>) currently invites applications for the position of an entry-level (equivalent to Assistant Professor) Associate Curator of Ornithology to conduct field and collections-related research.

The successful applicant will be expected to develop a program of externally funded scholarly research and publications; curate and continue building the disciplinary collection of birds; participate in the development and rotation of new permanent galleries and travelling exhibitions; and actively participate and contribute to development of public programming in a variety of formats from on-site to on-line. The successful candidate will be the public spokesperson for Ornithology at the ROM.

We seek a candidate who conducts conceptually driven, collection-based research on the systematics and evolution of birds. We seek applications from candidates whose research programs fit well with the highly collaborative and interdisciplinary research in the ROM's Department of Natural History and complements our close partnership with the Department of Ecology and Evolutionary Biology at the University of Toronto (<http://www.eeb.utoronto.ca/>). Successful applicants will have a Ph.D. in systematic biology and be well versed in modern phylogenetic methods for analyzing DNA and/or morphological datasets, phylogenomics, comparative genomics, evolutionary biology, historical biogeography, or

conservation biology; an outstanding record of scholarly publication in peer-reviewed journals; be qualified for cross-appointment to the University of Toronto, demonstrate potential for teaching undergraduate and graduate students, and be eligible for NSERC funding in support of their research (i.e. proven record of successful grant applications). Experience in a museum or equivalent environment is preferable.

The Royal Ontario Museum is a leading institution in the study of Systematics and Evolution with a recognized group of curators performing research in temperate and tropical regions of the Americas, Asia, Oceania and Africa. Strong links exist between the Department of Natural History and the Department of Ecology and Evolutionary Biology, University of Toronto, the Ontario Ministry of Natural Resources and Parks Canada.

Toronto is a vibrant and cosmopolitan city, one of the most desirable in the world in which to work and live. The Royal Ontario Museum is strongly committed to diversity within its community and especially welcomes applications from visible minority group members, women, Aboriginal persons, persons with disabilities, members of sexual minority groups, and others who may contribute to the further diversification of ideas.

Applications for the position will be accepted until March 1, 2015. Informal inquiries before application are welcome and should be directed to the Chair of the Search Committee, Dr. Hernán López-Fernández ([hernanl@rom.on.ca](mailto:hernanl@rom.on.ca)). Applicants should provide a curriculum vita, a summary of their research, and an outline of their proposed research program as a single PDF file, and should arrange to have three confidential letters of recommendation in PDF format sent on their behalf to:

Human Resources Department c/o Mara Gunner The Royal Ontario Museum 100 Queen's Park, Toronto, Ontario, Canada M5S 2C6 Fax: (416) 586-5827 Email: [humanresources@rom.on.ca](mailto:humanresources@rom.on.ca)

Kindly add "file No. 2015-005" to All qualified candidates are encouraged to apply. Salary and rank are commensurate with experience as stipulated in the Collective Agreement between the ROM and the ROM Curatorial Association.

Hernán López-Fernández

Hernán López-Fernández, Ph.D. Curator of Freshwater Fishes Royal Ontario Museum 100 Queen's Park, Toronto Ontario M5S 2C6, Canada

And

Assistant Professor Department of Ecology and Evolutionary Biology University of Toronto

Email: [hernanl@rom.on.ca](mailto:hernanl@rom.on.ca)

Hernan Lopez-Fernandez <hernanl@rom.on.ca>

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## StockholmU Evolutionary Zoology

Associate Professor in Terrestrial Vertebrate Ecology at the Department of Zoology Stockholm University.

Reference number SU FV-3325-14. Deadline for application: February 16, 2015.

Swedish “universitetslektor”; tenured position approximately equivalent to Senior Lecturer (UK) or Associate Professor (US).

The department consists of five divisions: Ecology, Ethology, Functional Morphology, Population Genetics, and Systematics and Evolution. The announced position will be part of the Division of Ecology where currently 10 teachers/researchers, 10 post-doctorial fellows and 18 PhD students are active. The Department of Zoology has in total 45-50 teachers/researchers and 45-50 PhD students. There is a long-standing tradition for researchers at the division of Ecology to collaborate with researchers from other fields, mostly at the other divisions at the Department, but also at other universities in Sweden and abroad.

Main tasks: Research and supervision. Teaching, primarily Ecology and Conservation Ecology.

Required qualifications: In order to qualify for employment as associate professor, the applicant must have demonstrated good teaching skills and have a doctoral degree, or equivalent research expertise, of relevance to the subject area and the main responsibilities of the position. All teaching positions at Stockholm University require the ability to collaborate and the general ability and suitability to perform one’s duties.

Assessment criteria: In the appointment process special consideration will be given to scientific and teaching proficiency, which will be weighted equally. Assessment of scientific proficiency will primarily focus on merits within the subject area of the position.

When merits are judged similar according to the general criteria, the following will be distinguishing: - Documented teaching proficiency regarding teaching in Ecology and Conservation Ecology.

Teaching and learning theory: Completed training in teaching and learning in higher education, or equivalent knowledge, is an advantage. An applicant who has not completed at least 7.5 credits of teaching and learning

in higher education and is not considered to have otherwise acquired equivalent knowledge should undergo such training within the first two years of employment.

Additional information: Female applicants are particularly welcome, as most associate professors at the department are men.

The language of instruction in first-cycle courses and programmes is Swedish. If the successful candidate does not speak Swedish at the time of appointment, he/she is expected to acquire the necessary language skills during the first two years of employment.

Administrative coordinator Katarina Gustafsson, telephone +46 (0) 8 16 2292, e-mail [katarina.gustafsson@su.se](mailto:katarina.gustafsson@su.se) will provide further information about the application and appointment procedure if required.

Trade union representatives: Anqi Lindblom-Ahlm, (SACO), Lisbeth Häggberg (Fackförbundet ST), telephone +46 (0)8 16 20 00 (switchboard) and Gunnar Stenberg (SEKO) +46 (0) 70 316 43 41.

In order to apply for this position please use the Stockholm University web-based application form. It is the responsibility of the applicant to ensure that the application follows the template and that it is submitted before application deadline. We appreciate if your application is written in English since it will be reviewed by international experts, English being the working language.

Further information about the position can be obtained from professor Anders Angerbjörn, e-mail: [anders.angerbjorn@zoologi.su.se](mailto:anders.angerbjorn@zoologi.su.se) , telephone +46 (0) 8 16 4035.

Stockholm University: [www.su.se/english](http://www.su.se/english) Department of Zoology: [www.zoologi.su.se/en/](http://www.zoologi.su.se/en/) Faculty of Science: [www.science.su.se/english](http://www.science.su.se/english) (Rules & regulations, Guidelines for employment & recruitment)

Anders Angerbjörn Department of Zoology, Stockholm University, S-106 91 Stockholm Sweden

Anders Angerbjörn <[angerbj@zoologi.su.se](mailto:angerbj@zoologi.su.se)>

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## TempleU Evolution Comp Sci

Evolutionary 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 [toigem@temple.edu](mailto:toigem@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, 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>) Institute for Genomics and Evolutionary Medicine Carnell Professor of Biology Temple University (SERC 710) Philadelphia, PA 19122, USA [https://twitter.com/kumar\\_lab](https://twitter.com/kumar_lab) <http://www.kumarlab.net> [s.kumar@temple.edu](mailto:s.kumar@temple.edu)

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### TempleU Phylogenomics Phylomedicine

Research Faculty Positions (iGEM@Temple)

Multiple multi-year research faculty positions (non

tenure-track) are available in the Institute for Genomics and Evolutionary Medicine (iGEM) at Temple University in Philadelphia, USA. We are interested in early and mid-career scientists who integrate concepts, methods, and tools from evolutionary biology to address significant questions in biomedicine and phylogenomics. Successful candidates will have a primary focus on one or more of the following: large scale analytics of sequence and expression data, and development of methods and computational tools. They will be core faculty of iGEM @ Temple and one of the academic departments (e.g., Biology or Computer Science). They will work closely with and benefit from our expertise in molecular evolution, population genetics, phylogenomics, phylomedicine, and computational biology.

Applicants should submit their detailed curriculum vitae and a summary of current and future research interests by e-mail to [igem@temple.edu](mailto:igem@temple.edu) (send a single PDF file). Successful candidates will be provided for salary support for an initial period and they will work closely with one or more of the current or future tenured faculty in iGEM (<http://igem.temple.edu/people>). They will be expected to develop a strong, extramurally funded, and collaborative research program. For all questions, please contact Sudhir Kumar by email ([s.kumar@temple.edu](mailto:s.kumar@temple.edu)).

Temple University located is in the heart of historic Philadelphia, and is the sixth largest provider of graduate school education in the USA. Situated in close proximity to New York City and Washington DC, Philadelphia is home to a large biotech industry and has many outstanding academic and research institutions.

Sudhir Kumar Director, iGEM@Temple

[s.kumar@temple.edu](mailto:s.kumar@temple.edu)

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### UAlabama Staff Computational Evolution

A research associate position is available in the laboratory of Janna Fierst in the Department of Biological Sciences at the University of Alabama. My lab works on a broad array of projects addressing evolutionary questions with computational approaches. This position is to support bioinformatics and computational projects through consultation, research and hands-on support, provide system administration for UNIX and Macintosh servers, assist in mentoring student projects, and coordinate lab activities. This is a full-time staff position with

an initial appointment of one year and renewal subject to performance.

The successful candidate will have:

- An MS in Computational Biology or a related field (Genetics, Evolution, Biology, Computer science, Physics, Mathematics, Statistics, or Bioinformatics)
- A strong bioinformatics and biostatistics background
- Experience with UNIX environments
- Programming proficiency (e.g. Python, Perl, C++)
- Software development experience
- Familiarity with the statistical computing language R

To apply, please submit an application to the University of Alabama jobs website <http://staffjobs.ua.edu/> for job #499830. The application should include a current CV/Resume, a cover letter discussing the applicants background, research experience, and career goals, and contact information for 3 references. Application review begins February 1 and the start date is negotiable.

Contact Janna Fierst ([jlfierst@ua.edu](mailto:jlfierst@ua.edu)) with questions regarding the position or application process.

The University of Alabama is an equal opportunity employer and women and minorities are encouraged to apply.

Janna L. Fierst

Assistant Professor

Department of Biological Sciences

The University of Alabama

Tuscaloosa, AL 35487

Office: SEC 1339

Phone: 205-348-1830

[www.jannafierst.wordpress.com](http://www.jannafierst.wordpress.com)

<[janna.lynn.fierst@gmail.com](mailto:janna.lynn.fierst@gmail.com)>

Janna Fierst

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## UCalgary Bioinformatics

Dear colleagues,

We currently have two open faculty positions in Bioinformatics & Computational Biology in the Faculty of Medicine, University of Calgary. These openings include a junior faculty position at the assistant professor level and a mid-career associate professor position supported

by a Canada Research Chair Tier 1 allocation.

If you know of any highly qualified trainees, or mid-career researchers, who might be interested in these opportunities, I would greatly appreciate it if you would forward on the attached ad.

Thanks!

Best wishes, - Jason de Koning

- A.P. Jason de Koning, Ph.D.

Assistant Professor University of Calgary, Faculty of Medicine and Alberta Children's Hospital Research Institute for Child and Maternal Health Dept. of Biochemistry and Molecular Biology Dept. of Medical Genetics

PLEASE NOTE NEW LOCATION: Health Sciences Centre 1150 Suite 3330 Hospital Drive N.W. Calgary, Alberta T2N 4N1 Canada

Office: 403-210-7638 | Fax: 403-270-8928 Email: [jason.dekoning@ucalgary.ca](mailto:jason.dekoning@ucalgary.ca) Web: <http://lab.jasondk.io>  
Faculty Positions in Bioinformatics & Computational Biology

The Department of Biochemistry & Molecular Biology, Cumming School of Medicine, University of Calgary and the Alberta Children's Hospital Research Institute for Child & Maternal Health invite applications for two full-time positions in the area of Bioinformatics or Computational Biology as applied to genomics-related problem:

1. A junior position at the Assistant Professor level.
2. A mid-career position, supported by a Tier 1 Canada Research Chair in Bioinformatics & Computational Biology, at the Associate/Full Professor level.

Qualifications for the Assistant Professor position include a Ph.D. degree or equivalent, at least two years of post-doctoral experience, and a strong record of research publications in high impact journals on the development or application of computational tools to address biological/biomedical problems. Qualifications for the Associate/Full Professor position additionally include a record of successful academic leadership experience in research, education and service. These positions are aimed toward bioinformaticians working on analysis of large scale genome, transcriptome, epigenome or related datasets. A background in statistics or machine learning will be viewed as an asset for either position.

The successful candidates will join a blossoming multidisciplinary and inter-Faculty team of bioinformaticians, clinical researchers and basic scientists whose research spans model organisms to human disease. They will also have an opportunity to contribute to the recruitment of two additional junior



academic bioinformaticians. The Cumming School of Medicine is home to both undergraduate ([cumming.ucalgary.ca/bhsc/program/bioinformatics](http://cumming.ucalgary.ca/bhsc/program/bioinformatics)) and graduate ([ucalgary.ca/bmb/ProspectiveStudents](http://ucalgary.ca/bmb/ProspectiveStudents)) training programs specializing in bioinformatics. Expectations for the current positions include the establishment of vigorous, sustainable, externally-funded research programs (for which 75% time will be protected), contributions to teaching and graduate student supervision and, in the case of the Associate/Full Professor position, to leadership in recruitment, research, education and service. This is an excellent opportunity to build and develop an innovative research program within a dynamic and collaborative environment. Competitive salaries and attractive start-up packages are available.

The Alberta Children's Hospital Research Institute encourages a translational approach to research with an emphasis on people, core programs and infrastructure. The Department, Institute and School are home to a number of excellent core research facilities, such as state-of-the-art proteomics and genomics labs, including a next-generation sequencing and bioinformatics platform. Please visit our websites at <http://www.ucalgary.ca/bmb/> and <http://research4kids.ucalgary.ca/> for more information.

Increasing scholarly capacity will help the University of Calgary meet its strategic goal to become one of Canada's top five research universities by 2016, where innovative teaching and groundbreaking research go hand in hand, and where we fully engage the communities we both serve and lead. The strategy is called Eyes High, inspired by the university's Gaelic motto, which translates as "The sky will lift up my eyes".

Calgary, Canada's fastest growing major city, offers a vibrant, multicultural and family-oriented environment with a population of more than one million. Situated near the Rocky Mountains, Banff National Park and Lake Louise, Calgary has great quality of life and outstanding recreational activities.

Interested candidates should submit by email, by January 18, 2015, a single PDF file containing: a cover letter stating to which position

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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/evodir.html>

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## UCambridge 2 Evolutionary Genetics

Two University Lectureships - Department of Genetics - University of Cambridge

Applications are invited for two research-oriented, tenure-track University Lectureships. The posts are available from 1 October 2015 or as soon as possible thereafter. Based in central Cambridge, the Department of Genetics is a world class research and teaching environment with particular strengths in quantitative approaches to genomics, epigenetics, population and evolutionary genetics, cell and developmental biology and has numerous links with other local institutions. We are searching for outstanding scientists undertaking cutting edge and fundable research in any field of contemporary genetics relating to or complementing our existing research programmes. (<http://www.gen.cam.ac.uk/research-groups/research-by-subject>).

The successful applicants will have a PhD in a relevant subject area and will have demonstrated the potential to achieve international recognition for their research. Applicants will also have an aptitude and enthusiasm for teaching at undergraduate and graduate level and will be expected to contribute to the teaching and other academic activities in the Department. They will be expected to contribute to the design and delivery of undergraduate and graduate lecture courses and to perform other academic duties such as Departmental administration, examinations and other forms of assessment.

Appointments will be made at University Lecturer level with a probationary period of five years, with appointment to the retiring age thereafter. The starting salary, depending on experience, will be in the range of £38,511 - £48,743 per annum. Once an offer of employment has been accepted, the successful candidates will be required to undergo a health assessment, with a satisfactory outcome determined by the University.

Prospective candidates are invited to contact the Head of Department, Professor Anne Ferguson Smith, for informal enquires (Tel: +44 (0) 1223 339984, e-mail: [head@gen.cam.ac.uk](mailto:head@gen.cam.ac.uk)).

The Department is committed to the Athena SWAN scheme to provide equal opportunities and to advance the representation of women in science. We welcome applications from all qualified candidates irrespective of gender and we strongly encourage applications from

female candidates. Appointment will be based on merit alone. The Department strongly supports DORA (<http://am.ascb.org/dora/>) and will assess research on its quality rather than on the basis of the journal in which it is published.

The University values diversity and is committed to equality of opportunity.

The University has a responsibility to ensure that all employees are eligible to live and work in the UK.

For further details of how to apply, see <http://www.jobs.cam.ac.uk/job/5870/> Chris Illingworth <cjri2@cam.ac.uk>

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## UMainz EvolutionaryGenomics

In the Faculty 10 Biology, Zoological Institute, Department of Evolutionary Biology at the University of Mainz is looking for an

Assistant Professor / Junior group leader

(Akademischer Rat at a University / Bes.Gr. A 13 BBesG)

Field: Evolutionary Genomics / Behavioral Genomics from April 15st 2015 on.

The contract is initially for 3 years with the possibility of extension to up to a total of nine years depending on previous employment at German universities (12-year rule). In case the prerequisites of civil service law are not fulfilled, an engagement as a Scientific Assistant (EG 13 TV-L) is possible. More information on potential contract length and position can be given on an individual basis.

We invite applications for an Assistant Professor (Akademischer Rat / A 13) position in the Department of Evolutionary (Prof. Dr. Susanne Foitzik) at the Institute of Zoology at Johannes Gutenberg University of Mainz, Germany. This young international research team focusses on the evolution, behavior, genetics, chemical ecology of social insects ([http://www.bio.uni-mainz.de/zoo/evobio/index\\_ENG.php](http://www.bio.uni-mainz.de/zoo/evobio/index_ENG.php)). Collaboration with other groups of in the department of Evolutionary Biology are desirable. Excellent research conditions are available at the newly renovated and well-equipped genetic and chemical laboratories in Mainz. Furthermore, new climate chambers are available for animal

maintenance. A NextGen sequencing facility is available on campus. For further information, please contact foitzik@uni-mainz.de.

We are seeking a highly motivated young researcher with a strong background in evolutionary genomics or behavioral genomics to establish a junior research group within Department of Evolutionary Biology. Candidates must hold a Ph.D. and postdoctoral experience is necessary. The successful candidate should address evolutionary or behavioral questions in social insects or other arthropods and should preferentially apply the newest genomic methods including the necessary bioinformatics (e.g. next-gen sequencing and transcriptomics).

The successful candidate should have an excellent publication record. Experience with grant acquisition and teaching is advantageous. The candidate should set-up an independent, competitive research group and is encouraged to apply for grants in Germany or the EU (e.g., DFG, ERC). The position comes with a teaching requirement of 4 h per week during the semester in the Master and Bachelor programme. Some basic zoology classes are preferably taught in German. Consequently, a willingness to learn German is required. The candidate has the option to acquire a "Habilitation". The working language of the lab is English.

Requirements of appointment:

- University degree and a PhD in biology (or related field) - a full-time employment of at least two years and six month after Master or PhD

The Johannes Gutenberg-University Mainz is interested in increasing the number of women in science. Applications from female scientists are strongly encouraged. Similarly, qualified candidates with disabilities will be preferred.

The University of Mainz hosts many excellent scientific institutions (<http://www.uni-mainz.de/eng/>) and Mainz is a historic city located on the Rhine River with many students and a rich social and cultural life (<http://www.mainz.de/WGAPublisher/online/html/default/hpkr-5nkek8.en.html>).

Interested candidates should send an application (as a single e-mail pdf attachment) containing a CV, a list of publications (including reprints of the three most important publications), research and teaching statements, and contact information for two potential referees to:

Prof. Dr. Susanne Foitzik Evolutionary Biology

Institute of Zoology Johannes-v.- Müller-Weg 6 55099 Mainz

Germany foitzik@uni-mainz.de

Closing date for the application is February 28th, 2015  
Starting date for the position is negotiable, earliest possible date is April 15th 2015

Prof. Dr. Susanne Foitzik Evolutionsbiologie Institut für Zoologie Johannes Gutenberg Universität Mainz Johannes von Müller Weg 6 55099 Mainz

Tel: +49 (0) 6131 39 27 840 Fax: +49 (0)6131 39 27 850 Email: foitzik@uni-mainz.de

“Foitzik, Susanne” <foitzik@uni-mainz.de>

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### UMissouri Columbia BioinformaticsCompBiol

Members of the EVOLDIR community that are attending the Plant and Animal Genomes meeting in San Diego and that might be interested in this position can talk to Jerry Taylor (speaking in Cattle/Swine and Buffalo Workshops on Saturday January 10).

\*\*\*\*\*

The Division of Animal Sciences at the University of Missouri-Columbia invites applications for a Research Assistant Professor in Bioinformatics and Computational Biology. The University recognizes that a more complete understanding of the genomes of agriculturally important species and humans will underpin most advances in agriculture and biomedicine. Future research will take advantage of the recent advances in next generation sequencing technologies to generate de novo genome and transcriptome assemblies, identify and annotate regulatory elements, and perform genotyping by sequencing. The successful candidate will become a member of large teams in reproductive biology and genomics focusing on improving the efficiency of livestock production and human reproductive health.

The candidate will be expected to design, develop and implement computational pipelines for analyzing genotype and sequence data of all varieties but primarily whole genome resequencing and RNA-seq. Experience in predicting non-coding RNAs and other functional elements is beneficial. The successful applicant should have programming experience, preferably in one compiled (C, C++, Fortran, etc.) and one interpreted language (Perl, Python, etc.). Knowledge of relational databases, particularly Postgres, and experience building/administering server hardware is also beneficial.

The successful candidate will be required to make a

major contribution to the development of the Animal Genomics and Reproductive Biology programs within the Division of Animal Sciences. This will include the development and submission of grant applications and of manuscripts to peer reviewed journals. It will also include the mentoring of graduate students and presenting guest lectures in undergraduate and graduate courses. Candidates for the position must have a Ph.D. degree in Bioinformatics, Computer Science, Statistics, Genetics or Molecular Biology; postdoctoral experience; and possess satisfactory verbal and written communication skills. The ability to critically assimilate information from a number of disciplines (molecular genetics, biology, comparative genetics and statistics), talent for structuring and analyzing data, and interest in teamwork and interdisciplinary cooperation are desirable. Background and/or interest in mammalian genomes is preferred. The position will be in the Division of Animal Sciences within the College of Agriculture, Food and Natural Resources. This is a professional track position with salary commensurate with experience and annual renewal of contract dependent on performance.

Applications should include: A letter describing interest in the position, curriculum vitae, and the names of at least three individuals who might act as references.

Applications Submission: Please visit <http://hrs.missouri.edu/find-a-job/academic/index.php> to submit an application. Questions regarding this position should be directed to Dr. Thomas Spencer, at [spencerte@missouri.edu](mailto:spencerte@missouri.edu).

Applications must be received by February 28, 2015.

The University of Missouri is an equal access, equal opportunity, affirmative action employer that is fully committed to achieving a diverse faculty and staff. For more information, call the Associate Vice Chancellor of Human Resource Services/Affirmative Action officer at 573-882-4256.

To request ADA accommodations, please call Human Resource Services at 573-882-7976. TTY users, please call through Relay Missouri, 1-800-RELAY (735-2966) or en Español at 1-800-520-7309.

MU's College of Agriculture, Food and Natural Resources strongly endorses the principles embodied in MU's values statement - respect, responsibility, discovery, excellence (<http://web.missouri.edu/~jesse105/-pages/values.htm>). In that context we seek to recruit and retain outstanding scholars who are: Committed to blending service with scholarship: Leaders; Good colleagues who will collaborate with others from diverse disciplines and backgrounds and be flexible and adaptable in an era of rapid change.

“Taylor, Jerry F. (Animal Science)”  
<taylorjerr@missouri.edu>

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### UMontana ResAssist AlgalEvolution

A laboratory technician (Research Assistant III) position is available with Dr. Matthew Herron. This position is based at the University of Montana in Missoula, MT (but may also involve work in collaborating labs. The Herron Lab Group uses experimental evolution of the unicellular green alga *Chlamydomonas reinhardtii* to understand the evolution of multicellularity. The person in this position will contribute to this project through collaboration with postdocs and graduate students; take on a specific line of investigation assigned by the principal investigator; and train and supervise undergraduate work-study students.

The Research Assistant III will maintain orderly, up-to-date written and electronic notebooks consistent with standard NIH guidelines; actively participate in weekly group meetings; and significantly contribute to research communications and grants by analyzing and interpreting data, preparing publication-quality figures and tables, and composing the methods and results sections of manuscript narratives in a quality that would merit manuscript co-authorship.

The person in this position will demonstrate expertise in molecular microbiology, microbial cell culture, and have a working knowledge of all aspects of nucleic acid preparation and analysis, PCR, and standard genetic analyses. Required skills include demonstrated ability to work independently, to recognize and creatively solve technical problems, to effectively transmit protocol knowledge to new students and postdocs, to assist lab personnel as needed, and to follow through on assigned tasks in a timely manner. Strong demonstrated ability in oral and written communication skills, demonstrated experience and expertise in molecular microbiology and microbial cell culture, and working knowledge of nucleic acid preparation and analysis, PCR, and standard genetic analyses are also required. Required Experience: bachelors degree in Biology, Chemistry or a related discipline and two (2) years of research experience or an equivalent combination of education and experience Preferred Qualifications: masters degree

About the University of Montana University of Montana is located in Missoula, a vibrant community of 67,000, surrounded by mountain grandeur. The city has

been singled out in national publications for its high quality of life and abundant recreational opportunities in surrounding state and national forests and nearby Glacier National Park and Yellowstone National Park complement a thriving intellectual atmosphere.

HOW TO APPLY: Submit a Letter of Interest, detailed resume, and names and contact information for three professional references at <https://university-montana-hr.silkroad.com/epostings/index.cfm?fuseaction=app.jobinfo&jobid=1156> .

– Matthew D. Herron, PhD Division of Biological Sciences University of Montana X.princeps@gmail.com <http://www.eebweb.arizona.edu/grads/mherron/> Matthew Herron <xprinceps@gmail.com>

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### UNewMexico FieldLabTech PlantAnimalInteractions

Field and Laboratory Technician

Ecology and evolution of plant-animal interactions

The Whitney & Rudgers Labs at the University of New Mexico will soon be posting a technician opening. Duties will include work in both field and laboratory settings on NSF-funded projects examining the ecology and evolution of plants, plant-animal interactions, and plant-microbe interactions. Candidates should have B.A./B.S. in biology (or related field) and some hands-on field and lab experience. Training will be provided, but experience with DNA techniques (DNA extraction, PCR, sequencing), plant care and greenhouse maintenance, plant identification and vegetation sampling, and/or general field methods in ecology, is a bonus. The position will involve supervision of undergraduate research assistants. This position would be an excellent fit for someone planning on graduate study in Ecology & Evolutionary Biology, as there will be the opportunity to gain experience in a number of research areas and to co-author papers.

For more information on the position, please send a CV and contact information for three references by email ([whitneyk@unm.edu](mailto:whitneyk@unm.edu)).

Ken Whitney Associate Professor Department of Biology University of New Mexico Albuquerque, NM 87131 [whitneyk@unm.edu](mailto:whitneyk@unm.edu) <http://biology.unm.edu/whitney/whitneyk@unm.edu>

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## UOtago 2 EvolutionaryEcol

Department of Zoology University of Otago Dunedin,  
New Zealand

Lecturers/Senior Lecturers - Behavioural and/or Evolutionary Ecology-1402226

Applications are invited from behavioural and/or evolutionary ecologists to teach at undergraduate and postgraduate levels, and to develop a strong research programme in their area of expertise. At least one appointee is expected to have research expertise in behavioural ecology.

Up to two positions will be offered as confirmation-path (tenure track) positions at the level of Lecturer (equivalent to Assistant Professor in the North American system). An appointment at Senior Lecturer Level (North American Associate Professor) may also be considered.

For more information, please see <https://otago.taleo.net/careersection/2/jobdetail.ftl?lang=en&job=1402226> Professor Hamish G. Spencer, FRSNZ Director & PI, Allan Wilson Centre Department of Zoology / Te Tari o Mātai Kararehe University of Otago / Te Whare Wānanga o Otāgo Dunedin / Ōtepoti New Zealand / Aotearoa

Email: [h.spencer@otago.ac.nz](mailto:h.spencer@otago.ac.nz) Postal: Department of Zoology, University of Otago, P.O. Box 56, Dunedin 9054 Courier: 340 Great King Street, Dunedin 9016 Phone: +64-3-479-7981 Fax: +64-3-479-7584

Departmental Website: <http://www.otago.ac.nz/zoology/staff/spencer.html> Allan Wilson Centre Website: <http://www.allanwilsoncentre.ac.nz/> Gravida Website: <http://www.gravida.org.nz/> NZ Mollusca Website: <http://www.molluscs.otago.ac.nz> [hamish.spencer@otago.ac.nz](mailto:hamish.spencer@otago.ac.nz)

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## USvalbard SpeciesAdaptation

Dear colleagues,

The University Centre in Svalbard (UNIS) is searching for a Full/ Associate Professor in terrestrial zoology. Application deadline 25 January.

The call can be found here: [http://www.unis.no/30\\_ABOUT\\_UNIS/4020\\_Vacant\\_Positions/documents/Korrigertutlysningstekstprofessor-forsteamanuensisizologi.pdf](http://www.unis.no/30_ABOUT_UNIS/4020_Vacant_Positions/documents/Korrigertutlysningstekstprofessor-forsteamanuensisizologi.pdf) List of vacant positions at UNIS: [http://www.unis.no/30\\_ABOUT\\_UNIS/4020\\_Vacant\\_Positions/vacant\\_positions.htm](http://www.unis.no/30_ABOUT_UNIS/4020_Vacant_Positions/vacant_positions.htm) Description of the position and qualifications: We are seeking a zoologist with strong international competence in terrestrial ecology. Candidates with experience from working in the field and from one or more of the following research areas will be considered: species evolutionary adaptations, interactions within and between populations and trophic levels, and community diversity. The collaborative skills and personal attributes of the successful candidate are essential. It is equally important that the person who is appointed has the ability to work independently, has a positive attitude and flexibility. The following qualifications are desirable: Fieldwork experience in the Arctic, a well-established national and international networks and teaching experience at different academic levels.

The appointed person is expected to conduct high quality research within her / his field of research and participate in the departments development of scientific quality combined with excellence in academic teaching. See: [www.bioceed.no](http://www.bioceed.no) The candidates field of expertise will be evaluated in relation to the existing plans and research profiles of the department. Potentials for research collaboration within the department will be emphasized.

Applicants are requested to document scientific, pedagogical and administrative experience and qualifications. Applicants for the position must be able to document their qualifications, as Full or Associate Professor as UNIS does not evaluate applicants for professorships. To be considered for the position of Associate Professor a Ph.D. in an appropriate field, or its equivalent, is the minimum requirement.

Regards, Øystein Varpe

Øystein Varpe Associate Professor University Centre in Svalbard

Adjunct researcher Akvaplan-niva

Øystein Varpe <[Oystein.Varpe@unis.no](mailto:Oystein.Varpe@unis.no)>

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## UWashington MarineConservation

The School of Aquatic and Fishery Sciences (SAFS; <http://fish.washington.edu>) at the University of Washington (UW) seeks a tenure-track Assistant Professor who will complement the diversity of research and education on aquatic systems and processes in SAFS, and enhance the work on the ecology and conservation of estuarine and nearshore marine ecosystems. For more information, see the full announcement at: <http://ap.washington.edu/ahr/-academic-jobs/position/aa9573/> Cheers- CT Curtis D. Tanner, Division Manager Environmental Assessment and Restoration U.S. Fish and Wildlife Service Washington Fish & Wildlife Office 510 Desmond Dr. SE, Suite 102 Lacey, WA 98503 office: (360) 753-4326 cell: (360) 951-6612 email: [curtis.tanner@fws.gov](mailto:curtis.tanner@fws.gov) <[https://mail.google.com/mail/?view=cm&fs=1&tf=-1&to=curtis\\_tanner@fws.gov](https://mail.google.com/mail/?view=cm&fs=1&tf=-1&to=curtis_tanner@fws.gov)>

“Tanner, Curtis” <[curtis.tanner@fws.gov](mailto:curtis.tanner@fws.gov)>

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## Vienna 2 FieldAssist AvianBehaviour

Two experienced field assistants in Reproductive Behaviour in city birds (Great Tits) needed (April-June 2014)

Two field assistant positions are available in a research project on reproductive biology in response to urbanity in Vienna, run by Sabine Hille.

Job description: The field assistants will help collecting breeding and behavioural data on urban Great Tits (*Parus major*) from the beginning of April 2015 to the end of June 2015. The aim of the research is to assess the effects of key urban environmental traits - physical and biological habitat variables - on the local avifauna. Assistants will work closely with an international team consisting of a PhD, Master and Bachelor students, as well as one the other assistant. Fieldwork will be done from beginning April until end of June 2015 in Vienna city. We are looking for two field assistants, with catching, handling and ringing experience in small passerines.

Candidates should preferably have a background in biological sciences. Field assistants will participate in systematic monitoring of breeding performance, individual growth patterns, in a nest box population. Field assistants will be responsible for the logistic organisation of the nest checks. Skills in ladder climbing and creative thinking and planning are expected. A European Driving license is required. Motivation will play a key role; the work is hard and demanding, takes place in changing weather and requires long hours at times. Timing of field work is fully to be adapted to the breeding activity of the birds and requires e.g. all May full day working hours. Work includes also entering data in a database.

Applicants are expected to stay for the entire field season. The language at the study sites will be English.

Applications: Review of the applications will begin Mid-January and continue until the positions are filled. To apply, please send (1) a statement of relevant experience, (2) a short resume or CV, and (3) contact information for two references. Applications should be in English. Bird ringers should indicate their level of experience and include their ringing licences into the application. Please provide names and email addresses of two persons who are willing to write a letter of recommendation, and send applications by email to the following address:

Dr. Sabine Marlene Hille Institute of Wildlife Biology and Game Management University of Natural Resources and Applied Life Sciences Gregor Mendel-Straße 33 1180 Vienna Austria Tel.: +431 47654 4463 (tel:%2B431%2047654%204463) Fax.: +431 47654 4459 (tel:%2B431%2047654%204459) [sabine.hille@boku.ac.at](mailto:sabine.hille@boku.ac.at)

Closing date: 5th of February 2015

Dr. Sabine Marlene Hille

Institute of Wildlife Biology and Game Management

University of Natural Resources and Life Sciences

Gregor Mendel-Straße 33 1180 Vienna Austria

Tel.: +431 47654 4463 Fax.: +431 47654 4459 skype: [sabinehille](https://www.skype.com/people/sabinehille)

Sabine Hille <[sabine.hille@boku.ac.at](mailto:sabine.hille@boku.ac.at)>

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**WestChesterU**  
**PlantMolecularGeneticist**

**Plant Molecular Geneticist**

Tenure track ASSISTANT PROFESSOR position available August 2015. Earned doctorate in Plant Molecular Biology or related discipline; research focused on some aspect of plant molecular genetics. The successful applicant must be qualified to teach Molecular Genetics, Recombinant DNA Methodology, Cell Physiology lecture and lab, as well as special topics courses or graduate courses, and may be required to teach labs in Botany and General Biology. Candidate is expected to establish an active, externally funded research program involving graduate and/or undergraduate students. Finalists must successfully complete an interview process that includes a research seminar

and teaching demonstration. To apply, upload a letter of application, statements of teaching and research philosophies, curriculum vitae, and all unofficial university transcripts to <http://agency.governmentjobs.com/wcupa/default.cfm>. Have three letters of reference sent by email to [search-bio@wcupa.edu](mailto:search-bio@wcupa.edu) or mail to Dr. Jessica Schedlbauer, 750 S. Church St., Department of Biology, West Chester University, West Chester, PA 19383. Review of completed applications begins on March 16, 2015 and continues until position is filled. For more details and full ad visit the website above or contact Dr. Jessica Schedlbauer at the email above. The filling of this position is contingent upon available funding. All offers of employment are subject to and contingent upon satisfactory completion of all pre-employment criminal background checks. Developing and sustaining a diverse faculty and staff advances WCU's educational mission and strategic Plan for Excellence. West Chester University is an Affirmative Action/Equal Opportunity Employer. Women, minorities, veterans, and persons with disabilities are encouraged to apply.

"Auld, Josh R." <[JAuld@wcupa.edu](mailto:JAuld@wcupa.edu)>

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**Other**

Alabama K-12ScienceStandards Draft .....	88	Passing of Bruce Wallace .....	95
Awake letter .....	88	PlantEvolSymposia funding .....	95
Bern Switzerland 2 VolFieldAssist AvianEvolution	89	PLANTS Grants .....	96
CallProposals NouraguesTravelGrant .....	90	Sample management software .....	96
ChihuahuanDesertBiodiversity UndergradExperience	90	Software DAMBE update .....	96
Exchange grants microMorph .....	91	Software Phylogeny LVB .....	97
GodfreyHewitt ESEB Award .....	91	SouthAfrica VolResAssist SocialMolerats .....	97
IIASA Austria SummerFellowships .....	92	Survey EvolBiolResearch Directions .....	98
NESCent 2015 VideoContest .....	93	Switzerland Internship BatEvolution .....	98
OmennPrize EvolutionAndMedicine Deadline Jan21	93	Systematics Research Fund .....	98
OmennPrize EvolutionAndMedicine Deadline Jan21	3	TravelAwards EvolMedicine DeadlineJan10 .....	99
93		TravelGrants ConservationGenetics .....	99
OxfordU VolFieldAssist SeabirdEvolution .....	94	TVMef model .....	100

UAlberta RedSquirrelVolunteers .....	100	USussex VolFieldAssist SpainWasps .....	102
UBern FieldAssist BirdEvolution .....	101	UTexas Austin Switchgrass Undergrads .....	102
UKansas UndergraduateResearchExperiences .....	101	Video suggestions .....	103
USaskatchewan PrairieDogVolunteers .....	101		

[www.ljrisler.org](http://www.ljrisler.org)    rissler@ua.edu    205-348-4052  
[www.speakingevolution.org](http://www.speakingevolution.org)    rissler@ua.edu

## Alabama K-12ScienceStandards Draft

Dear EvolDir Members, The new Alabama Course of Study in Science is now available for public comment until 30 January 2015. This is the framework for K-12 science education in Alabama's public schools. We encourage members of the EvolDir to comment on this draft. The link to the standards can be found on this page: <http://www.alsde.edu/dept/coss/Pages/welcome.aspx> . Why Comment?

1. The standards do not include evolution. If you search the document, "evolution" (n=4) is found only in the Preface. For example: "Since natural selection has been observed to play a role in influencing small changes in a population, it is assumed, based on the study of artifacts, that it produces large changes, even though this has not been directly observed." 2. Alabama requires an evolution disclaimer in every public high school biology textbook, and this has been the case since 1996! (<http://ncse.com/news/2011/03/-creationism-alabama-standards-006570>) The new standards include much of this language in the Preface. 3. Alabama has been rated by the NCSE in 2009 as the state with the lowest quality K-12 science standards. The current draft is only a draft. With enough substantive comments from the public, the new standards could be improved. 4. It is easy to comment. See <http://www.alsde.edu/dept/coss/Pages/forms.aspx> . We suggest reviewing and commenting on the Front Matter (Preface) and 9-12 Biology sections because they are most relevant to evolutionary biology.

Please help us make a difference to improve science literacy by adding your suggestions to the public draft (<http://www.alsde.edu/dept/coss/Pages/forms.aspx>).

Sincerely, Leslie Rissler

Dr. Leslie J. Rissler Professor Co-Director:  
Evolutionary Studies Minor (<http://evolutionarystudies.as.ua.edu/>) Chair: Evolution  
Working Group Curator of Herpetology Department  
of Biological Sciences Room 307 Mary Harmon Bryant  
Hall University of Alabama Tuscaloosa, AL 35487

## Awake letter

Dear EvolDir

The following letter was written in response to misquotation of my work by Jehovah's Witnesses in their magazine Awake, making me appear as if I support creationist view of the origin of life. I thought it might be of interest to the membership of EvolDir. I would welcome your comments and/or similar experiences.

Rama Singh

Evolution, Religion, Reason - An open letter to Jehovah's Witnesses

Editor of Awake (Magazine) Jehovah's Witnesses

Dear Editor,

I am writing to protest your Awake Magazine article, "The origin of life - five questions worth asking", dated January, 2015, in which you have misquoted me by taking half a sentence out of context from my article on evolution. Contrary to what you imply, I do not support a creationist view, nor do I suggest that even a minority of scientists support such a view. Anyone who reads my article can see that I fully support the theory of evolution (Singh 2011).

In my article, I follow the paragraph from which you have misquoted me with material showing why the facts of evolution are hard to comprehend for many people. My article is meant for people who want to understand evolution but who do not have the expertise to do so, not for creationists like you who oppose evolution on religious grounds.

Your misquotation amounts to intellectual dishonesty and reflects on your character and dignity as editor as well as a man of God. I can understand that you do not accept evolution as an explanation for the biodiversity on this planet, but I cannot understand why you would knowingly misuse a scientist's work to make him appear



supporting the creationist point of view.

I have received inquiries from many evolutionists, atheists and former members of your organization (ex-JW) who brought the above misquotation to my attention. I agree with them that your misquotation of my work is deliberate and meant to convince your followers in the truth of creationism by perpetuating false support from scientists.

So I am asking you first to remove the misquotation from your article immediately and second print an unconditional apology for what I consider is a deliberate damaging action on your part to my reputation.

The goal of religion is to seek truth, to remove ignorance and fear, not to perpetuate myths and lies. As a man of religion you may have the need for God and as a man of science I may not. But we both should be on the same side when it comes to the pursuit of truth. Believers need truth as much as non-believers do.

If I may suggest, as an organization you should stop wasting your time in perpetuating lies against evolution. Religion and science need each other. As Einstein remarked, religion is lame without science, and science is blind without religion. Religion and science are both driven by reason but they operate in different domains. Religion seeks absolute truth, science proceeds through incremental steps. Religion is the reason to keep science marching.

The Catholic Church and its leaders, including Pope Pius XII, Pope John Paul II, and most recently Pope Francis, have albeit slowly but progressively accepted evolution and do not see conflict between religion and science. God is not a magician, as Pope Francis said, and it's insulting to human intelligence to put everything at God's door. Jehovah's Witnesses should feel liberated in supporting evolution as it would free you from proselytizing false doctrine and allow you to dig deeper into the meaning and the mystery of life.

Accepting evolution does not bar you from believing in God and vice versa. This is exactly what many Hindus, Buddhists, and Jains do. All these religions came from the same trunk and yet Buddhism and Jainism were atheistic in their origins. Hindus' theory of reincarnation making God progressively appear in the different eons in the form of fish, turtle, boar, lion, a small man, a full man, Rama, Krishna, Buddha, and the future Kalki, represent an evolutionary ladder in higher organisms. According to Hindu texts, there are 8.4 million life forms (yoni/species) and the life (jiv) in all of them comes from the same source, implying a common origin. The literal theory of rebirth meaning life going through all 8.4 million life forms is obviously an evolutionary pro-

gression up the ladder if life. Hindus have no problem with believing in evolution and God at the same time.

Furthermore, not believing in religion and God does not mean that one has no interest in the origin and evolution of the universe and in the bigger questions of life. Atheists do not believe in organized religions or faiths, but atheists are as much interested in the bigger questions life and death as you are. Atheists too can be loving and kind. Let me give you an example:

"When Gandhi was developing his non-violent struggle movement for the freedom of India, he was also mounting a campaign against the social ills

— / —

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

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## Bern Switzerland 2 VolFieldAssist AvianEvolution

Two field assistant positions to study oxidative stress in relation to social status in house sparrows in Switzerland. We are seeking for two (2) research assistants for the upcoming breeding season to join a project investigating the impact of oxidative stress and social status on the development of reproductive strategies in house sparrow. The research will be conducted in Bern, Switzerland. The work will start on 1st of April and will continue through early/mid July. Our project investigates how males with different positions in a dominance hierarchy allocate their antioxidant resources to the protection of their sperm vs. the protection of their somatic functions, and how such allocation strategies affect the quality of the sperm they produce. The project is based at the University of Neuchatel, Switzerland (PI Prof. Fabrice Helfenstein, PhD student Alfonso Rojas), but will be conducted at Hasli, Bern, Switzerland. The work of the volunteers will consist in carrying out an experiment in aviaries with house sparrows. This includes assisting the PhD student with catching and banding birds, behavioural observations, sample collection, data management and data analysis. During the conduct of the experiment we work 7 days a week and 10-12 hours a day. Qualifications: (1) BSc or higher in Biology or similar qualification (2) Ability to work and live in small groups and sociable personality (3) Fluent in English

(French and/or German are a plus, but not essential) (4) Ability to endure long working days (5) Knowledge in observing & handling birds is a plus (6) Driving license. This is a volunteer field assistant position, thus the applicant should cover his/her travel expenses and food. Accommodation expenses will be covered (up to 500.-CHF/month). Applications - including a CV and a letter of motivation (1 pg.) - should be send to both: Fabrice Helfenstein: [fabrice.helfenstein@unine.ch](mailto:fabrice.helfenstein@unine.ch) and Alfonso Rojas: [alf.roja@gmail.com](mailto:alf.roja@gmail.com) Please use "Volunteer Assistant in Switzerland" as the subject and note your availability during this time period in the body of the e-mail. Applications received until 15th of February 2014 will be given full consideration. Do not hesitate to contact us for further information.

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Alfonso Rojas Ph.D. Student Evolutionary Ecophysiology Institute of Biology University of Neuchâtel Rue Emilie-Argand 11 CH-2000 Neuchatel Tel: 0041 (0) 32 718 3037 Switzerland

Alfonso Rojas <[alf.roja@gmail.com](mailto:alf.roja@gmail.com)>

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### CallProposals NouraguesTravelGrant

\*The Nouragues Travel Grant 2015\*

The Nouragues annual call for proposals is aimed at facilitating access to the Nouragues station for scientists of all research fields. Graduate students, post-doctoral researchers, and established scientists may apply.

Submitted proposals will be evaluated by a Science Advisory Board and selected based on their excellence, the quality of expected publications, and the feasibility of the project. The grants will not exceed 9,000 euros in total, and will be for a duration of one year. Reapplications will be evaluated based on the achievements of the previous years. Grant recipients will be expected to contribute to the dissemination of knowledge in French Guiana, via participation in outreach programs of the collaborating Nouragues Natural Reserve.

In 2015, experimental projects and projects related to the new COPAS instrument (Canopy Operational Permanent Access System) will be especially considered.

Deadline for application: March 6th, 2015.

For more information : <http://www.nouragues.cnrs.fr/-spip.php?article42> Amaia IRIBAR-PELOZUELO

Chargée de coordination scientifique CEBA

Laboratoire Evolution et Diversité Biologique UMR 5174 Université Paul Sabatier, bÂt 4R1, bureau 124 118 route de Narbonne, 31062 Toulouse Cedex 9 - France

tél : + 33 (0)5 61 55 64 95 fax : + 33 (0)5 61 55 73 27

link: [www.labex-ceba.fr](http://www.labex-ceba.fr) Amaia Iribar-Pelozuelo <[amaya.pelozuelo@univ-tlse3.fr](mailto:amaya.pelozuelo@univ-tlse3.fr)>

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### ChihuahuanDesertBiodiversity UndergradExperience

REU Opportunity Summer 2015: "Research Experience for Undergraduates in Chihuahuan Desert Biodiversity"

The University of Texas at El Paso (UTEP) Department of Biological Sciences invites applicants for the NSF sponsored Research Experience for Undergraduates (REU) in Chihuahuan Desert Biodiversity. This is a 10 week summer program. The goal of this program is to provide undergraduate students with experience in hypothesis-driven collaborative research utilizing field based and/or laboratory methods and fully engage students in projects associated with the ecology and evolution influencing Chihuahuan Desert biodiversity.

The program provides: \* High quality research experience in ecology and evolutionary biology in the field and/or lab \* Research opportunities at the Indio Mountains Research Station (IMRS), a 40,000 acre facility controlled by UTEP \* One-on-one and group mentoring from active research faculty in multidisciplinary fields \* Training in bioethics and other relevant professional skills

The program includes \* \$5000 stipend for 10 weeks \* Housing in shared apartments and field station \* Travel reimbursement of up to \$600

For more information on the program, research projects or to apply please visit: <http://cosrvfile00.utep.edu/-cdb-reu/> Enquiries: [CDB-REU@utep.edu](mailto:CDB-REU@utep.edu)

[mlmoody@utep.edu](mailto:mlmoody@utep.edu)

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## Exchange grants microMorph

### Cross-Disciplinary Visits and Training Grant

The microMORPH RCN promotes and fosters cross-disciplinary training and interaction through a series of small grants that allow graduate students, post-doctoral researchers, and early career faculty to visit labs and botanical gardens. Being listed on the microMORPH community web page is required of all successful applicants (and encouraged for everyone else!).

**Award Amount:** Each Year, microMORPH is able to fund five graduate student, post-doctoral, or early career faculty cross-training research opportunities for up to \$3,500 to cover travel, lodging, and per diem.

**Submission Deadline:** The next microMORPH Cross Disciplinary Training Grant deadline is 11:30 pm March 1st, 2015.

**Eligibility:** To be eligible for a microMORPH training grant you must fulfill one or more of the following requirements: 1) you must be a U.S. citizen or, 2) you must be affiliated with a U.S. university or institution (in a graduate program or working as a post-doc or faculty member), or 3) the lab you plan to visit for your training experience must be at a U.S. university of institution.

**How to Apply:** For full application instructions (including list of required documents) and to submit applications, please visit the microMORPH website(<http://projects.iq.harvard.edu/micromorph>).

**Proposal Evaluation:** Two members of the steering committee (one organismic and one molecular) and a third individual from outside the core participants (chosen by the steering committee) are charged with evaluating applications.

**Questions or Comments?:** Contact Becky Povilus at [RCNmicromorph@gmail.com](mailto:RCNmicromorph@gmail.com)

[pamela.diggle@uconn.edu](mailto:pamela.diggle@uconn.edu)

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## GodfreyHewitt ESEB Award

**\*\*Godfrey Hewitt Mobility Award 2015 Call for Applications\*\***

Godfrey Hewitt (1940-2013) was President of the European Society for Evolutionary Biology (ESEB) from 1999-2001. He was exceptionally influential in evolutionary biology both through his research and through his mentoring of young scientists. He was also a great believer in seeing organisms in their environment first-hand and in exchanges of ideas between labs. Therefore, ESEB has decided to offer, annually, mobility grants for young scientists in his name.

**Closing date:** Friday 16 January 2015, 12.00 GMT.

**Eligibility:**

The award is open to PhD students or postdoctoral scientists who are, at the closing date for applications, both within 6 years of the start date of their PhD and ESEB members. The maximum single award will be 2000 Euros. It must be used to support fieldwork or a period of research at a lab that you have not previously visited. There is no restriction on the country of residence or nationality of the applicant but preference will be given to applicants who are unlikely to be able to fund the proposed work by other routes. Preference will also be given to self-contained or 'seed-corn' projects, rather than fundamental elements of already-funded PhD or postdoctoral projects, and to projects with a definable output that is achievable within the scope of the GHM award. A report will be required by 30 April 2016, by which time the funds must have been used.

**Application procedure:**

Your application should be sent as a single PDF file to Ute Friedrich at the ESEB office, [office@eseb.org](mailto:office@eseb.org). It should include your name, current status and institution, your PhD start date, your ESEB membership number, a description of the work to be carried out (maximum 500 words), an outline budget with brief justification (maximum 100 words) and a signed statement from your PhD supervisor or postdoctoral adviser (maximum 100 words) explaining why the work cannot be funded from your institution.

Applications will be considered by a committee chaired by Roger Butlin. The aim will be to announce decisions before the end of March 2015.

Sincerely, Ute Friedrich ESEB Office Manager

European Society for Evolutionary Biology  
 Email: [office@eseb.org](mailto:office@eseb.org) Homepage: [www.eseb.org](http://www.eseb.org)  
[office@eseb.org](mailto:office@eseb.org)

## IIASA Austria Summer Fellowships

Summer Fellowships for Young Scientists at the International Institute for Applied Systems Analysis, Austria

Funding is available for PhD students interested in three months of collaborative research during June-August 2015 on

Evolutionary and Ecological Modeling

at the International Institute for Applied Systems Analysis (IIASA) in Laxenburg, Austria.

Young scientists from all countries are eligible for stipends provided by IIASA's Evolution and Ecology Program (EEP) that contribute to travel and accommodation costs. Students from Australia, Austria, Brazil, China, Egypt, Finland, Germany, India, Indonesia, Japan, Korea, Malaysia, Mexico, the Netherlands, Norway, Pakistan, Russia, South Africa, Sweden, Ukraine, USA, and Vietnam are furthermore eligible for fellowships that provide full coverage of travel, accommodation, and living expenses.

Model-based summer research projects are invited in the following indicative areas:

Evolution of cooperation Governance of common goods Systemic risk and network dynamics Eco-evolutionary dynamics Evolutionary community ecology Food-web evolution Vegetation dynamics Adaptive speciation Disease ecology and evolution Evolutionary conservation biology Fisheries management Fisheries-induced evolution Adaptive dynamics theory and models Spatial models in ecology and evolution

Applicants are encouraged to prepare a research proposal that corresponds to their scientific interests and to the research agenda of their hosting IIASA Program. Accepted applicants will begin work before the summer, by planning their research in collaboration with their IIASA supervisors. Previous experiences with implementing and studying evolutionary or ecological models are important assets for working in EEP. To improve chances of being selected, potential applicants are welcome to send informal inquiries regarding their specific research interests and plans to EEP's program director

Ulf Dieckmann ([dieckmann@iiasa.ac.at](mailto:dieckmann@iiasa.ac.at)).

Online applications will be accepted until Monday, January 12, 2015 (24:00 CET).

Since 1977, IIASA's annual Young Scientists Summer Program (YSSP), has attracted 1750+ students from 80+ countries. The YSSP 2015 will take place from June 1 to August 31. IIASA is located in the former summer palace of Austria's royal family, ca. 15 km south of Vienna. IIASA's summer program offers exceptional opportunities for acquiring experience in an international and interdisciplinary research environment. Research training is based on regular personal interaction with advising scientists, and typically leads to a publication in an international journal, as well as to a chapter in a candidate's PhD thesis.

Some useful links:

+ Details about the summer program, and online application <http://www.iiasa.ac.at/web/home/-education/yssp/Apply/ConditionsEligibility/-Conditions-and-Eligibility.en.html> + Information about IIASA's Evolution and Ecology Program <http://www.iiasa.ac.at/web/home/research/-researchPrograms/EvolutionandEcology/New-page.en.html> + Examples of successful YSSP projects <http://www.iiasa.ac.at/web/home/-research/researchPrograms/EvolutionandEcology/-AbouttheProgram/Student-Participation-in-EEP.en.html> + General information about IIASA [http://www.iiasa.ac.at/web/home/about/whatisiiasa/-what\\_is\\_iiasa.html](http://www.iiasa.ac.at/web/home/about/whatisiiasa/-what_is_iiasa.html) Ulf Dieckmann Program Director Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

Email [dieckmann@iiasa.ac.at](mailto:dieckmann@iiasa.ac.at) Phone +43 2236 807 386 Phone secretary +43 2236 807 231 Fax +43 2236 807 466 or +43 2236 71313 Web <http://www.iiasa.ac.at/-Research/EEP> Online reprints <http://www.iiasa.ac.at/~dieckman> FroSpects Network <http://www.iiasa.ac.at/-Research/EEP/FroSpects> FinE Network <http://www.iiasa.ac.at/Research/EEP/FinE> FishACE Network <http://www.iiasa.ac.at/Research/EEP/FishACE> DIECKMANN Ulf <[dieckmann@iiasa.ac.at](mailto:dieckmann@iiasa.ac.at)>

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## NESCent 2015 VideoContest

NESCent 2015 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) 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.)

First- and second-place winners will receive up to \$1,000 and \$500, respectively.

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](https://www.skype.com/jory.weintraub)

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

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## OmennPrize EvolutionAndMedicine Deadline Jan21

The International Society for Evolution, Medicine, & Public Health invites nominations for the Omenn Prize

of \$5000 to be awarded in March 2015 for the best article published in 2014 in any scientific journal on a topic related to evolution in the context of medicine and public health.

The prize, provided by the generosity of Gilbert S Omenn, will be awarded to the first author of the winning article. Authors are encouraged to nominate their own articles, but nominations of articles by others are also welcome. Nominations, including a brief statement in the body of the email (max. 250 words), a copy of the article (if distribution is permitted) or abstract and article link, must be submitted by 21 January, 2015 at 5 PM US Eastern Standard Time. All applications should be sent to [OmennPrize@evolutionarymedicine.org](mailto:OmennPrize@evolutionarymedicine.org)

Any relevant peer-reviewed article published online or in print in 2014 is eligible, but the prize is intended for work that uses evolutionary principles to advance understanding of a disease or disease process. The prize committee will give priority to articles with implications for human health, but many basic science or theoretical articles have such implications.

The Prize Committee for this year is chaired by Sarah Tishkoff, and its members are Joe Alcock, Noah Rosenberg, and Alison Galvani. Papers by committee members, their students and lab group members are not eligible, and articles by their co-authors or close associates are subject to special conditions.

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

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be sent to [OmennPrize@evolutionarymedicine.org](mailto:OmennPrize@evolutionarymedicine.org)

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

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### OxfordU VolFieldAssist SeabirdEvolution

Dear EvolDir,

We are looking for a voluntary research assistant to help us during our field season for our ongoing seabird research. The deadline for applications is the 31st Jan 2015 and we can only accept applicants who have permission to work in the UK. I would be highly grateful if you could post/circulate the advert below in the EvolDir community.

Many thanks and best wishes,

Oliver Padget

Zoology Department, Oxford University, United Kingdom

Voluntary research assistantship in seabird behaviour & ecology Skomer Island & University of Oxford

We are looking for an enthusiastic, hardworking young biologist to work as a voluntary Research Assistant to help with our pelagic seabird research on Skomer Island, Pembrokeshire, Wales, in Spring and Summer 2015. The work will involve several research projects coordinated by Prof Tim Guilford at Oxfords Department of Zoology (see the OxNav website). We utilise state-of-the-art tracking technologies (miniature GPS, geolocators, time-depth recorders & on-board video) on several species (Manx Shearwaters, Atlantic Puffins, Common Guillemots, Razorbills). Most work will involve assisting doctoral students with the day-to-day maintenance

of the study burrows, weighing and monitoring breeding birds and their chicks, and the deployment and retrieval/downloading of tracking devices. It will also involve entering data collected in the field into appropriate databases. There will be a significant amount of nocturnal work, since the primary study species is the Manx Shearwater, which only arrives at the colony after dark. There will also be scope for involvement in other conservation and ecological projects on the island, which is a National Nature Reserve administered by the Wildlife Trust of South and West Wales.

Unfortunately we cannot provide a stipend but accommodation (shared and basic) on Skomer will be covered. However, the project is a great opportunity to gain valuable experience in modern field ornithology. There will also be opportunities for the assistant to learn some analytical techniques applied to animal movement data. Skomer has mobile coverage and some access to Internet, however movements to and from the mainland are limited because of unpredictable wind conditions. There is a small community of wardens, assistants and volunteers, who are involved in the running and conservation of the Nature Reserve, monitoring the seabird populations, and managing the daily and over-night visitors. There might be opportunities to visit other UK island reserves during the project.

Profile: we are looking for a motivated and hardworking biologist, who likes working in the field and can cope with difficult working and living conditions. Previous experience in the field or in harsh conditions is desirable, but not essential. Work on Skomer requires long hours (with some work at night and at dawn) spent in a cold and wet environment and considerable manual work. A good candidate should be able to work independently and have a reasonable level of fitness. Planning to embark on further research degrees in the future would be a plus (previous assistants have engaged in doctoral studies afterwards). It is also important that the assistant feels comfortable sharing sometimes crowded accommodation with a number of colleagues over long periods of time, and can cope with the occasional untidiness inevitably associated with fieldwork. Unfortunately, for administrative reasons, we can only accept applications from people having permission to work in the UK (UK and EU citizens, UK residents, or persons with a UK work permit).

We are looking for an assistant to work with us between April and September 2015. If you are interested, please email a CV and a statement of interest and arrange for two letters of reference to be emailed to [tim.guilford@zoo.ox.ac.uk](mailto:tim.guilford@zoo.ox.ac.uk) (with [oliver.padget@zoo.ox.ac.uk](mailto:oliver.padget@zoo.ox.ac.uk) in cc). The deadline for submitting applications (including reference letters) is

the 31st January 2015. We will interview the shortlisted candidates (on Skype) shortly after and we expect to make a decision by late February.

Oliver Padget <oliver.padget@linacre.ox.ac.uk>

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## Passing of Bruce Wallace

It is my sad duty to inform his colleagues and friends here that Prof. Bruce Wallace passed away on Monday, January 12, 2015, at the age of 94. Details of any memorial services, obituaries, etc. will be posted here as they are forthcoming from his family.

Bruce Turner

Please post this elsewhere as you think appropriate,

Bruce Turner <fishgen@vt.edu>

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## PlantEvolSymposia funding

\*Funding of up to £43k is available to run symposia with slots available from 2017 onwards. Application deadline is 28th February 2015.\*

If you are interested in organising a New Phytologist Symposium, please complete the proposal pro forma ( [http://www.newphytologist.org/app/webroot/img/upload/-files/NPS%20proposal\\_pro%20forma2015\(1\).docx](http://www.newphytologist.org/app/webroot/img/upload/-files/NPS%20proposal_pro%20forma2015(1).docx) ) and email this to the Managing Editor (np-managed@lancaster.ac.uk) by the end of February. Feel free to get in touch with any queries or for guidance on completing the proposal.

The internationally renowned series of New Phytologist Symposia (NPS) aim to support emerging and key areas of research. Usually these meetings would be expected to extend over one to three days, with invited speakers and a maximum of 120 delegates. In this way we hope to provide an informal atmosphere for the stimulation and exchange of ideas and the building of collaborations. We particularly encourage the involvement of early career scientists and as such a number of travel grants will be awarded in association with each meeting.

Information about past and upcoming symposia can be found here: <http://www.newphytologist.org/>

**symposia** We also welcome workshop proposals throughout the year and we can support workshops scheduled from 2016 onwards. To submit a proposal for a workshop download and complete the proposal pro forma ( [http://www.newphytologist.org/app/webroot/img/upload/files/-NPWorkshopProposal\\_proforma2015%281%29.docx](http://www.newphytologist.org/app/webroot/img/upload/files/-NPWorkshopProposal_proforma2015%281%29.docx) ) and email this to the Managing Editor (np-managed@lancaster.ac.uk). Further details can be found on the website: <http://www.newphytologist.org/workshops> or feel free to get in touch with any queries.

New Phytologist Workshops aim to facilitate advances in plant science by bringing together a small number of scientists (up to 20) who wish to focus and brainstorm a particular topic or issue. The format is intentionally flexible to suit a range of projects, but this might, for example, include a working group that intends to focus on analysing new data or indeed analysing old data in the light of new techniques and planning the way forward. Awards are usually in the region of £5-10k.

Dr MICHAEL PANAGOPULOS Development Coordinator, New Phytologist

New Phytologist Central Office, Bailrigg House, Lancaster University, Lancaster, LA1 4YE, UK  
Tel: + 44 1524 592839 Fax: + 44 1524 594696 Email: [m.panagopulos@lancaster.ac.uk](mailto:m.panagopulos@lancaster.ac.uk) Website: [www.newphytologist.org](http://www.newphytologist.org) Twitter: @NewPhyt Facebook: [fb.com/NewPhytologist](https://www.facebook.com/NewPhytologist)

The New Phytologist Trust, registered charity number 1154867

2013 Impact factor 6.545

New Phytologist Symposia 2015 Genomes of forest trees (Boston, USA) // Plant-microbe interactions (Munich, Germany)

[m.panagopulos@lancaster.ac.uk](mailto:m.panagopulos@lancaster.ac.uk)

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## PLANTS Grants

Applications for the PLANTS program are now open and due by March 1, 2015. This program will fund up to 12 US undergrads to attend the Botany 2015 meeting of the Botanical Society of America and affiliated societies July 25 - 29, 2015 in Edmonton, Alberta, Canada. Meeting topics range across all levels of botany, including ecology, conservation, biodiversity, plant genomics, evolution, plant systematics, and botanical education. Peer mentors and senior mentors work with PLANTS students and attend talks with them, introduce them to colleagues, and generally make the meetings a welcoming place for them. There are also a number of social functions and career-oriented activities, specifically targeted at students for networking and fun. The meetings are a great way to understand the breadth of botanical research and education, to meet undergraduate and graduate students with similar interests, and to network with professionals in your area of interest. The program covers the normal costs of travel, registration, and food and accommodation at the meeting. An overview of the scientific conference will be available at [www.botanyconference.org](http://www.botanyconference.org) APPLICATIONS DUE BY MARCH 1, 2015: Applications ([http://www.botany.org/Awards/F\\_PLANTS.php](http://www.botany.org/Awards/F_PLANTS.php)) are open and due by March 1, 2015 and include your statement of interest, a letter of recommendation, and unofficial transcripts. Applications are welcome from all undergraduates who have interest in plant science; the admissions goal is to create a diverse pool of students attending the meetings. For questions, please contact the organizers Heather Cacanindin (HCacanindin@Botany.org), Ann Sakai (aksakai@uci.edu), or Ann Hirsch (ahirsch@ucla.edu).

aksakai@uci.edu

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## Sample management software

Dear colleagues,

we are searching a way to get rid of Excel tables of our samples in Dropbox or network drives. Would you be so kind and suggest solutions regarding the management

of samples? Our samples are regular molecular ecology stuff. Sometimes we have multiple samples from the same individual, and also multiple samples types. Otherwise we do not need anything special. It would be nice if the sample management could be online etc. To be honest: We do not exactly know what we need ;-) We rather wish to explore some options. If you can suggest a software/system, would you as well very briefly let me know which are the pro and cons in your daily use, and for what applications you have it? I'll of course repost all collected info here on EvolDir in a few days.

Thanks in advance!

Cheers, Robert

robert.kraus@uni-konstanz.de

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## Software DAMBE update

Dear Colleagues,

I have uploaded a new version of DAMBE with two major revisions:

1. The addition of the index of translation elongation (LTE, with four different implementations, and a number of codon tables for a subset of bacterial species). The paper detailing LTE has been published by Genetics been chosen as one of the highlights for the February issue of Genetics (Xia, X. 2015. A Major Controversy in Codon-Anticodon Adaptation Resolved by a New Codon Usage Index (<http://www.ncbi.nlm.nih.gov/pubmed/25480780>))
2. An improvement of the search algorithm for DNAML and DNAMP. You may compare the tree from DAMBE against trees from PHYLIP's DNAML and other programs to see the difference.

Please download to use it (I have also added quite a number of undocumented features mostly related to translation initiation and prokaryotic operon structure. I will explain them in the future).

For those not familiar with DAMBE, it is a comprehensive software package for data analysis in molecular biology and evolution, available free at:

<http://dambe.bio.uottawa.ca/dambe.asp> A recent release was documented in Xia, X. 2013. DAMBE5: A comprehensive software package for data analysis in molecular biology and evolution. *Molecular Biology and Evolution* 30:1720-1728



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 <Xuhua.Xia@uottawa.ca>

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## Software Phylogeny LVB

Dear Evoldir,

Phylogeny reconstruction software, LVB 3.2 Beta, has been released.

Compared to earlier releases of LVB it is much faster, more flexible and now has a full Open Source license.

Download LVB here:

<http://eggg.st-andrews.ac.uk/lvb> - Daniel

– Daniel Barker <http://biology.st-andrews.ac.uk/staff/-db60> The University of St Andrews is a charity registered in Scotland : No SC013532

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## SouthAfrica VolResAssist SocialMolerats

SouthAfrica.ResearchAssistant.SocialMolerats

Cooperative breeding in Damaraland mole-rats (*Fukomys damarensis*), South Africa.

2 Positions:

15th of March 2015 to 14th of June 2015.

Mid-June 2015 to mid-September 2015.

We are looking for two voluntary field research assistants to conduct field research on the completely subterranean, highly social Damaraland mole-rat (*Fukomys damarensis*). Specifically, this project investigates the group augmentation hypothesis and how benefits of living large groups can generate selection for altruism in animals. We plan a large scale capture-mark and recapture experiment running over one year in which the voluntary research assistant would play an important role. Field work takes place in the southern Kalahari, Northern Cape province of South Africa. Entire groups of mole-rats will be captured and individually marked. Morphological measurements and tissue samples will be obtained before the release of the animals. The work is

physically extremely demanding (long hours, heavy digging to capture mole-rats) and weather conditions are very challenging (heat during the day, very cold during the night). Field work will make trapping during the night necessary. The assistant will mostly be working along one more experienced scientist but will need to work independently at times.

Applicants should be enthusiastic, willing to work hard and keen to get involved in an ecological research project in the African bush. Research assistants are expected to be willing to work at night when trapping schedules require it and need to be fit as capturing mole-rats requires the capacity to do hard physical work (digging) in a challenging environment. Applicants must be holders of a driving license. A zoology related degree and/or previous field experience will be considered an asset. The successful applicants will work in a small team of 2 persons and hence need to be a team player and generally a person that enjoys collaboration under sometimes challenging and isolated circumstances.

Accommodation is provided, and research assistants are paid a monthly allowance to cover their food.

Applications received until the 12th of February 2015 are ensured full consideration. Later applications can be considered (particularly for the second time period). Dates for the second period are more flexible and applicants can indicate if they wish to commit for a longer period.

Further Information:

<http://bit.ly/1zG67hJ> To apply (CV + cover letter) or enquire further information contact:

Dr Markus Zöttl

Research associate

University of Cambridge

+441223336673

Mz338@cam.ac.uk

<http://www2.zoo.cam.ac.uk/larg/-MARKUSZOETTL.html>  
<mz338@cam.ac.uk>

Markus Zoetl

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## Survey EvolBiolResearch Directions

Dear Fellow Evolutionary Biologists and Ecologists:

Please help us identify and prioritize future directions for long-term ecological research by taking the survey below, funded by the National Science Foundation and administered through Yale and Michigan State Universities.

Link to the online survey: [https://yalesurvey.qualtrics.com/SE/?SID=-SV\\_0SqycN6h3AUMUvz](https://yalesurvey.qualtrics.com/SE/?SID=-SV_0SqycN6h3AUMUvz)

Your participation is very important to ensure that viewpoints from a representative cross-section of ECOLOGISTS AND EVOLUTIONARY BIOLOGISTS shape the outcomes of this initiative.

Thank you for taking the time to share your expertise.

Jennifer Lau Associate Professor Kellogg Biological Station and Dept. of Plant Biology Michigan State University [jenlau@msu.edu](mailto:jenlau@msu.edu) phone: 269-671-2107 fax: 269-671-2104

[jenlau@msu.edu](mailto:jenlau@msu.edu)

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## Switzerland Internship BatEvolution

Internship for undergraduate/ Master's degree student for the bat project

Topic: Impact of oxidative stress on alternative reproductive tactics in bats.

Context: Oxidative stress is considered to be a major mechanism impacting on life history trade-offs. *Carollia perspicillata*, a neo-tropical bat, shows two reproductive tactics, with harem males defending a territory, and bachelor males. Our hypothesis is that bachelor males, because they have less mating opportunities will invest more in sperm quality than harem males. The project is based at the university of Neuchâtel, Switzerland. We study a captive bat colony (Papiliorama <http://www.papiliorama.ch>). Bats can fly freely under a 40m-diameter dome, which includes an artificial cave. The light cycle is reversed, allowing us to work during the

day. Therefore, it is a unique opportunity to study bats, animals still largely unknown.

Tasks of the intern, in collaboration with the two PhD students working on the project:

- Planning of the experiment
- Help to feed the bats that are in cages during the experiment
- Participation in blood and sperm collect
- Behavioral observation
- Possibility of lab work

About the position:

- It can be part of your studies. Therefore, the candidate is welcome to conduct a personal research project.
- Not paid, but housing could be reimbursed for two month maximum
- Minimum duration of two months, possibly starting at the end of February.

Please feel free to contact us if you have any questions. To apply, please send a CV and a cover letter to [magali.meniri@unine.ch](mailto:magali.meniri@unine.ch), [nicolas.fasel@iee.unibe.ch](mailto:nicolas.fasel@iee.unibe.ch) and [fabrice.helfenstein@unine.ch](mailto:fabrice.helfenstein@unine.ch)

MENIRI Magali <[magali.meniri@unine.ch](mailto:magali.meniri@unine.ch)>

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## Systematics Research Fund

Reminder: application deadline is Friday 16th January 2015. See: <http://bit.ly/1vkRZC0> Systematics Research Fund - 2014/15 call for applications

The Systematics Research Fund is a joint fund of the Linnean Society of London and the Systematics Association. It provides grants for small-scale research projects in the field of systematics. The 2014/2015 application round is now open. The deadline for applications is Friday 16th January 2015.

The SRF typically supports fieldwork expenditure, the purchase of scientific equipment or expertise (e.g. buying time on analytical equipment), specimen preparation (including the cost of temporary technical assistance), and publication costs.

Projects of a more general or educational nature may also be considered, provided that they include a strong systematic component.

The fund is unable to cover article processing charges

and it does not provide support for attendance at scientific meetings, student maintenance or tuition fees, nor for bench fees.

Projects already substantially funded by other bodies may be disadvantaged.

Successful projects are selected by a panel of systematists who represent a wide range of conceptual interests and taxonomic groups. The value of any single award will not exceed £1500.

Please note that the applicant named on the application form must be a current member of the Linnean Society of London or the Systematics Association to be eligible for funding.

For more information, please see: <http://bit.ly/1vkRZC0> Mark Carine <M.Carine@nhm.ac.uk>

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### TravelAwards EvolMedicine DeadlineJan10

The International Society for Evolution, Medicine, & Public Health meeting March 19-21 in Arizona has support for student and faculty travel awards, thanks to the National Evolutionary Synthesis Center, the Triangle Center for Evolution and Medicine, and donations to the Foundation for Evolution, Medicine, & Public Health. Meeting details are at <http://evmedmeeting.org>. Applications for travel awards may be submitted without first registering for the conference.

#### STUDENT TRAVEL AWARDS

Travel awards of \$500 to \$1,000 US dollars (possibly more depending on applications) each to students to defray a portion of the costs of lodging and travel to the ISEMPH inaugural meeting.

-The applicant must be a student in good standing as an undergraduate, graduate student, postdoctoral fellow, veterinary student, medical student or medical resident, in a degree program at an accredited university.

-\$5,000 of the available awards are committed for support of students from under-represented groups in science, including women, thanks to funding from the the National Evolutionary Synthesis Center (NESCent) and the Triangle Center for Evolutionary Medicine (TriCEM). If you would like to be considered for one of the awards for students from underrepresented groups, please indicate that in your statement.

-Students presenting papers or posters at the conference

are prioritized; followed by students who are co-authors of papers or posters to be presented at the conference. However, students who will not be presenting are still encouraged to apply and will be supported if possible. Travel distance and overall costs are also considered when making awards.

Submission Deadline: January 10, 2015 Notification: January 31, 2015 Application information at <http://evmedmeeting.org> FACULTY TRAVEL AWARDS

Funding is available from the National Evolutionary Synthesis Center (NESCent) and the Triangle Center for Evolutionary Medicine (TriCEM) to support travel by faculty from under-represented groups in science to the International Society for Evolution, Medicine, & Public Health meeting in Arizona March 19-21. Applicants must be from an under-represented group in science and be on the faculty at a Minority Serving Institution or Historically Black College or University.

Submission Deadline: January 8, 2015 Notification: January 15, 2015 Apply at <http://goo.gl/forms/T9tRztmVt4> [rmnesse@gmail.com](mailto:rmnesse@gmail.com)

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### TravelGrants ConservationGenetics

#### TravelGrants - ConservationGenomics

Dear colleagues,

The European Research Networking Programme “ConGenOmics” invites applications for travel grants intended to foster collaborations between European researchers working on topics related to conservation genomics.

We will support the exchange of researchers within Europe, ideally targeting at early careers researchers such as PhD students and postdocs. We invite applications for short visits (up to 2 weeks) or longer exchanges (up to 3 months) to foster scientific interactions between institutions from different countries. The planned visits should be directly relevant to the scope of the ConGenOmics network programme, which include topics such as:

- Development and transfer of genomic knowledge and approaches in a conservation context
- Experimental study of the (genomic) mechanisms behind important biological processes of relevance for conservation
- Application and development of data handling and

processing strategies in conservation genomics

- Application of community and metagenomics in conservation biological context

Please note that the congenomics programme is funded by the European Science Foundation and that only exchanges between European countries can be considered. Exchanges between member countries of the congenomics network will be prioritized. After assessment of scientific merit and relevance to the ConGenOmics network, priority will be given to applications in the following order:

- knowledge exchange between contributing countries of the ESF ConGenOmics network
- knowledge exchange between a contributing country and a non-contributing ESF member country or the associated USA Ecogenomics network Ecological Genomics Institute (EGI) at Kansas State University (KSU)
- knowledge exchange between a contributing country and a non-ESF member country in Europe

(Researchers from countries with ESF Observer status not contributing to the ConGenOmics network are considered non-ESF)

\*\*Contributing member countries are: Belgium, Denmark, Finland, Germany, Greece, Italy, Luxembourg, Netherlands, Norway, Portugal, Spain, Sweden and Switzerland.

Further information and instructions on how to apply are available at

<http://www.ru.nl/congenomics/grants-application/-travel-grants/> Deadline for submission: 1 March 2015

philippine.vergeer@wur.nl

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## TVMef model

Hello .

Does anyone can tell me if the model TVMef (molecular evolution) is derived from TrN model ??

Thanks a lot. Rodrigo

Rodrigo Augusto Torres <rodrigotorres@ufpe.br>

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## UAlberta RedSquirrelVolunteers

Field Assistants Required-North American red squirrels Kluane, Yukon, Canada

We are looking for 3 volunteers to assist with fieldwork for the period of February 20 to the end of May, 2015, and a further 5 volunteers from May through August (please note: there is the exciting possibility of linking this position with a 'sister study' on Columbian ground squirrels in Alberta. See below). The positions are part of a long-term study of red squirrel population dynamics. As a member of the study, assistants will be involved with monitoring the reproduction and survival of individuals. Fieldwork will involve live-trapping and handling of animals, radio-telemetry, behavioural observation, and climbing trees to find young in nests. This is an excellent opportunity to gain experience working with a collaborative research team on a long-term study of a wild mammal.

All fieldwork is carried out in the beautiful backdrop of southwestern Yukon, Canada. We will be staying at a rustic field station two hours from Whitehorse. Food and accommodation are provided. Volunteers are required to provide for their own travel to Edmonton, Alberta; however, travel from Edmonton to the field station (and back again!) is provided.

Training will be provided and no experience is necessary, but candidates should have an interest in a number of the following: ecology, evolutionary biology, wildlife, field biology, and animal behaviour. The field camp is remote and low tech (no showers, cell phone service, or internet), so successful applicants must enjoy the outdoors and be able to remain a positive and responsible team member under relatively isolated and demanding conditions. Candidates must be in good physical condition, be willing to climb trees, and have an enthusiasm for learning. We work on 'squirrel time', which often involves long work days; as such, applicants must have a strong work ethic. That said, the atmosphere at squirrel camp is friendly and inclusive, and this area is one of the most beautiful in Canada.

Columbian ground squirrel study: We are also involved with a similar long-term study on Columbian ground squirrels in Kananaskis, Alberta. We are thus able to provide the opportunity for interested applicants to be involved with both programs. Volunteers would begin work on red squirrels in February and switch to

ground squirrels for May to August 31. Both projects use a similar approach (lifetime monitoring using live-trapping and observation), but are conducted in two different landscapes and on species differing in natural history (e.g., winter-active vs. hibernating). If you are interested in this joint opportunity, please see our advertisement on this webpage and mention it in your application.

If you wish to apply for one of these posts then please send a CV with a cover letter and contact details for three references (with e-mail addresses), by email to Ainsley Sykes (contact info below), by January 30, 2015.

Contact: Ainsley Sykes via email: [asykes@ualberta.ca](mailto:asykes@ualberta.ca)  
Department of Biological Sciences, University of Alberta  
Twitter: @KluaneSquirrels

[jeffrey.lane@usask.ca](mailto:jeffrey.lane@usask.ca)

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### UBern Field Assist Bird Evolution

University of Bern, Switzerland: Field assistant bird evolution

We are seeking one (1) enthusiastic field assistant interested in taking part in a field study in Bern, Switzerland. The field assistant will be part of the Evolutionary Ecology Lab (Institute of Ecology & Evolution, University of Bern, Switzerland). I am a post-doctoral research fellow at the Institute and will be conducting a field experiment that aims at quantifying the magnitude of phenotypic plasticity in sperm performance. We will be working on a natural population of great tits (*Parus major*) that breed in ca. 3-400 nest-boxes in forests surrounding the city of Bern. I will require one (1) field assistant that will help with all aspects of the work, including checking nest-boxes, ringing and taking measures of adult & offspring birds, catching adults, and more. The applicant should i) hold a BSc/Msc in Biology/Ecology or equivalent, ii) be independent and motivated: we work up to 12h/day and 7 days/week at peak periods, iii) be fluent in English (or in French), and iv) hold a valid European driving license. Bird handling experience would be an advantage. The study will start around mid-March 2015 and go on until mid-June 2015. Travel expenses and accommodation will be covered.

Applications (letter + CV) should be sent to 's.losdat@gmail.com'. Applicants are welcome to contact me for any additional questions or details.

Sylvain Losdat Post-doctoral research fellow Insti-

tute of Ecology & Evolution University of Berne  
Baltzerstrasse 6 3012 Bern Switzerland +447580056289  
[s.losdat@gmail.com](mailto:s.losdat@gmail.com)

Sylvain Losdat <[s.losdat@gmail.com](mailto:s.losdat@gmail.com)>

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### UKansas Undergraduate Research Experiences

The Models in Ecology, Evolution and Systematics Research Experiences for Undergraduates (REU) Program at The University of Kansas is now accepting applications. The NSF-funded program will occur over ten weeks this summer (May 26-July 31) in the Department of Ecology and Evolutionary Biology. In the program, students will participate in mentored, independent research. Students will receive a stipend, room and board, and course credit.

Applications are encouraged from biology majors and mathematics (or computer science) majors with an interest in biology. Students must be in good academic standing and enrolled at a community college, college or university. Members of underrepresented groups are strongly encouraged to apply. Students must be United States citizens or permanent residents. More information, including available projects, and an online application form are available at <http://eebreu.ku.edu> and inquiries should be directed to [eebreu@ku.edu](mailto:eebreu@ku.edu). The application deadline is February 16, 2015.

Dr. Jennifer Gleason, Program director Ecology and Evolutionary Biology University of Kansas [eebreu@ku.edu](mailto:eebreu@ku.edu)  
[jgleason@ku.edu](mailto:jgleason@ku.edu)

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### USaskatchewan Prairie Dog Volunteers

Field Assistants Required - Black-tailed prairie dogs  
Grasslands National Park, Saskatchewan, Canada

I am looking for 3 volunteers to assist with fieldwork beginning March 10 and continuing until July 10 (with a possibility of extension to Oct 10 for at least 1 of the positions). The project investigates the ecology of Black-tailed prairie dogs and will involve live-trapping,

handling and monitoring of individuals. Prairie dog towns are home to (among others): burrowing owls, swift fox and, the recently reintroduced, black-footed ferret. Assistants will have the opportunity of seeing all of these iconic grassland species, plus the many more resident in the Park.

This is an excellent opportunity to gain experience working with a population of wild mammals in a spectacular setting and in collaboration with university, park and zoo researchers. All fieldwork is carried out in Grasslands National Park, southern Saskatchewan, one of the largest remaining tracts of native prairie in Canada. We will be staying in Parks Canada housing in the heart of the park. Food and accommodation are provided. Volunteers are required to provide for their own travel to Saskatoon, Saskatchewan. Travel between the field station and Saskatoon is provided.

Training will be provided and no experience is necessary, but candidates should have an interest in the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and conservation biology. The field house and study population is isolated (the nearest town is approx. 45 min away) and, as such, successful applicants need to be able to cope under these conditions, enjoy the outdoors, be up-beat, positive, responsible and work well as a member of a team.

If you wish to apply for one of these posts then please send a CV with a cover letter and contact details for three references (with e-mail addresses), by email to Jeff Lane (contact info below) by January 31, 2015.

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

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## USussex VolFieldAssist SpainWasps

VOLUNTEER FIELD ASSISTANT sought for 6 weeks starting mid-March 2015, to help with a study of paper wasp (*Polistes*) behavioural ecology in southern Spain. The work will involve helping a PhD student/postdoctoral researcher to census and observe colonies as part of experiments to elucidate the basis of helping behaviour in these wasps, which live in small colonies of <20 individuals. The successful applicant must be prepared to work hard and have an interest in behavioural/evolutionary biology and enthusiasm for fieldwork. Successful applicants will obtain excellent experience of cutting-edge insect behavioural

ecology. A driving licence and any ability to speak Spanish would be an advantage, but are not essential. Because the work involves recording colour marks on individual animals, the job would not be suitable for someone who is colour-blind. See our research group website for more information about the kind of work we do (<http://www.sussex.ac.uk/lifesci/fieldlab/>).

Air fare (from the UK or mainland Europe) and accommodation expenses will be provided, with the applicant needing to pay for only their own food/personal expenses, which are relatively cheap in Spain (a successful applicant will also receive a £300 contribution towards their expenses). Accommodation will be a room in a flat shared with the PhD student/postdoctoral researcher and/or other members of the research group - including shower, cooking facilities, TV etc. Accommodation is in a medium-sized coastal town with nice beach.

Send a covering letter and CV, including contact details (including e-mail addresses/tel nos.) for the applicant and 2-3 referees who would be available to provide references during January/February 2015. Email as a single Word document to: [j.field@sussex.ac.uk](mailto:j.field@sussex.ac.uk), and copy in [c.acclتون@sussex.ac.uk](mailto:c.acclتون@sussex.ac.uk)

Or post a hard copy to: Prof Jeremy Field, School of Life Sciences, John Maynard Smith Building, University of Sussex, Brighton BN1 9QG, UK.

Applicants must be available for interview at Sussex University, and review of applications will begin on 31 January. Informal enquiries: [j.field@sussex.ac.uk](mailto:j.field@sussex.ac.uk)

Professor Jeremy Field School of Life Sciences, John Maynard Smith Building, University of Sussex, Falmer, Brighton BN1 9QG, UK

[j.field@sussex.ac.uk](mailto:j.field@sussex.ac.uk) <http://www.sussex.ac.uk/lifesci/fieldlab/> Tel 01273 877135

Jeremy Field <[J.Field@sussex.ac.uk](mailto:J.Field@sussex.ac.uk)>

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## UTexas Austin Switchgrass Undergrads

Dr. Tom Juenger's research group is currently seeking undergraduates interested in conducting research in Switchgrass biology. We are seeking undergraduate applicants for the The University of Texas at Austin Switchgrass Summer Research Program. This program is an opportunity for undergraduate students to participate in mentored independent research on the biology

of Switchgrass. The program is funded through the NSF Research Experience for Undergraduates (REU) program and is associated with our ongoing interdisciplinary work on the ecology, physiology, and genomic responses of switchgrass to future climate change.

Summer students will be immersed in research and learn basic and applied biology through active participation. Working as part of our research team, they will contribute to group research projects, design short research projects, and present their work in an end-of-summer student symposium.

**Who Should Apply?** Undergraduates in the second or third year. Each REU position is supported for ten weeks, with a stipend of \$4,500. The program runs from the first week in June until the first week of August 2013. Students will be housed in a UT dormitory, and the costs of the dormitory and meal plan are included in the program. Some funds will be available to help defray the cost of traveling to Austin.

**Applications** The application deadline is February 15, 2015. Applicants should submit a cover letter describing experience, interests and future career plans, along with a copy of their transcripts. Applicants should also ensure that two letters of recommendation are submitted on their behalf. Only applications that are complete will be considered. If acknowledgement of receipt is required, please request this in the application. Applications and requests for further information should be directed to:

Dr. Brandon Campitelli e-mail: brandon.campitelli@utexas.edu Subject: Switchgrass REU 2015 Mail: 1 University Station CO930, Austin 78712

For current information regarding ongoing re-

search in the Juenger lab, please visit [https://w3.biosci.utexas.edu/juenger\\_lab/?q=people/thomas-juenger](https://w3.biosci.utexas.edu/juenger_lab/?q=people/thomas-juenger) – Brandon E Campitelli, PhD Postdoctoral Fellow, Dept. of Integrative Biology College of Natural Sciences Research Educator, Biology of Biofuels Freshmen Research Initiative University of Texas at Austin

brandon.campitelli@utexas.edu

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### Video suggestions

I am teaching a second year evolution course for the first time, and am wondering if anyone can recommend any videos that illustrate any aspects of evolution, from basic HW theorem through adaptation (e.g. sexual selection, form-and-function, senescence, human health) to evo-devo. I am using Herron & Freeman as the text, so that is the level of education that I am aiming for. I just want to give the students (and me) a couple of breaks from regular lectures. 50 minute videos would be ideal, but shorter ones would also be useful. Thank you.

Dr. Vicki Friesen, Professor Department of Biology, 4443 Biosciences, 116 Barrie Street, Queen's University, Kingston, ON K7L 3N6, Canada Tel: 613-533-6156 Fax: 613-533-6617

Haida Saying: Treat the Earth well: it is not given to us by our parents, it is loaned to us by our children.

Vicki Friesen <vlf@queensu.ca>

Antwerp BacterialGenomics .....	104	StockholmU PopulationGenomics .....	126
ArizonaStateU CancerPhylogeneticMethods .....	105	SyracuseU PlantEvolution .....	127
Barcelona EvolutionaryNeurobiologist .....	106	TempleU PlantReproductiveEvolution .....	128
Calgary AdaptationGenomics .....	107	TexasAMU PopulationBehaviourGenomics .....	128
CardiffU FishAdaptation .....	108	TrentU 2 ConservationGenomics .....	129
Chicago Conservation .....	108	UArizona SimpsonFellowship EvolutionSystematics	130
DukeU EvolutionFastMovement .....	109	UBritishColumbia SingleCellGenomics .....	130
ISTAustria EvolutionOfSexChromosomes .....	109	UCalifornia Berkeley EvolutionaryPhysiology .....	131
KansasStateU ComparativeTranscriptomics .....	110	UGuelph Biodiversity .....	132
KelloggBiologicalStation MSU MicrobialAdaptation	110	UHelsinki LifeHistoryEvolution .....	132
Linkoping Sweden BehaviouralEvolution .....	111	UJerusalem Evolution MicroRNAs .....	133
:LundU 3Postdocs NewLink .....	112	UKent Blastocystis adaptations .....	134
LundU EvolutionaryBiology .....	112	ULausanne BarnOwlPolymorphism .....	134
Lyon GenomeStability .....	113	ULund MolecularEvolutionaryEcol .....	135
Maynooth Ireland FungalGenomics .....	114	UMichigan ComputationalEvolutionaryBiol .....	135
MichiganStateU Evolution DeadlineExtended .....	114	UMichigan HostParasiteInteractions .....	136
Montpellier CropAdaptation .....	115	UMinnesota PlantMicrobeEvolution .....	137
MontpellierIBC EvolutionaryGenomics .....	115	UNatlAutoMexico PlantEvolution .....	137
Moulis France DragonflyInvasionProcesses .....	116	UNotreDame ConservationBiology .....	137
NIH US HPVGenomics .....	117	UOttawa SingleCellGenomics .....	138
NTNU UMuseum InvertBarcoding .....	118	UPittsburgh PlantEvolGenomicsEcophysiology .....	139
Okinawa AntBiodiversityEvolution .....	118	UppsalaU EvolPlantGeneticsGenomics .....	139
RBG Kew Early Career Research Fellowships .....	119	UppsalaU EvolutionaryPlantGenomics .....	140
Roscoff KelpLifeHistoryEvol .....	119	UToledo FishGenomicsGenetics .....	141
RutgersU PopulationGenomics .....	119	UUtah HerbivoreMicrobiomeBiodiversity .....	141
StellenboschU AntelopeGenomics .....	120	UZurich GeneticsMaternalEffects .....	142
StellenboschU Biogeography .....	121	Vienna DrosophilaThermalAdaptation .....	142
Stockholm EvolutionaryGenetics .....	122	VirginiaTech ComparativeGenomics .....	143
Stockholm MammothGenomics .....	123	YaleU 2 EvolutionaryBiol .....	143
Stockholm MeiofaunaTaxonomy .....	124	YaleU PrimateGenetics .....	144
StockholmU ancientDNA .....	124		
StockholmU EvolutionaryGenomics .....	125		

## Antwerp BacterialGenomics

Postdoctoral scientist in bacteria genomics

Department of Biomedical Sciences - Unit of Diagnostic Bacteriology

The Institute of Tropical Medicine (ITM) is internationally recognized as a center of excellence for education, research and service delivery in the field of tropical medicine. The Unit of Diagnostic Bacteriology at the Department of Biomedical Sciences is developing and validating innovative diagnostic tests for tropical bacterial infections. We recently launched several new projects in which we use metagenomics and genomics to identify and study pathogens in clinical samples. To support these activities and to develop new projects, we are

looking for a postdoctoral scientist in genomics data analysis.

Assignment: \* Coordinate the bioinformatics activities at the Diagnostic Bacteriology Unit. \* Develop and validate a metagenomics approach to identify bacteria in clinical samples. \* Develop the data analysis for a study on whole genome sequencing of Salmonella isolates. \* Assist in the data analysis of genomics, transcriptomics and proteomics projects in the unit. \* Develop your own research lines and apply for competitive grants. \* Coach MSc and PhD students.

Profile: \* You have a Master degree in biology, bioengineering or bioinformatics (or equivalent) and a PhD degree in sciences, preferably in the field of genomics or metagenomics. \* You have strong skills in bioinformatic analysis of whole genome sequence data. \* Additional skills in the analysis of transcriptomics and proteomics data are an asset. \* Additional skills in bacteriology and molecular biology are an asset. \* You have excellent



knowledge of English. \* You have proven that you can work in a multi-disciplinary context and lead research lines.

Offer: \* An intellectually stimulating, international and socially committed environment, with room for personal initiative. \* A full time contract as postdoctoral scientist for one year, extendable. Starting date is as soon as possible. \* A salary set according to the pay scales of the ITM and the Flemish universities. \* Reimbursement of public transport costs, bicycle compensation and luncheon vouchers. \* You will work at the ITM headquarter in the bustling city of Antwerp.

Interested? For more information about this position, please contact Prof. Stijn Deborggraeve, Head of the Diagnostic Bacteriology Unit (sdeborggraeve@itg.be). Applications with motivation letter, application form and contact details of at least 3 references should be received by email at [vacatures@itg.be](mailto:vacatures@itg.be) by February 16, 2015. Please use the application form available as a download on [www.itg.be/vacatures](http://www.itg.be/vacatures). \* Please consider the environment before printing this e-mail

Disclaimer: [Http://www.itg.be/disclaimer](http://www.itg.be/disclaimer) Directions to our location(s): <http://g.co/maps/ua89b> Stijn Deborggraeve <[sdeborggraeve@itg.be](mailto:sdeborggraeve@itg.be)>

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## ArizonaStateU CancerPhylogeneticMethods

The Biodesign Institute at Arizona State University and the Center for Evolution and Cancer is searching for a Postdoctoral Research Associate to help develop methods to reconstruct the phylogenies of cell lineages from within neoplasms. This will require the development of new likelihood models and the integration of multi-modal data (e.g., point mutations and chromosomal alterations). Initial data will derive from SNP arrays and exome sequencing of Barrett's esophagus tissue samples. We will also work on developing methods to extract regularities across forests of phylogenetic trees from tumors.

The Center for Evolution and Cancer was the first of its kind to apply evolutionary biology to cancer biology both at the cell level, studying the evolutionary dynamics of carcinogenesis and therapeutic resistance, and at the organismal level, studying the evolution of cancer suppression in whales, elephants and other species. Scholars will be part of a highly interdisciplinary re-

search team led by Dr. Carlo Maley, will collaborate with Mary Kuhner in Joe Felsenstein's lab, and also be part of a larger community of interdisciplinary researchers at Arizona State University in the Center for Evolution and Medicine and the Centre for Evolution and Cancer at the Institute for Cancer Research in London, bringing together evolutionary biologists, ecologists, computational biologists, mathematical modelers, cancer biologists and oncologists to make fundamental discoveries in understanding cancer and improving cancer prevention and management.

Interactions among faculty, Postdocs and students across the Institute and the University are central to a variety of ongoing research and educational programs. These interactions allow our Postdoctoral Research Associates to develop their expertise in research and build towards an independent research program. Faculty, Postdocs and students are actively involved with a number of other centers, institutes, and research groups on campus that promote transdisciplinary approaches to issues of local and national significance, affording outstanding research and training experiences that extend beyond traditional disciplinary boundaries. The Biodesign Institute is a research hub that makes an important contribution to the advancement of ASU as a leader of knowledge generation and utilization.

### Qualifications:

Ph.D. in evolutionary biology, computational biology, bioinformatics, biostatistics, or related field. Experience in developing phylogenetic methods is required. Experience with the BEAST software package is preferable but not required. Relevant publications in high quality peer review journals is desired.

To apply, please submit to [maley@asu.edu](mailto:maley@asu.edu) as a single pdf document the following materials: 1) a cover letter specifying relevant qualifications and training, 2) curriculum vitae, 3) statement of current research interests and expertise (2 page maximum), 4) two letters of reference, and 5) one peer-reviewed publication. Please include 'Application for Postdoc- Phylogeneticist' in the email subject line. Initial review of applications will begin on February 1, 2015; if not filled, review will continue every week thereafter until the search is closed. A background check is required for employment.

Arizona State University is a new model for American higher education, an unprecedented combination of academic excellence, energy and broad access. This New American University is a single, unified institution comprising four differentiated campuses positively impacting the economic, social, cultural and environmental health of the communities it serves. Its research is inspired by real world application blurring the boundaries that

traditionally separate academic disciplines. ASU serves more than 80,000 students in metropolitan Phoenix, Arizona, the nation's fifth largest city. ASU champions intellectual and cultural diversity, and welcomes students from all fifty states and more than one hundred nations across the globe.

Arizona State University is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will be considered without regard to race, color, sex, religion, national origin, disability, protected veteran status, or any other basis protected by law.

– Carlo C. Maley, Ph.D. Associate Professor Director, Center for Evolution and Cancer at UCSF School of Life Sciences Arizona State University

carlomaley@gmail.com

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## Barcelona Evolutionary Neurobiologist

\*Postdoctoral Position for Evolutionary Neurobiologist at the EMBL/CRG Systems Biology Unit\*

Our laboratory, at the EMBL/CRG Systems Biology Unit in Barcelona, is looking for an excellent and highly motivated postdoc to study the functions and evolutionary impact of neural-specific alternative splicing in vertebrates.

The major goal of the project - funded by the European Research Council (ERC) - is to understand the in vivo functions and evolutionary impact of a program of neural-specific protein isoforms that are conserved across all vertebrates. These isoforms, sometimes diverging by only one or two aminoacids from the onneural isoforms due to microexons (see Cell 2014, 159:1511-23), are expected to be crucial for terminal neurogenesis and synaptic function, and unique to vertebrate species. The applicant will mainly use zebrafish as a model organism to investigate these questions. In addition to these, the candidate will be encouraged to develop his/her own scientific ideas.

The applicant is expected to be passionate about evolution, neuroscience and/or developmental biology.

Strong experience on zebrafish research, particularly on nervous system development and/or in vivo neuronal differentiation, is required. Previous experience with the CRISPR-Cas9 system, and interest on transcriptomic analyses are an advantage, but not necessary. The

applicant should be able to work rigorously, independently and flexibly. The candidate will be responsible for his/her own project within the research group, including carrying out experiments, data analysis and interpretation. Fluency in English (spoken and written) is expected.

The position has a fully covered, competitive salary for up to five years, but the applicant will also be encouraged to apply for independent funding.

\*The Institute\* The Centre for Genomic Regulation (CRG), is an international biomedical research institute of excellence, based in Barcelona, Spain, whose mission is to discover and advance knowledge for the benefit of society, public health and economic prosperity.

The breadth of topics, approaches and technologies at the CRG permits a broad range of fundamental issues in life sciences and biomedicine to be addressed. Research at the CRG falls into four main areas: gene regulation, stem cells and cancer; cell and developmental biology; bioinformatics and genomics; and systems biology.

With more than 350 scientists from 41 countries, the CRG excellence is based on an interdisciplinary, motivated and creative scientific team that is supported by high-end and innovative technologies.

The centre's other main strategic goals are: to translate basic scientific findings into benefits for health and economic value for society; to provide advanced and excellent training to our scientists; and to communicate and establish a bilateral dialogue with society.

For further information: [www.crg.eu](http://www.crg.eu) \*Requirements\*

\*Studies\*:

- PhD in Biology-related areas

\*Technical skills required\*:

- Experience on zebrafish research, particularly on nervous system development and/or in vivo neuronal differentiation.

\*Additional beneficial skills\*:

- Experience with CRISPR-Cas9 system. - Interest and experience on transcriptomic analysis.

\*Languages\*:

- Fluent level of English

\*Soft skills\*:

- Passion for evolutionary biology. - A highly motivated and organized candidate. - Capable of working in group, and with a high degree of work autonomy.

\*The Offer\*

- Duration: 1 year renewable contract up to 5 years. - Estimated annual gross salary: A competitive salary will be provided, which will be well matched relative to the cost of living in Barcelona, and adjusted according to experience. - Starting date: as soon as possible from April 2015.

We offer work in a highly stimulating environment with state-of-the-art infrastructure, providing the successful applicant with unique opportunities to develop a strong technical portfolio.

**\*Application Procedure\*** All applications must include:

1. A presentation letter addressed to Dr. Manuel Irimia
2. A full CV including contact details.
3. Two contacts for further references.

All applications must be addressed to Dr. Irimia and be submitted to the following email address: [rrhh@crg.es](mailto:rrhh@crg.es). Please include as email subject the reference "Postdoc-NeuralAS".

**\*Deadline:** Please submit your application by \*13th February 2015\*

Centre de Regulació Gen<sup>À</sup>mica (CRG) Doctor Aiguader 88, 08003 Barcelona (Spain)

Manuel Irimia <[mirimia@gmail.com](mailto:mirimia@gmail.com)>

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## Calgary Adaptation Genomics

POSTDOCTORAL RESEARCH POSITIONS at the UNIVERSITY of CALGARY

Local adaptation and the architecture of complex traits: theory and comparative genomics Sam Yeaman AIHS CAIP Chair in computational evolutionary biology

I'd like to take this opportunity to invite prospective postdocs to apply for positions in the lab that I will be starting in the Department of Biological Sciences at the University of Calgary in September 2015. In particular, I am looking for candidates that have strengths in de novo genome assembly, mapping, and comparative genomics. I have received full funding from AIHS and U of C to cover a project on "Comparative genomics of rearrangements involving genes associated with local adaptation" (see description below for more details).

Positions will run for 2+ years, with the possibility of extension for another 2+ years. Full funding is available through either a dedicated two-year fellowship of-

ferred through the University of Calgary (\$50k/year) or through my research budget. For this project, I would like to find a collaborator that has experience with NGS library preparation and de novo genome assembly or linkage mapping, although candidates without direct experience in these areas but with strong bioinformatics AND wetlab skills would also be most welcome.

**TO APPLY:** Please send a CV and a short description of your interest in the position to [yeaman@zoology.ubc.ca](mailto:yeaman@zoology.ubc.ca), along with the names and emails of three people I could contact for reference letters. Please be sure to clearly highlight skills and experience related to genome assembly, NGS library prep, statistics, bioinformatics, or programming. I will begin reviewing applications on February 1st, 2015, but please contact me to check in if you need to make a quick decision.

**Project description:** Theory shows that migration-selection balance favours the fixation of rearrangements that build clusters of genes involved in local adaptation (Yeaman 2013, PNAS). Recent empirical work has shown that loci with signatures resembling local adaptation in the threespine stickleback tend to be clustered together (Jones et al. 2012, Nature; Miller et al. 2014, Genetics). To test whether these putative clusters have evolved through rearrangements, this project will undertake de novo assembly of the genomes of several close and distant relatives of the threespine stickleback. In combination with existing and emerging genomic resources, we will reconstruct the long-term patterns of genome rearrangement in this group and test hypotheses about the involvement of selection and local adaptation. This study has full funding for 7 years, and will employ a combination of Illumina short reads, PacBio long reads, and potentially some physical and linkage mapping, or other innovative methods. I also plan to undertake comparative genomic studies in other taxa where more genomes have already been assembled (Arabidopsis, Helianthus, Solanaceae, Cichlids, etc.).

[yeaman@zoology.ubc.ca](mailto:yeaman@zoology.ubc.ca)

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## CardiffU FishAdaptation

A position is available for a Research Associate (Post-doc) to conduct research on fish biology, disease and bioinformatics, in the topic:

Minimising the Impacts of Intensive Aquaculture in the face of Climate Change

Institutions Involved: Cardiff University, Swansea University and Aberystwyth University Collaborators: Natural Resources Wales (NRW), Cardiff Harbour Authority (CHA), Wye & Usk Foundation (WUF), Natural Aptitude, Fishgen, Skillfish, Pontus Aqua, CIBIO

Worldwide demand for fish and shellfish has increased 9% annually over the last few decades and is expected to reach c. 180 million tons by 2015, most of which will have to come from farmed fish, as the majority of wild fisheries are either stagnant or grossly over-exploited. However, to achieve long-term sustainability and meet food security demands, aquaculture needs to diversify and to step-up the domestication of aquatic species, which will have to thrive on less food, less space, and less water, all compounded by warmer temperatures and disease.

The AquaWales Research Cluster combines academic (Swansea, Cardiff and Aberystwyth Universities) and non-academic participants, including stakeholders and local government involved in policy and regulation, and will target these challenges by capitalising on the diverse and complementary expertise of the group (from behavioural ecology to genomics, citizen-science and fisheries policy). We will use a multidisciplinary approach to disentangle the basis of domestication and the response to crowding (stress and parasite susceptibility), an aspect often neglected in breeding programs, and to investigate the potential effects of climate change on the risk of expansion and establishment of non-native aquatic species associated with aquaculture and fisheries using state-of-the-art methods. Specific aims include to:

1. bridge, for the first time, the behavioural, genetic and environmental (epigenetic) components of fish undergoing domestication
2. disentangle the role of domestication in disease resistance in response to stress and temperature change, and
3. model pathways of introduction and dispersal of aquaculture-related invasive species (AIS) under different environmental conditions, combining state-of-the-art methods for early detection

(environmental DNA) and citizen science.

The Research Associate will work in collaboration with a Research Associate based at Swansea and 2 PhDs affiliated with this research cluster; the Research Associate must also be prepared to work for short periods of time in Swansea and/or Aberystwyth.

The main tasks of the Research Associate will be to work on the relationship between domestication and disease resistance under stressful conditions of crowding and disease in tilapia and salmon, developing infection protocols, culture assay methods and performing genomic/transcriptomic analyses.

The successful candidate will have a PhD in related subject area or relevant industrial experience, experience in two of the following fields, fish behaviour, epidemiology, genetics/genomics background or experience programming in R/Python and proven ability to publish in international journals.

This is a full-time position, fixed-term until 30 September 2018

Salary: £31,342 - £37,394 per annum (Grade 6). It is not anticipated that an appointment will be made above 6.31, currently £32,277 per annum.

Closing data for application: Wednesday 21st January, 2015 Please use the following link to apply: Cardiff University - Job details

Cardiff University - Job details Job Details: Vacancy Number 2951BR Research Associate A position View on [krb-sjobs.brassring.com](http://krb-sjobs.brassring.com)

For additional information please contact: [CableJ@cardiff.ac.uk](mailto:CableJ@cardiff.ac.uk) and/or [orozco-terwengelpa@cardiff.ac.uk](mailto:orozco-terwengelpa@cardiff.ac.uk)

Pablo Orozco-terWengel  
<[orozco-terwengel@yahoo.com](mailto:orozco-terwengel@yahoo.com)>

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## Chicago Conservation

Postdoctoral Fellow: Species Conservation Methods

Chicago Zoological Society

This Species Conservation Methods postdoc will work within a new Species Conservation Toolkit Initiative – a partnership to ensure that the new innovations and tools needed for species risk assessment, evaluating conservation actions, and managing populations are developed, globally available, and used effectively. Further

information about the conservation tools is available at [www.vortex10.org](http://www.vortex10.org).

The postdoc will participate in the design of computer modeling tools for conservation assessments and planning for wildlife populations in the wild and in captivity. You will make use of your experience in computer programming to implement new methodologies for species conservation through extending existing software tools (Vortex, PMx, Outbreak, and MetaModel Manager) or developing new tools, and will provide technical support and help to provide training to conservation professionals and graduate students using modeling methods and tools.

The position is funded for 3 years and can start immediately. The position will be based at the Chicago Zoological Society (Brookfield Zoo, in the Chicago suburbs), but will work closely with (and require occasional travel to) colleagues in Washington, Minneapolis, and occasionally overseas. The position will remain open until an ideal candidate is hired.

Position Requirements include:

Ph.D. degree in biology or related field or Ph.D. in information science with considerable training also in biology. Expertise in population biology. One year experience in conservation biology research or species management required. Experience in computer programming for Windows applications required, including prior experience with or ability to learn C#.NET programming or related object-oriented languages. Excellent verbal and written communication skills, including proven ability in writing of reports and scientific papers, grant proposal preparation, and oral presentations. Demonstrated ability to work independently.

Desirable qualifications include:

Broad research and conservation interests preferred. Experience with software program VORTEX or other PVA models, and PMx or other pedigree analysis tools desirable. Experience with software development for multiple platforms (web, tablet, etc.) a plus. Experience with user interface design highly desirable.

To apply:

Applicants can find the position posting and apply online by going to <http://www.czs.org/Brookfield-ZOO/-Careers/Job-Openings.aspx>, click on Enter Career Center, click on Search Openings, and then search for "Auto req ID" of 766BR.

Further information, contact Robert Lacy ([rlacy@ix.netcom.com](mailto:rlacy@ix.netcom.com))

[rlacy@ix.netcom.com](mailto:rlacy@ix.netcom.com)

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## DukeU EvolutionFastMovement

Post-doctoral Scientist Integrative Organismal Biology

A postdoctoral position is available in the Patek laboratory at Duke University < <http://www.pateklab.org/> > to examine the evolution and biomechanics of fast movements across the tree of life. Our integrative and comparative research program links biomechanical analyses and field work with phylogenetic comparative analyses and modeling. We are looking for a candidate with experience in one or more of these areas. The candidate may have a background in biology, engineering and/or physics. A publication record reflecting significant contributions to the primary scientific literature is required. A Ph.D. is required.

The appointment will be for 12 months with the possibility for renewal contingent on performance. The annual salary range for this position will be commensurate with experience. The start date is flexible, preferably in summer or fall of 2015.

Applications will be accepted and evaluated on an ongoing basis until February 24, 2015. Please email a letter explaining your interest in and qualifications for the position, a curriculum vitae, research statement, up to three pdf reprints, and contact information of three references to:

Dr. Sheila Patek Associate Professor  
[sheila.patek@duke.edu](mailto:sheila.patek@duke.edu) [www.thepateklab.org](http://www.thepateklab.org)  
[snp2@duke.edu](mailto:snp2@duke.edu)

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## ISTAustria EvolutionOfSexChromosomes

A postdoctoral position in evolutionary genomics is available in the newly established Vicoso group at the Institute of Science and Technology, Austria. The general focus of the lab is the evolution of sex chromosomes, which we approach using a combination of experimental and computational approaches. Questions that motivate our research include: why do some Y/W chromosomes degenerate while other remain homomorphic; what forces drive some species to acquire global dosage

compensation, while others only compensate specific genes; what are the frequency and molecular dynamics of sex-chromosome turnover? The successful applicant will apply comparative genomics analyses to a wide variety of species, and combine them with population DNA and gene expression data, to achieve a better understanding of the evolutionary and molecular forces driving sex chromosome differentiation. Candidates wishing to work on a specific project in sex chromosome evolution are also encouraged to apply.

Applicants should have obtained, or anticipate obtaining by the start date, a PhD in biology, genetics, bioinformatics, or a related field. A strong background in one or more the following areas is highly desired: - comparative genomics - molecular evolution - population genetics - bioinformatics

The initial appointment is for one year, with the possibility of extension and a minimum salary of 49,070 Euros per year (gross).

IST Austria is a young and vibrant international institute dedicated to basic research and graduate education in the natural and mathematical sciences, located on the outskirts of Vienna ([www.ist.ac.at](http://www.ist.ac.at)). The official language of the institute is English. Aside from the evolution cluster at IST Austria, Vienna is home to a large community of evolutionary biologists: [www.univie.ac.at/evolvienna/](http://www.univie.ac.at/evolvienna/). To apply, send a summary of research interests, CV, up to three relevant publications/manuscripts, and the names and contact information for three references to Beatriz Vicoso (bvicoso@ist.ac.at). The start date is negotiable, but an earlier start would be preferred.

Beatriz Vicoso Assistant Professor IST Austria website: <http://ist.ac.at/research/research-groups/vicoso-group/> email: bvicoso@ist.ac.at

bvicoso@ist.ac.at

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## KansasStateU ComparativeTranscriptomics

### POSTDOC POSITION ON COMPARATIVE TRANSCRIPTOMICS OF DROUGHT TOLERANCE IN WILD GRASSES

A postdoctoral position currently is available in the Division of Biology at Kansas State University as part of a collaborative project between laboratories of Mark Ungerer and Jesse Nippert. Goals of this work are

to integrate morphological, physiological and transcriptomic approaches to better understand the evolution of drought tolerance in wild grass species.

While involvement at all levels of the research is encouraged, primary responsibilities will include comparative analyses of RNA-seq datasets and thus the successful candidate will have appropriate bioinformatics skills for the handling of next generation sequence data and a publication record demonstrating research expertise in evolutionary genomics, molecular evolution, or a related field. Salary will be based on a 12-month appointment and commensurate with experience. Full benefits will be provided. The appointment is for one year and will be renewable contingent on sufficient progress.

To apply, send a cover letter describing your research interests and/or past research achievements, a C.V., relevant PDF reprints, and the names and contact information of two individuals willing to provide letters of recommendation. Questions can be addressed to Dr. Mark Ungerer at [mcungere@ksu.edu](mailto:mcungere@ksu.edu). Materials should be sent to [biology@ksu.edu](mailto:biology@ksu.edu) with "EEB Postdoc" in the subject line. Review of applications will begin on January 30, 2015, and continue until the position is filled. PhD degree must be completed by start date with expertise in evolutionary genomics, molecular evolution, or related field. Kansas State University is an Equal Opportunity Employer of individuals with disabilities and protected veterans and actively seeks diversity among its employees. Background check required.

Mark Ungerer Division of Biology Kansas State University Manhattan KS 66506 [mcungere@ksu.edu](mailto:mcungere@ksu.edu) office: 785.532.5845 fax: 785.532.6653

[mcungere@ksu.edu](mailto:mcungere@ksu.edu)

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## KelloggBiologicalStation MSU MicrobialAdaptation

Title: Postdoctoral Researcher available in the Evans Lab at Michigan State University's Kellogg Biological Station (Hickory Corners, MI).

A postdoctoral position is available in microbial ecology and soil biogeochemistry at Kellogg Biological Station, Michigan State University. The Evans Lab ([www.saraheevanslab.weebly.com](http://www.saraheevanslab.weebly.com)) is interested in how microbes respond to climate change and how these responses influence ecosystem processes. To investigate these questions, we use molecular techniques, physiolog-

ical assays, modeling, and terrestrial climate manipulations.

The postdoctoral candidate will have the opportunity to conduct work at the KBS Long Term Ecological Research Site ([kbs.lter.edu](http://kbs.lter.edu)) or Great Lakes Bioenergy Research Center ([glbrc.msu.edu](http://glbrc.msu.edu)), where long-term data on natural and agro-ecosystems and inter-disciplinary research teams provide an excellent context for scientific questions in the time period of a postdoctoral position. Research questions could focus on, but are not limited to, interactions among changes in rainfall patterns, nitrogen dynamics, and microbial community function.

Responsibilities include: data collection in existing climate manipulation or crop management experiments, microbial community or physiological analysis, participation in lab and KBS community, data management, and manuscript preparation. The successful candidate will have the opportunity to interact with the many researchers working on KBS long-term projects, distinguished faculty at KBS, as well as faculty on campus in Departments of Microbiology and Molecular Genetics and Integrative Biology. The candidate will also have the ease and efficiency that comes with access to much available data and state-of-the-art field sites outside their door. KBS and the Evans Lab prioritize postdoctoral research career development, and it is a fun place to spend two years.

The ideal candidate will have a strong background in microbial ecology, including experience with metagenomic/metatranscriptomic protocols and data and statistical analyses. However, other specific and well-refined skillsets that can be applied to these types of questions will be equally considered. Demonstration of strong written and oral communication skills is a must, and a PhD and research experience in appropriate disciplines is required.

The postdoctoral appointment will be for 2 years. Start date is May 2015, but requests for other start dates near this time will be considered (indicate in cover letter). To apply, please send a cover letter (including research interests and an indication of field, lab, and data analysis skills), CV, and contact information (name, position, phone, email) for 3 references to [evanssar@gmail.com](mailto:evanssar@gmail.com). We will begin reviewing applications in mid-February, 2015.

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

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## Linköping Sweden BehaviouralEvolution

Postdoc position: Why do animals have personality?

It's a pleasure to announce a postdoctoral position in the research group of Dr Hanne LÅvlie at Linköping University, Sweden, on the topic of animal personality.

The project will focus on mechanisms underlying variation in personality, the link to variation in cognition and learning, and the role of underlying variation in the monoamine systems (i.e. serotonin, dopamine), and is in collaboration with Prof. Svante Winberg (Uppsala University).

Despite intense recent research interest, we still do not know why animals have personality. This is partly because the architecture of animal personality is poorly understood. The aim of the announced position is to improve our overall understanding of the causes and consequences of variation in animal personality. More specifically the aim is to investigate the relationship between variation in personality and learning (together with other aspects of cognition), and their underlying genetic and physiological bases, with particular focus on the brain monoamines serotonin and dopamine. In other words, an exciting interdisciplinary project is offered that aims to improve our understanding of the relationships between personality and cognition, and their underlying mechanisms. We use the charismatic red junglefowl and domestic chickens as our main models, which together with excellent molecular tools enables a strong experimental approach.

The post includes responsibility for conducting lab/fieldwork, carrying out behavioural and/or physiological experiments, analysing data and writing up results for publication. The postdoc will have access to previously collected behavioural, physiological and genetic data. To some extent is the topic of the project is flexible and can be tailored to fit the skills and interests of the successful candidate.

Funding is available for two years, but is contingent on satisfactory progress in year one. The post doc is a stipend (i.e. no tax will be deducted) of 20,000SEK/month. The stipend does not give entitlement to sickness benefit, parental allowance, holiday pay or pension. Funding is awarded from Carl Trygger's Foundation.

Requirements The successful candidate should be enthusiastic and dedicated to science, with a PhD and possibly some postdoctoral experience in a field of relevance to the project (e.g. animal behaviour, evolutionary biology, molecular biology, quantitative genetics and/or neurobiology). The candidate should have demonstrated excellent quantitative and analytic skills, and excellent communication abilities, particularly in written English. The latter should be demonstrated by a proven track record of publication. The candidate should also demonstrate their ability to work as part of a team. Previous experience of working with vertebrates, especially birds, is advantageous, but not necessary.

If you are interested in this position, please send: (1) a letter of motivation (including a brief description of research experience and why you are suitable for the announced position), (2) a CV including a list of publications and contact details of two referees to: [hanne.lovlie@liu.se](mailto:hanne.lovlie@liu.se). Please merge all documents into a single pdf-file and include your name in the file name. Deadline for submitting an application is 9th of March 2015. The position has a negotiable start, but a start date before summer 2015 is preferred.

Please feel free to contact me if you have any questions about the position!

Linköping University is a modern university with a consistently growing biology division. A major research focus at the Biology division is on animal behaviour, including behavioural genetics and animal welfare. Linköping is located central in Sweden, only a couple of hours away from other university cities, like Stockholm, Uppsala and Lund.

Hanne LÅvlie, Assistant professor IFM Biology, AVIAN Behavioural Genomics and Physiology Group Linköping University 58183 Linköping, Sweden [hanne.lovlie@liu.se](mailto:hanne.lovlie@liu.se) Home page and more information: <https://www.liu.se/-forskning/foass/hanne-lovlie?l=en&sc=true> Hanne Lovlie <[hanne.lovlie@liu.se](mailto:hanne.lovlie@liu.se)>

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### :LundU 3Postdocs NewLink

The link to the previously (Jan 4) advertised postdoc to study sexual selection and hybridisation in lizards is now unfortunately broken. To access information about this position (Official Records Number: NPA 2014/747) and two other postdoc opportunities in my group at Lund University, please see information posted on Jan 5 on the following link (which allows you to continue to

the list of vacancies and the application system):

<http://exelund.blogspot.se/> Apologies for any confusion caused.

Dr Tobias Uller Wallenberg Academy Fellow Department of Biology Lund University

[tobias.uller@biol.lu.se](mailto:tobias.uller@biol.lu.se)

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## LundU EvolutionaryBiology

2 Post doc scholarships in Evolutionary Biology

Placement: Department of Biology, Lund University, Sweden Ref No: V 2014/2299 Duration: 24 months Starting time: April 1 2015 or later following agreement Last day for applying: January 31 2015

Research Area

Evolutionary biology is in a vibrant phase where data from ecology, molecular and developmental biology are coming together to shape our understanding of how organisms evolve. These two postdoctoral scholarships are intended to provide the opportunity to develop an independent research project in organismal evolutionary biology within a highly creative and supportive environment. The successful applicants will be invited to develop their projects in collaboration with the host investigator Dr Tobias Uller.

We particularly welcome applications from those interested in the relationship between developmental, ecological, and evolutionary processes. This includes, but is by no means limited to, experimental and comparative studies of the evolutionary causes and consequences of phenotypic plasticity, non-genetic inheritance and developmental bias, and research projects on populations in novel environments or at range margins. The focal study organisms of the host research group are lizards and water fleas (*Daphnia*), and we will therefore aim to develop a suitable project on these systems, but alternative study organisms will be supported if they are better suited to the question and the research project is logistically feasible. Projects can be lab or field based and can be experimental, observational or comparative. We can support a range of methods, from molecular genomics to desk-based approaches, including comparative and meta-analytical methods and mathematical modelling.

Why apply?

The intention with these scholarships is to enable early career researchers to develop an interesting, cutting-



edge, research project and give them sufficient time to complete the project and learn a wide range of skills. We want to work with people who are passionate, intelligent, and dedicated to advance our understanding of phenotypic evolution through collaboration and exchange of ideas and expertise.

The successful applicants will be based in Dr Tobias Uller's research group at the Department of Biology, Lund University. They will join a growing team of students and postdoctoral researchers with a broad research agenda and a large international collaborative network as full members of the Experimental Ecology, Evolution and Behaviour group and the Evolutionary Ecology Unit. Scholarships and research projects are funded as part of a Wallenberg Academy Fellowship to Dr Uller.

For further information about the host research group and informal contact please visit <http://www.biology.lu.se/tobias-uller> or email Tobias Uller on [tobias.uller@biol.lu.se](mailto:tobias.uller@biol.lu.se).

#### Qualifications required

Applicants must have a PhD in a suitable area for conducting postdoctoral research in evolutionary biology and show evidence of high scientific potential. Such evidence may include a strong track record of publications in scientific journals, documentation of successful completion of research projects, high intellectual capacity and problem-solving ability, technical know-how, organizational skills, enthusiasm, dedication, and an ability to work both independently and in a team. Where possible, statements to these effects in the personal letter should be accompanied by objective or independent assessment of the candidate's track record and potential (e.g., via letters of support; see below).

Applicants must have been awarded their PhD no earlier than three years before the application deadline (this may be adjusted based on, for example, documentation of parental leave or military service).

Further details on the scholarships and how to apply can be found at <http://www.biology.lu.se/article/postdoc-scholarships> Dr Tobias Uller Wallenberg Academy Fellow Department of Biology Lund University [tobias.uller@biol.lu.se](mailto:tobias.uller@biol.lu.se)

[tobias.uller@zoo.ox.ac.uk](mailto:tobias.uller@zoo.ox.ac.uk)

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## Lyon GenomeStability

Post Doctoral position in epigenetics and genome stability

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.

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 essential. Excellent written and oral skills in English are required.

Environment The host laboratory (LBBE) 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)

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

applications will be selected by the end of March

- 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. 0472448198 <http://lbbe.univ-lyon1.fr/-Equipe-Elements-transposables-.html> Cristina Vieira <[cristina.vieira@univ-lyon1.fr](mailto:cristina.vieira@univ-lyon1.fr)>

## Maynooth Ireland FungalGenomics

Dear all,

Applications are invited for a bioinformatics postdoctoral position in the research group of David Fitzpatrick (Department of Biology, Maynooth University, Ireland). My group is interested in genomics, transcriptomics, proteomics and molecular evolution of fungal species. The project start date is the 1st of February 2015 and sets out to investigate the genome of *Agaricus bisporus*.

*Agaricus bisporus* strain A15 is the most widely cultivated white mushroom strain in Europe. Currently there are significant financial and time costs associated with ensuring A15 inoculum is genetically identical to parent culture. This project sets out to undertake an extensive genetic analysis of *A. bisporus* A15, via genomic and transcriptomic sequence analysis. Ideally this genetic characterisation will act as the starting point for development of a molecular diagnostic test to determine if new inoculum is genetically identical to parent culture. We also aim to produce a high quality map for the genome of *A. bisporus* A15. This will be invaluable for future breeding of new *A. bisporus* strains.

The position will last for 18 months, with the possibility of extension. I am looking for somebody who has experience in genome/transcriptomic assembly and experience in handling large datasets. The successful candidate will have published in peer-reviewed literature and have their PhD awarded by the start of the project.

Send a CV and covering letter to [david.fitzpatrick@nuim.ie](mailto:david.fitzpatrick@nuim.ie) with the subject line

“post-doc position on *Agaricus bisporus*”

Please pass this notice on to anybody you think might be interested.

Regards

David.

Dr. David Fitzpatrick Genome Evolution Laboratory Department of Biology Maynooth University Maynooth Co. Kildare Ireland.

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## MichiganStateU Evolution DeadlineExtended

\*BEACON Center for the Study of Evolution in Action\*

\*BEACON Distinguished Postdoctoral Fellows Program\*

\*\*\*\*APPLICATION DEADLINE EXTENDED\*\*\*\*

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BEACON is an NSF Science and Technology Center headquartered at Michigan State University with partners at North Carolina A&T State University, University of Idaho, University of Texas at Austin, and University of Washington. BEACON brings together biologists, computer scientists, and engineers to study evolutionary dynamics using biological and computational techniques and to apply evolutionary principles to engineering problems. We seek outstanding post-doctoral scholars to pursue interdisciplinary research on evolution in action with BEACON faculty members, in the fields of biology, computer science, and/or engineering.

Applicants will propose a research project within the scope of BEACON's mission and must have two BEACON faculty sponsors who will serve as research mentors should the fellowship be awarded. One sponsor must be MSU faculty; the other sponsor may be from any of the five BEACON institutions. Preference is given for interdisciplinary research. The post-doc fellow will be based at Michigan State University in East Lansing. Please see our website (<http://www.beacon-center.org>) for information about BEACON mission, participants and ongoing research projects.

Applicants must submit the following, in a single PDF,

to BEACON Managing Director Danielle Whittaker via email (djwhitta@msu.edu):

- 1.CV
- 2.A two-page description of their research plan
- 3.A one-page summary of their doctoral research
- 4.Letters of support from two BEACON sponsors (one must be from MSU)
- 5.Two additional letters of recommendation

Fellowships last two years and include a salary of \$50,000/year and modest funds to support research and travel. The successful applicant will help foster collaborations among faculty and disciplines and serve as a professional model for pre-doctoral trainees.

A Ph.D. in biology, computer science, engineering or related fields is required. Current MSU graduate students or postdocs are not eligible for this fellowship. US citizens or permanent residents only. Minority applicants are especially encouraged to apply. MSU is an Equal Opportunity/Affirmative Action Employer.

The deadline for applications is January 23, 2015.

– Danielle J. Whittaker, Ph.D. Managing Director BEACON Center for the Study of Evolution in Action 567 Wilson Road, Room 1441E Michigan State University East Lansing, MI 48824 (517) 884-2561 djwhitta@msu.edu <http://beacon-center.org> “Danielle J. Whittaker” <djwhitta@msu.edu>

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## Montpellier CropAdaptation

18 months Postdoctoral fellowship: Investigating adaptive introgression in crops

at the Institut de Recherche pour le Développement, Montpellier, France

The position is offered through a project supported by the Agropolis foundation to study wild-to-crop adaptive introgression. The project investigates pattern of introgression and signature of selection through wide genome scans on three native African crops. The postdoc fellow will primarily work on NGS data from whole genome resequencing or gene enrichment approaches from wild and cultivated populations. The postdoc fellow is expected to use different modelling approaches and Bayesian statistics to identify genomic regions under selection through wide genome screening. The postdoctorate will interact with PhD students working on

the same project.

Required skills: Strong knowledge in modelling demographic scenarios- ABC methods Knowledge in bioinformatics pipelines for identifying SNPs from NGS data, BLAST, Gene Ontology Knowledge in programming perl, bash, C++ Knowledge in plant evolution and domestication is a plus. Good English written and verbal communication skills Able to spend some 1-2 months travelling abroad Able to train master/PhD students Able to manage research and administrative activities

Eligibility: If possible, candidate should not have passed more than 12 month over the last 36 months in France. Candidates not filling this condition should still apply. Closing of the applications: 15/03/2015 approximate effective start date: 01/06/2015 Gross monthly salary: ~1850 € *~freeoftaxes, Frenchhealthinsuranceisincluded*

Thank you for sending CV, cover letter and at least two references letters.

Applications to be sent to / Information to be taken with: Dr. Yves Vigouroux Dr. Cécile Berthouly-Salazar Email : yves.vigouroux@ird.fr Email : cecile.berthouly@ird.fr Phone : 33 (0)4 67 41 62 45

– Cécile Berthouly-Salazar IRD - Institut de Recherche pour le Développement 911 avenue AGROPOLIS BP 64501 34394 Montpellier cedex 5 France Tel : 33 (0)4 67 41 64 39 ; Fax : 33 (0)4 67 41 62 22 Email : cecile.berthouly@ird.fr Web : <https://sites.google.com/site/plantbiodiversityadaptation/>

Cecile Berthouly <cecile.berthouly@ird.fr>

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## MontpellierIBC EvolutionaryGenomics

Postdoc:

WHERE : Institute of Computational Biology (IBC), Montpellier (France), <http://www.ibc-montpellier.fr>  
WHAT : Methodological developments in evolutionary genomics

Three-year post-doctoral position at the Institute of Computational Biology (IBC), Montpellier (France) : Methodological developments in evolutionary genomics.

One young investigator position opens immediately at the Institute for Computational Biology (IBC, <http://www.ibc-montpellier.fr>) of Montpellier (France) to work

on the development of innovative inference methods and software in population genomics or phylogenetics to analyze large-scale genomic data in the fields of health, agronomy and environment (Work Package 2 « evolutionary genomics » of the IBC). The candidate will develop its own research on some of the following topics : selective processes, demographic history, spatial genetic processes, very large phylogenies reconstruction, gene/species tree reconciliation, using maximum likelihood, bayesian and simulation-based inference. We are seeking a candidate with a strong background in mathematical and computational evolutionary biology, with interest in applications and software development. The successful candidate will work on his own project, build in collaboration with any researchers\* involved in the WP2 project and working at the IBC labs (AGAP, CBGP, ISEM, I3M, LIRMM, MIVEGEC).

IBC hires young investigators, typically with a PhD plus some post-doc experience, a high level of publishing, strong communication abilities, and a taste for multidisciplinary research. Working full-time at IBC, these young researchers will play a key role in Institute life. Most of their time will be devoted to scientific projects. In addition, they are expected to actively participate in the coordination of workpackages, in the hosting of foreign researchers and in the organization of seminars and events (summer schools, conferences...). In exchange, these young researchers will benefit from an exceptional environment thanks to the presence of numerous leading international researchers, not to mention significant autonomy for their work. Montpellier hosts one of the most vibrant communities of biodiversity research in Europe with several research centers of excellence in the field. This position is open for up to 3 years with a salary above the French post-doc standard.

Living at Montpellier: <http://www.agropolis.org/english/guide/index.html> Contacts WP2 « Evolutionary Genetics » : Jean-Michel Marin : <http://www.math.univ-montp2.fr/~marin/> François Rousset : <http://www.isem.univ-montp2.fr/recherche/teams/evolutionary-genetics/staff/roussetfrancois/?lang=en> Vincent Ranwez : <https://sites.google.com/site/ranwez/> Olivier Gascuel : <http://www.lirmm.fr/~gascuel/> Submit my application : <http://www.ibc-montpellier.fr/open-positions/young-investigators#wp2-evolution> \* WP2 researchers : Vincent Berry, François Chevenet, Jean-François Dufayard, Olivier Gascuel, Mathieu Gautier, Raphaël Leblois, Jean-Michel Marin, Miguel Navascués, Fabio Pardi, Martine Peeters, Pierre Pudlo, Vincent Ranwez, François Rousset, Céline Scornavacca, Renaud Vitalis.

raphael.leblois@supagro.inra.fr

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## Moulis France Dragonfly Invasion Processes

\*20 months Postdoctoral fellowship: Experimental studies on invasion process in a dragonfly species.\*

At the Field Station of Experimental Ecology in Moulis, France (CNRS V USR 2936)

\*Project objectives\*

The position is offered within a pan-European project, Probis (Biodiversa, <http://biodiversa-probis.weebly.com/>). PROBIS aims at characterizing patterns of traits variation, and test for the underlying evolutionary processes along an invasion succession. More generally we aim at determining how the genetic and phenotypic heterogeneity of invasive populations along and age-gradient of invaded habitats is expressed, and how this may influence the invasion success and rate of non-native species establishment.

The post-doc fellow will primarily work on the dragonfly aspect of the project. This project will focus on *Crocothemis erythraea*, a dragonfly originated from Mediterranean areas and naturally expanding its range northwards through Europe. In 2014, we first sampled populations along a South-North gradient to isolate changes in the genetic diversity of populations, so as to then identify specific populations that will be used for experimental works. For the next steps, we will use 6 populations of different ages since the invasion started across Europe.

The post-doc fellow will quantify the variation and plasticity of phenotypic traits associated to each invasion steps and create semi-natural populations into an experimental metapopulation system (Metatron, <http://www.ecoex-moulis.cnrs.fr/spip.php?rubrique5>) to experimentally measure population invasiveness.

\*Task of the postdoctoral fellow\*

The recruited researcher will be in charge of 1) collecting dragonfly larvae in 6 populations across Europe, 2) maintaining larvae in lab facilities, 3) planning and performing phenotypic measurements (morphological and behavioral), 4) maintaining and monitoring semi-natural populations and movements between populations and 5) analyzing data and writing articles.

This work will likely lead to, at least, two articles as a first author.

**\*Required skills\***

Able to manage research and administrative activities

Knowledge in biological invasions and/or evolutionary ecology in general.

Knowledge in entomology and possibly dragonfly biology and rearing.

Able to actively participate as a member of a research team.

Good written and verbal communication skills

Able to spend some time travelling abroad

Experience in experimental design

Experience with data manipulation and statistical analysis (including mixed models)

\*Closing of the applications: \*15/02/2015\*Effective start date: \*01/04/2015

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\*Gross monthly salary: ~\*1850 £á free of taxes

\*Applications to be sent to / Information to be taken with:\*

Thank you for sending CV, cover letter and contact details of at least two references.

\*Contact\*

Dr. Simon Blanchet

Email : [simon.blanchet@ecoex-moulis.cnrs.fr](mailto:simon.blanchet@ecoex-moulis.cnrs.fr)

Phone : 05 61 04 03 61

Dr. Julien Cote

Email : [julien.cote@univ-tlse3.fr](mailto:julien.cote@univ-tlse3.fr)

Phone : 0 5 61 55 61 97

– Dr Julien Cote laboratoire Evolution & Diversite Biologique UMR 5174 CNRS UPS Universite Toulouse 3 - Paul Sabatier 118 route de Narbonne 31062 Toulouse cedex 9 France phone: +33 (0) 5 61 55 61 97 email: [julien.cote@univ-tlse3.fr](mailto:julien.cote@univ-tlse3.fr)

Julien Cote <[julien.cote@univ-tlse3.fr](mailto:julien.cote@univ-tlse3.fr)>

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## NIH US HPVGenomics

Post-doctoral Research Opportunity at the NIH

Human Cancer Genomics/Carcinogenic HPV Genomics

A postdoctoral position is available within the Genetic Epidemiology Branch of the Division of Cancer Epidemiology and Genetics ([www.dceg.cancer.gov](http://www.dceg.cancer.gov)), National Cancer Institute.

We are using high-throughput genomic approaches to examine carcinogenic HPV genome-wide variation to investigate the molecular basis of HPV carcinogenicity. Another goal of our research is to identify and characterize human genome variants that underlie the development of human pediatric cancers. To these ends, we use next-generation sequencing data to evaluate the HPV genome and human genome in large case-control or cohort studies. We are applying bioinformatics methods, phylogenetics, and genetic epidemiologic analyses to analyze these data.

Applicants with a doctoral degree or background in genetics/genomics, genetic epidemiology, or related field, are encouraged to apply. Experience in analyses of large complex genomic datasets, next-generation sequencing, and/or bioinformatic methods is a plus. A successful candidate will have excellent communication skills, be highly motivated and able to work in a large multidisciplinary team. Salary and benefits are highly competitive and commensurate with experience and accomplishments.

See the Division Fellowship Information page <<http://dceg.cancer.gov/fellowship-training/become-a-fellow>> for an overview of the fellowship experience.

To apply: Interested candidates should submit their curriculum vitae, a cover letter containing a statement of research interests, and the names and contact information for three referees to:

Lisa Mirabello, Ph.D., M.S. Earl Stadtman Investigator, Genetic Epidemiology Branch Division of Cancer Epidemiology and Genetics, NCI, NIH E-mail: [mirabellol@mail.nih.gov](mailto:mirabellol@mail.nih.gov) <http://dceg.cancer.gov/about-staff-directory/biographies/K-N/mirabello-lisa> This position is subject to a background investigation. The NIH is dedicated to building a diverse community in its training and employment programs.

[yeagerm@mail.nih.gov](mailto:yeagerm@mail.nih.gov)

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## NTNU UMuseum InvertBarcoding

The NTNU University Museum is seeking a highly qualified postdoctoral researcher for a project on environmental barcoding/metabarcoding of freshwater invertebrates. The position is for 3 years, preferably with start June 1, 2015 and is connected to a project funded by the Research Council of Norway and the Norwegian Environment Agency that involves partners from Canada, Germany and Norway.

Please see the full announcement for details and how to apply: <http://www.jobbnorge.no/ledige-stillinger/-stilling/109370> Best regards Torbjørn

– Dr. Torbjørn Ekrem Systematics and Evolution Group Department of Natural History NTNU University Museum Tel: +47 73597812 Email: [torbjorn.ekrem@ntnu.no](mailto:torbjorn.ekrem@ntnu.no)

Coordinator Norwegian Barcode of Life (NorBOL < <http://www.norbol.org> >) Co-editor Chironomus Newsletter on Chironomidae Research < <http://www.ntnu.no/ojs/index.php/chironomus/index> >

[torbjorn.ekrem@ntnu.no](mailto:torbjorn.ekrem@ntnu.no)

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## Okinawa AntBiodiversityEvolution

The Economo Lab (<http://arilab.unit.oist.jp/>) at the Okinawa Institute of Science and Technology ([www.oist.jp](http://www.oist.jp)), Japan, is seeking applicants for a postdoctoral position.

Our research investigates ecological and evolutionary processes generating and maintaining biodiversity across spatial scales and levels of biological organization, with an empirical focus on ant biodiversity. Ongoing projects (<http://arilab.unit.oist.jp/research/>) include understanding the macroevolutionary dynamics of the hyperdiverse ant genus *Pheidole*, global biodiversity patterns in ants, the island biogeography of Pacific Island ants, genomic approaches to community ecology, and biodiversity theory. Towards those ends, we integrate a variety of approaches including quantitative theory, phylogenetics, high-performance computing, ecoinformatics, morphometrics, field sampling, and traditional

collections-based taxonomy. Within these general research areas, the postdoc project is flexible and can be adapted to the interests and skills of the postdoc. Applicants having experience with model-based inference of population and evolutionary processes and working with next-generation sequence data are especially encouraged to apply.

The successful candidate will be provided funding to pursue their research and attend meetings, technician support, and access to state-of-the art facilities and equipment on the OIST campus. These resources include a 4000-core computer, a high-throughput ecological genomics pipeline, an X-ray micro-CT, SEM/TEM, confocal microscopes, etc. There will be numerous opportunities to work closely with other research groups at OIST and elsewhere.

To apply, please send your CV, including a list of references, and a cover letter describing your scientific background and interests as a combined PDF by email to <[arilab.oist@gmail.com](mailto:arilab.oist@gmail.com)> with 'Postdoc Application' in the subject line. Review will begin immediately and continue until the position is filled. Informal enquiries or questions are also welcome at <[economo@oist.jp](mailto:economo@oist.jp)>. The start date is flexible. Candidates must have a PhD in Ecology/Evolution or related field at the time of commencing the position.

About OIST: The Okinawa Institute of Science and Technology ([www.oist.jp](http://www.oist.jp)) is a new interdisciplinary graduate university located in the seaside village of Onna-son. The institute is international by design; the working language is English and researchers are split between Japanese and foreign nationalities. Knowledge of Japanese is not required, and our relocation staff will assist you with moving to Okinawa and setting up your living situation. The institute is located in a beautiful ecological setting adjacent to coral reefs and subtropical forest, and offers a competitive package for postdoctoral scientists. For more information on OIST, see recent articles in Nature (<http://www.nature.com/news/2011/110629/full/474553a.html>) (<http://www.nature.com/nature-journal/v474/n7353/full/474541b.html>), the Economist (<http://www.economist.com/node/21540228>), and info on our lab website (<http://arilab.unit.oist.jp/lab-oist-okinawa-oist/>).

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Evan P. Economo Assistant Professor Biodiversity and Biocomplexity Unit Okinawa Institute of Science and Technology 1919-1 Tancha Onna-son, Kunigamigun Okinawa, Japan 904-0495 <http://arilab.unit.oist.jp/evaneconomo@gmail.com>

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## RBG Kew Early Career Research Fellowships

Ten Early Career Research Fellowships in the Science Directorate at the Royal Botanic Gardens, Kew are now open for applications. Fellowships are available in the following departments:

Comparative Plant and Fungal Biology Biodiversity Informatics and Spatial Analysis Identification and Naming Natural Capital Conservation Science Collections

Details of these and other open positions in science at Kew are available at <https://careers.kew.org/home.html>. The deadline for applications is 15 February 2015.

W.Baker@kew.org

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## Roscoff KelpLifeHistoryEvol

\*/Postdoc position in evolutionary biology//

Kelp life history evolution and selection for aquaculture.\*

A two year postdoctoral research position is available immediately at the Roscoff Marine Laboratory, UMI "Evolutionary Biology and Ecology of Algae" in France (<http://www.sb-roscoff.fr/umi-3614.html>). The aim of the project is to use a combination of crossing experiments and genetic analyses in order to improve our basic knowledge of life history traits evolution in brown algae and to implement kelp selection for aquaculture. This position is funded in the context of the IDEALG project (<http://www.idealg.ueb.eu/>).

Artificial selection is crucial to algal aquaculture development, and contrarily to many terrestrial plant species, selection process in seaweed is in infancy, particularly in Europe. The aim of the project IDEALG is to develop basic research for selection process in seaweed aquaculture incorporating rigorous evolutionary thinking into it. Generally, seaweed populations are characterized by large level of genetic differentiation suggesting that populations are adapted to their local environment. In this context, parents that are too similar genetically may suffer from reduced crossing compatibility due to inbreed-

ing depression, whereas crosses between parents that are too different genetically may lead to an outbreeding depression by disrupting adaptive complexes. An intermediate optimal outcrossing distance is therefore expected as a compromise between inbreeding depression and outbreeding depression. In addition, seaweeds display complex life cycles, involving an alternation of haploid and diploid individuals. The consequences of such cycles for the reproductive system have been little studied experimentally. In particular, inbreeding depression is expected to be reduced as deleterious mutations are removed from the genome during the haploid phase.

The objective of this project is to address these questions combining crossing experiments with genetic analyses in different kelps (in particular *Saccharina latissima*). The effects of crosses on reproductive success will be investigated by examining the evolution of crossing compatibility with increasing geographic distance. Number of fertilizations and abortion rate will be measured in single-male crosses in laboratory conditions, as estimates of prezygotic and early postzygotic compatibility between mates.

Applicants must have a PhD in evolutionary ecology, in plant breeding or genetics. They must have a good background in population genetics and demonstrable experience in breeding experiments. Specific experience on seaweed ecology and culturing is preferable.

Salary will be 2000 EUR to 2500EUR per month (net) depending on experience. Applications are accepted until 15 February, 2015 and should include CV together with a description of research experience, relevant publications and 2 letters of references. Interview of the selected candidates will be made from the 15 to the 28 February 2015.

Applications should be sent to Christophe Destombe ([destombe@sb-roscoff.fr](mailto:destombe@sb-roscoff.fr)) and Myriam Valero ([valero@sb-roscoff.fr](mailto:valero@sb-roscoff.fr)). We prefer applications in electronic form. For more information please contact Christophe Destombe and/or Myriam Valero.

[destombe@sb-roscoff.fr](mailto:destombe@sb-roscoff.fr)

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## RutgersU PopulationGenomics

Postdoctoral position in Population Genomics at Rutgers University

Seeking qualified applicants for a post-doctoral position with Andrew Kern in the Department of Genetics and

the Human Genetics Institute of New Jersey at Rutgers University. The position is NIH funded to work on methods development for parameter inference in Isolation with Migration (IM) models. This work will be done in collaboration with the lab of Jody Hey at Temple University.

More information about the Kern lab can be found here: <http://kernlab.rutgers.edu>. More information about the department can be found here: <http://genetics.rutgers.edu/>. The Kern lab is located on the Busch campus of Rutgers University, in central New Jersey, and is in easy commuting range to New York City.

The ideal candidate would hold a Ph.D. and have a record of research achievement in population genetics, computational biology, computer science, statistics, or a related field. A background in comparative/population/evolutionary genomics is of course highly desirable. In addition the candidate should have experience programming in C, a scripting language (Ruby, Python, or Perl is fine), and would ideally be comfortable with cluster computing environments.

Review of applications will begin immediately and continue until the positions are filled. The position could begin as early as February, 2015. Interested candidates should submit an electronic version of their CV along with a cover letter describing their qualifications and relevant experience to Andrew Kern ([kern@biology.rutgers.edu](mailto:kern@biology.rutgers.edu))

Andrew Kern Assistant Professor of Genetics Rutgers University website: <http://kernlab.rutgers.edu> email: [kern@biology.rutgers.edu](mailto:kern@biology.rutgers.edu)

[Kern@dls.rutgers.edu](mailto:Kern@dls.rutgers.edu)

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## StellenboschU AntelopeGenomics

The Evolutionary Genomics Group at Stellenbosch University has a post-doctoral position available in the Department of Botany and Zoology to investigate the structural organization (architecture) and genomic plasticity of the meiotic genomes of African antelope. Large-scale chromosomal changes such as inversions, translocations, fusions and fissions “reshuffle” genomic segments providing new chromosomal forms on which natural selection can work. Since these new forms are produced in the germ line they can, at least potentially, be fixed in populations thereby providing new heritable allelic variants

that are essential for the maintenance of genetic diversity (*Heredity* 108 (1): 28-36).

There is extensive karyotypic diversity among African antelope where genomic reshuffling is often rapid and many closely related species possess different karyotypes indicating that chromosomal differentiation often occurs during, or shortly after cladogenesis. Our recent data suggest that the number of meiotic DSBs initiated in the early stages of meiosis and final crossover events are influenced by how the genome is organized into chromosomes, and that there is a phylogenetic component in recombination rates (*Proc Biol Sci* 280(1771):20131945). This appears to be directional, strongly punctuated and subject to selection. However, the mechanism(s) underlying this remain elusive and one of the aims of this investigation will be to determine if antelope species (with lower RR due to chromosomal fusions) similarly show a lower number of ZnF repeats suggesting that some Rb fusions may result in a modification of PRDM9, or its promoters, and thus facilitate speciation.

The ideal candidate will have a published track record in molecular cytogenetics, especially in meiosis. A strong background in one or more the following areas would be advantageous:

comparative genomics

molecular systematics

bioinformatics

The incumbent will work closely with researchers in two other groups: Dr Aurora Ruiz-Herrera (Universitat Autònoma de Barcelona, Spain, <http://grupsderecerca.uab.cat/evolgenom/>) and Professor Jiri Rubes (Veterinary Research Institute, Czech Republic) but will be located in the Stellenbosch lab. The appointment is for one year with the possibility of renewal contingent upon satisfactory progress. This position is available immediately.

Expressions of interest should be sent to Terry Robinson ([tjr@sun.ac.za](mailto:tjr@sun.ac.za)) and should include the names and contact details of 2-3 referees, a full CV and a covering letter that highlights the appropriateness of your expertise and why you are interested in the position.

Professor Terence J. Robinson Evolutionary Genomics Group Stellenbosch University Private Bag X1 Matieland 7602 South Africa E-mail: [tjr@sun.ac.za](mailto:tjr@sun.ac.za) Tel: +27 21 808 39 55 Fax: +27 21 808 24 05 <http://academic.sun.ac.za/botzoo/robinson/index.htm> <http://scholar.google.co.za/citations?sortby=pubdate&user=--npsyZdcAAAAJ> The integrity and confidentiality of this email is governed by these terms / Hierdie terme bepaal die integriteit en vertroulikheid van hierdie



epos. <http://www.sun.ac.za/emaildisclaimer> The integrity and confidentiality of this email is governed by these terms / Hierdie terme bepaal die integriteit en vertroulikheid van hierdie epos. <http://www.sun.ac.za/-emaildisclaimer> “Robinson, TJ, Prof <tjr@sun.ac.za>” <tjr@sun.ac.za>

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## StellenboschU Biogeography

Postdoctoral position, Stellenbosch University, South Africa

Postdoctoral position in island biogeography (ecological interaction networks)

Understanding the historic biogeographic processes that shaped current species distributions, and thus the evolution of different biotas, has become a central theme in ecology. Such knowledge is crucial for understanding how biodiversity is generated and maintained and for developing effective management strategies. Specifically, biogeography is assumed to play an important role in the structure of biological interaction webs (mutualisms, antagonisms, etc.) and their co-evolutionary histories. This assumption remains difficult to test under field conditions.

Truly puzzling and curious examples of biogeographic anomalies exist in nature; these are ideal systems for testing how biological interactions have diverged and the extent to which geography explains these patterns. For example, the diverse and speciose genus *Acacia* Mill. (sensu stricto; previously grouped in *Acacia* subgenus *Phyllodineae*) consists of about 1012 species, most of them confined to Australia, with a few taxa found in south-east Asia and Oceania. Two particularly peculiar extra-Australian taxa are the closely-related island endemics *Acacia koa* A. Gray found in the Hawaiian Islands in the Pacific Ocean and *A. heterophylla* Willd. from La Réunion Island in the Indian Ocean. This geographic disparity is truly remarkable, with ca. 18 000 km separating these two insular landmasses. What makes this even more interesting is that these two species are considered each other’s closest living relatives. Recent work in our laboratory has revealed that *A. heterophylla* from La Réunion Island represents a secondary colonization event from the Hawaiian Islands and is therefore the same species as *A. koa* (Le Roux et al. 2014). These two taxa therefore represent one of the most astonishing examples of long-distance dispersal.

This project will aim to compare and better understand

the ecological interaction networks of these two island endemics by studying their interactions with other biota (fungi and insects) in their native ranges (Hawaii and La Réunion Island). This research will shed light on how quickly speciation can happen and to what extent geographic isolation can shape evolutionary trajectories of interaction networks. Preference will be given to applicants with strong interest in mycology and/or entomology, molecular ecology, genetics, and evolutionary biology. Applicants should hold a PhD degree. Preference will be given to candidates with postdoctoral research experience, demonstrated skills in one or more of the fields listed above, and an excellent academic track record (i.e. publications in international journals). Successful candidates will be fully funded for 1 year, to be extended for an additional 1-2 years depended on satisfactory performance. An attractive annual salary will be offered along with additional expenses for research, international travel and subsistence, and conference attendance. Individuals of all nationalities are eligible. Applicants should be prepared to spend extended periods in Hawaii and La Réunion Island.

To apply, please send a CV, contact details for at least two academic references, and a brief outline of research interests to Dr Jaco Le Roux (jleroux@sun.ac.za), Prof. David Richardson (rich@sun.ac.za) and Prof. Mike Wingfield (Mike.Wingfield@up.ac.za) by 16 February 2015. Informal inquiries are welcome. Review of applications will begin immediately, and short-listed candidates will be contacted to set up phone/Skype interviews. The envisaged start date for the project would be March/April 2015.

Further reading:

Le Roux, J.J., Strasberg, D, Rouget, M., Morden, C., Koordom, M. and Richardson, D.M. (2014) Relatedness defies biogeography: the tale of two island endemics (*Acacia koa* and *A. heterophylla*). *New Phytologist* 204: 230-242.

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## Stockholm Evolutionary Genetics

A two-year postdoctoral position in Evolutionary Genetics is currently available at Stockholm University and Science for Life Laboratory in the research group of Dr. Tanja Slotte.

The complete ad for this position is available on the Stockholm University webpage: <http://www.su.se/english/about/vacancies/post-doctoral-positions/-postdoctoral-associate-in-evolutionary-genetics-1.217899> Project description We are recruiting a postdoctoral research associate to work within the project “Evolutionary consequences of dominance at a locus under long-term balancing selection” which is funded by the Swedish Research Council. The aim of this project is to investigate evolutionary processes at the self-incompatibility locus (S-locus) in the Brassicaceae. In particular, we wish to characterize the genetic basis of recurrent losses of self-incompatibility and the evolutionary consequences of S-locus dominance, both at the sequence and phenotypic level. The project will entail sequencing and analysis of S-locus alleles, phenotypic characterization of progeny from controlled crosses, and analyses of large-scale expression and methylation data. We will mainly focus on the crucifer genus *Capsella* (Brassicaceae), an emerging model for the study of mating system evolution.

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

Eligibility The applicant must hold a doctoral degree from an accredited college/university in evolutionary genetics, evolutionary functional genomics, or a related subject relevant to the project. Previous experience of bioinformatic analyses and molecular genetic lab work is

desirable. Previous experience of de novo assembly and annotation of genomes or genomic regions, and analyses of RNAseq or bisulfite sequencing data is an advantage, but not a requirement. Experience of plant experimental work is beneficial. The successful candidate must be highly motivated, creatively thinking and have a record of high quality scientific publications. Excellent written and spoken English language skills are required.

Terms of employment The position is a two year full-time appointment as a postdoctoral research associate, or as a researcher, if the successful candidate received their PhD more than three years ago. The position is available immediately. The starting date is negotiable.

Selection criteria The successful applicant will be selected based on the qualifications specified above. References and interviews will be used during the selection process to assess the qualifications of the applicants.

Information For further information, please contact the project leader Tanja Slotte, [tanja.slotte@su.se](mailto:tanja.slotte@su.se), the Department of Ecology, Environment and Plant Sciences. Personal webpage: <http://tanjaslottelab.se> University webpage: <http://www.su.se/emb/english/about-us/staff/r-s/tanja-slotte-1.174088> Science for Life Laboratory: <http://www.scilifelab.se> Union representatives Anqi Lindblom-Ahlm (Saco-S) and Lisbeth Häggberg (Fackförbundet ST), tel. 08-16 2000 (switchboard), and Gunnar Stenberg (SEKO), tel. 070-316 43 41.

### Application

Applications should consist of the following in a single electronic file (pdf) 1 Cover letter 2 Copy of diploma or other proof of PhD degree 3 Curriculum vitae, including publication list 4 Copies of three representative publications 5 Brief statement (no longer than two pages) describing research interests, research experience and career goals 6 Contact information (name, address, phone number and email address) for 2-3 references

Welcome with your application, marked with the reference number SU FV-0072-15, no later than March 1st, 2015, by e-mail to: [registrator@su.se](mailto:registrator@su.se). Please state the reference number SU FV-0072-15 in the subject line of your e-mail.

Stockholm University strives to be a workplace, which is free from

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## Stockholm MammothGenomics

**POSTDOC:** A two-year postdoctoral position on woolly mammoth genomics at the Swedish Museum of Natural History.

**DESCRIPTION:** We are seeking a highly motivated postdoctoral researcher to join the ancient DNA research group at the Swedish Museum of Natural History (see [www.palaeogenetics.com/adna](http://www.palaeogenetics.com/adna)). The position is for two years, and the postdoc is expected to play a key role in our project on woolly mammoth genomics, funded by the Swedish Research Council. The research will be focused on computational analysis of NGS data obtained from a large number of radiocarbon dated woolly mammoth samples, with the aim to track changes in genome-wide diversity leading up to the mammoth's extinction on Wrangel Island. The principal goals of the project are to investigate the genetic consequences of small population size by assessing the timing and rate of changes in heterozygosity, inbreeding coefficients and deleterious genetic variation. Moreover, the samples span a time period that encompasses several well-known environmental changes, and there is thus an opportunity to explore the effect of changes in selection pressure in real-time. From our perspective, an equally important goal of the position is that it will constitute an important step for the postdoctoral researcher towards securing a position as an independent researcher. Because of this, we will also encourage the postdoctoral researcher to design and pursue additional projects, to obtain experience in student supervision, and to develop his/her scientific network through collaborations and participation in scientific meetings.

**ENVIRONMENT:** The position will be based at the Department of Bioinformatics and Genetics at the Swedish Museum of Natural History (SMNH). The museum is located in Stockholm, which by many is regarded as one of the most beautiful capitals in the world and is home to a vibrant scientific community with several leading research institutes, including Stockholm University and the Science for Life Laboratory. The SMNH has a strong mission in natural history research, and its research division has more than 170 employees. The department of Bioinformatics and Genetics hosts three research groups, focused on ancient DNA and population genetics (PI: Dr. Love Dalén), avian systematics and biogeography (PI: Dr. Martin Irestedt), and phylogenomics (PI: Prof.

Fredrik Ronquist).

**QUALIFICATIONS:** The ideal candidate is a creative and independent researcher, who by the start of the project has obtained a PhD in biology or a related field. The PhD degree should have been received no more than three years before the deadline for applications. A record of scientific achievement in bioinformatics and computational genomics is essential, as is previous experience in handling NGS data using scripts and analysis pipelines. Additional merits include experience in computer programming, population genetics and wet lab analyses, as well as proficiency in genome assembly and annotation.

**OTHER INFORMATION:** The start date of the position is flexible, but should ideally be during the spring of 2015. The position is for two years full-time. For further questions regarding the position, please contact Dr. Love Dalén ([love.dalen@nrm.se](mailto:love.dalen@nrm.se)). Union representative is Bodil Kajrup SACO-S. Both can be reached at telephone number +46 8 519 540 00.

**HOW TO APPLY:** Applicants should submit a CV including a publication list, and cover letter describing their research interests, qualifications and reasons for applying. The cover letter should also indicate the applicant's ideal starting date and a list of two persons who may provide references. Please submit the application as a single pdf document, marked with dnr 2.3.1-36-2015, to [rekrytering@nrm.se](mailto:rekrytering@nrm.se) or to Swedish Museum of Natural History, P.O. Box 50007, SE-104 05 Stockholm, Sweden, no later than March 1, 2015.

Love Dalén <[Love.Dalen@nrm.se](mailto:Love.Dalen@nrm.se)>

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## Stockholm Meiofauna Taxonomy

Post-doctoral researcher

A postdoc position is available in the research group of Ulf Jondelius at the Swedish Museum of Natural History, Stockholm.

We are looking for a highly motivated postdoc with interest in animal diversity and taxonomy for a project aiming to survey the diversity of the flatworm group Macrostomorpha with emphasis on the Swedish fauna. Macrostomorphs are free-living microscopic worms that live predominantly in the marine environment, but also in fresh water. They are an abundant component of the littoral meiofauna.

Live specimens will be collected, documented and preserved for histology and DNA-sequencing. Sequence data will be used to delimit named and newly discovered species, which will be taxonomically described. The phylogeny of various groups within Macrostomorpha will be reconstructed. Sediment samples for a metagenetic study of several meiofauna groups will be collected and analyzed within the project aiming to provide new insights into meiofauna distribution and abundance patterns.

**Qualifications** The ideal candidate has a recent PhD in zoology or marine biology, an interest in marine and limnic fieldwork, experience in taxonomy of microscopic animals, proficiency in analysis of DNA sequence data and a record of publishing in scientific journals.

**Criteria for selection** Selection will be based on scientific merits including the quality of the PhD thesis and published scientific work, the applicants documented competence in subjects of relevance for the research field, proficiency in English and teamwork skills. The PhD degree should have been received no more than three years before the deadline for applications.

Starting date is May 1, 2015, although this is negotiable. Initial appointment is for one year with the possibility of extension for a further two years. The project will be carried out in cooperation with colleagues at the University of Basel.

For more information, please contact professor Ulf Jondelius (ulf.jondelius@nrm.se). Union representative is Bodil Kajrup, SACO-S. Both can be reached at telephone number + 46 8 519 540 00.

How to apply Applicants should submit (1) a cover letter describing your research interests and background, (2) a detailed CV (including publications), and (3) the contact details of three references as a single pdf document to rekrytering@nrm.se or to Swedish Museum of Natural History, P.O. Box 50007, SE-104 05 Stockholm, Sweden, no later than February 27, 2015. Mark your application with dnr 2.3.1-49-2015

Ulf.Jondelius@nrm.se

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## StockholmU ancientDNA

A two-year postdoc position in ancient DNA is currently available at Stockholm University and the Science for Life Laboratory.

The successful candidate will join the collaborative research project "Testing the utility of massively parallel sequencing on ancient sediments". This project is aimed at retrieving and analyzing metagenomic data sets from environmental DNA from 11,000-16,000-year old lake sediments. The postdoctoral position is shared between the groups of Barbara Wohlfarth (Department of Geological Sciences, Stockholm University), Tanja Slotte (Department of Ecology, Environment and Plant Sciences, Stockholm University, and Science for Life Laboratory) and Laura Parducci (Department of Plant Ecology and Evolution, Uppsala University). The post-doctoral fellow will be employed by the Department of Geological Sciences, but will have his/her main working place at the Science for Life Laboratory in Stockholm.

Link to the full ad on Stockholm University's website:

<http://www.su.se/english/about/vacancies/post-doctoral-positions/postdoctoral-fellow-in-testing-the-utility-of-massively-parallel-sequencing-on-ancient-sediments-1.217290>

Project Ancient lake sediments store a wealth of biological, chemical and physical information that allow reconstructing past climatic and environmental conditions in great detail. Although a wealth of paleoclimatic and paleoenvironmental information has been obtained, it is clear that the analysed microscopic and macroscopic fossil assemblages only represent a tiny fraction of the organisms that had existed at a certain time in the past and that each of the analytical methods employed has its specific limitation. Recent advances in environmental DNA analyses that make use of new large-scale sequencing technologies now offer the unprecedented opportunity to unravel a complementary spectrum of ancient faunal

and floral remains than those identified by micro- or macrofossil analyses. As such, aDNA analysis can provide a completely new understanding of how ecosystems responded to dramatic climatic changes.

The postdoctoral fellow will work in close collaboration with molecular ecologists, paleoecologists, paleoclimatologists and bioinformaticians and will utilize state-of-the-art approaches to retrieve and analyze the metagenomic data sets and to lead hypothesis-driven genomic analyses in an evolutionary context. He/she will also be involved in fieldwork (coring lake sediments), lab-work to sub-sample the sediment cores and DNA extraction in facilities specifically dedicated to ancient DNA extraction. Bioinformatics work will be done in collaboration with the Bioinformatic Service (<https://www.bils.se>) available at the Science for Life Laboratory in Stockholm.

**Terms of employment** This is a full-time position for two years, financed by the Faculty of Science at Stockholm University. Salaries at Stockholm University are set on an individual basis. The preferred starting date is May 2015.

**Qualification requirements** The applicant must hold a doctoral degree from an accredited college/university in a subject area relevant to the project. The ideal candidate must have very good experience in molecular biology, genetics, and bioinformatic analyses or equivalent. Candidates with a strong record in genetics/genomics, and previous experience in the field of ancient DNA will be preferred. Experience beyond the doctoral degree is not required. However the successful candidate must be highly motivated, creatively thinking and have a record of high quality scientific publications. He/she must demonstrate independency in working and be able to collaborate with scientists from different disciplines (biology, paleoscience, bioinformatics). Excellent English language skills, both written and spoken, are required.

**Selection criteria** The successful applicant will be selected based on the qualifications specified above. References and interviews will be used during the selection process to assess the qualifications of the applicants.

**Infrastructure and environment** Stockholm University is a leading European university offering a multicultural environment in one of the world's most dynamic capital cities. With more than 60,000 students and 5,000 staff, the University facilitates individual and societal development by providing top quality education that is tightly linked to its internationally recognized research programs.

The Department of Geological Sciences (<http://www.geo.su.se/index.php/en>) is located in the Frescati Campus of Stockholm University. Our research combines classical geology with geochemistry, marine geology and paleoclimate and is strongly integrated with the interests of the Bolin

[www.geo.su.se/index.php/en](http://www.geo.su.se/index.php/en)) is located in the Frescati Campus of Stockholm University. Our research combines classical geology with geochemistry, marine geology and paleoclimate and is strongly integrated with the interests of the Bolin

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## StockholmU Evolutionary Genomics

Postdoctoral position in Evolutionary Genomics

Project description

We are seeking a highly motivated postdoctoral researcher to join our ongoing ecological and evolutionary functional genomics (EEFG) research on a range of butterfly species. The research will be focused on 1) exploiting our extensive in-house population genomic data from 10 different Nymphalidae species, and 2) assembling and studying the genomes of 4 additional species in an analysis of gene family dynamics and ecological speciation.

The principal goals of the project are to investigate the genetic basis of local adaptation and species differences in physiological performance (e.g. flight) and host-plant usage. We have developed sufficient in-house experience for genome assemblies and now we wish to start using these resources to address fundamental questions. From our perspective, an equally important goal of the position is that it will constitute an important step for the postdoctoral researcher towards securing a position as an independent researcher. Because of this, we encourage the postdoctoral researcher to design and pursue additional projects, to obtain experience in student supervision, and to develop his/her scientific network through collaborations and participation in scientific meetings.

The Department of Zoology has an excellent history of studying butterfly ecology and evolution. The position will be in the lab of Christopher Wheat (see website < <http://www.christopherwheat.net/> >), which consists of 4 PhD students and 1 Postdoc. Currently we are primarily focused upon integrating our various studies of overwintering diapause, immune performance, and

wing coloration with our genomic and transcriptomic data for the *Pieris napi* butterfly.

#### Environment

The position will be based at the Department of Zoology, in the division of Population Genetics, at Stockholm University. The Department hosts six research groups focused on butterfly ecology and evolution, which have a long history of fruitful collaboration. PIs: Dr. Christopher Wheat, Dr. Karl Gotthard, Dr. Christer Wiklund, Dr. Sören Nylin, Dr. Niklas Janz and Dr. Bengt Karlsson

We have extensive rearing facilities, recently renovated wet lab space, and extensive computational and genomic resources, provided in part by generous funding from the Wallenberg Foundation and the Swedish Research Council. The campus is located 4 metro stops from the center of Stockholm, which by many is regarded as one of the most beautiful capitals in the world and is home to a vibrant scientific community with several leading research institutes, including the Science for Life Laboratory (SLL) and the Swedish Museum of Natural History. The SLL is a leading genomics core facility that we routinely use.

#### Eligibility and selection criteria

The applicant must hold a PhD in biology or a related field, and the degree should have been received no more than three years before the deadline for applications. The ideal candidate is a creative and independent researcher that can work well in a team environment. A record of scientific achievement in computational genomics is essential, as is previous experience in handling NGS data using scripts and analysis pipelines. Experience with butterflies is not necessary, but documented experience with linux is required. Additional merits include experience in computer programming, population genetics and gene family dynamics.

#### Terms of employment

The position is for two years full-time. The start date of the position is flexible, but should ideally be before June 2015.

#### Information

For further questions regarding the position, please contact Dr. Christopher Wheat ([chris.wheat@zoologi.su.se](mailto:chris.wheat@zoologi.su.se)).

#### Union representative

Anqi Lindblom-Ahlm (Saco-S) and Lisbeth Häggberg (Fackförbundet ST), telephone: +46 8 16 20 00 (switchboard), and Gunnar Stenberg (SEKO), telephone: +46 70 316 43 41.

#### Application

Applicants should submit a CV including a publication list, and a cover letter describing their research interests, qualifications and reasons for applying. The cover letter should also indicate the applicant's ideal starting date and a list of two persons who may provide references. Please submit the application as a single pdf document, marked with the reference number SU FV-0217-15, no later than March 1, 2015, by e-mail to [registrator@su.se](mailto:registrator@su.se).

Please state the reference number SU FV-0217-15 also in the subject line of your e-mail.

Christopher Wheat <[chris.wheat@zoologi.su.se](mailto:chris.wheat@zoologi.su.se)>

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## StockholmU PopulationGenomics

A two-year postdoctoral position in population genomics of plant mating system shifts is currently available at Stockholm University and Science for Life Laboratory in the research group of Dr. Tanja Slotte.

The complete ad for this position is available on the Stockholm University webpage: <http://www.su.se/english/about/vacancies/post-doctoral-positions/-postdoctoral-associate-in-evolutionary-genetics-1.218214> Background Plant mating systems, such as shifts from outcrossing to selfing, have profound effects on levels and structuring of genetic variation, and are expected to have a marked effect on the impact of natural selection. We are interested in quantifying the effects of mating system shifts on the efficacy of selection using population genomic and phylogenomic data. For a recent example of our work on this topic in *Capsella rubella*, see e.g. Slotte et al. 2013 *Nature Genetics* 45:831-5.

Project The post-doc will contribute to population genomic analyses of several parallel mating system shifts in the Brassicaceae. This will include investigating population structure, demographic shifts and assessing the impact of natural selection in different populations and species that vary in their outcrossing rates. Whole-genome and whole-transcriptome sequence data sets are already available, and more are currently being generated in the lab. The project offers plenty of opportunities for post-docs to pursue their own ideas using available genomic data.

Infrastructure and environment The postdoctoral associate will be based in the Slotte lab (<http://-tanjaslottelab.se>), a part of the Dept. of Ecology,

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

**Eligibility** The applicant must hold a doctoral degree from an accredited college/university in population genetics, phylogenetics, phylogeography, or a related subject relevant to the project. Previous experience of population genetic analyses and molecular genetic lab work is desirable. Previous experience of population genetic analyses of mating system effects, phylogeographic analyses, and/or phylogenetic analyses of factors determining rates of diversification is especially advantageous. Experience of plant sampling/field work and knowledge in R/Python is beneficial. The successful candidate must be highly motivated, creatively thinking and have a record of high quality scientific publications. Excellent written and spoken English language skills are required.

**Terms of employment** The position is a two year full-time appointment as a postdoctoral research associate. The position is available immediately. The starting date is negotiable.

**Selection criteria** The successful applicant will be selected based on the qualifications specified above. References and interviews will be used during the selection process to assess the qualifications of the applicants.

**Information** For further information, please contact the project leader Tanja Slotte, [tanja.slotte@su.se](mailto:tanja.slotte@su.se), the Department of Ecology, Environment and Plant Sciences. Personal webpage: <http://www.tanjaslottelab.se> University webpage: <http://www.su.se/emb/english/about-us/staff/r-s/tanja-slotte-1.174088> Science for Life Laboratory: <http://www.scilifelab.se> Union representatives Anqi Lindblom-Ahlm (Saco-S) and Lisbeth Häggberg (Fackförbundet ST), tel. 08-16 2000 (switchboard), and Gunnar Stenberg (SEKO), tel. 070-316 43 41.

#### Application

Applications should consist of the following in a single electronic file (pdf) 1 Cover letter 2 Copy of diploma or other proof of PhD degree 3 Curriculum vitae, including publication list 4 Copies of three representative publications 5 Brief statement (no longer than two pages) describing research interests, research experience and ca-

reer goals 6 Contact information (name, address, phone number and email address) for 2-3 references

Welcome with your application, marked with the reference number SU FV-0088-15, no later than February 10th, 2015, by e-mail to:

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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/evodir.html>

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## SyracuseU PlantEvolution

### Post-Doctoral Position in Plant Evolution

A post-doctoral position is available in the laboratory of Jannice Friedman, in the Department of Biology at Syracuse University. Work in my lab is focused on the evolution of reproductive strategies in plants, and understanding both the genetics and ecology of divergent reproductive strategies. Current NSF-funded work is focused on understanding life history transitions between annual and perennial strategies in *Mimulus guttatus*, yellow monkeyflower. Other projects include the evolution of wind pollination and mating system evolution.

Our research on *Mimulus* addresses the following questions: What is the genetic basis of differences between annual and perennial strategies in *M. guttatus*? How do seasonal cues determine flowering versus vegetative strategies? What are the fitness consequences and adaptive significance of this variation in the field? We use a combination of QTL mapping, next-gen sequencing, common garden experiments in the native range (western N. America), and greenhouse and laboratory work at Syracuse.

The particular focus of this post-doc position will be tailored to the skills and expertise of the successful applicant, and the opportunity exists to develop new systems. The ideal candidate will use this appointment as an opportunity to develop and pursue novel and exciting questions. Preference will be given to candidates with a strong background in evolution, and experience with population or quantitative genetics and next-gen sequencing would be valuable.

The position is available for 2 years, and will include a competitive salary and full benefits. The ideal start date would be April 2015 or earlier. Interested candidates should contact me by email at [friedman@syr.edu](mailto:friedman@syr.edu)

and include: a brief description of past research accomplishments and interests, CV, and contact information for three referees. Review of applications will begin immediately and continue until the position is filled.

Jannice Friedman Assistant Professor Department of Biology Syracuse University 107 College Place Syracuse NY 13244 315.443.1564 [friedman@syr.edu](mailto:friedman@syr.edu) <http://friedmanlab.syr.edu> [jannicefriedman@gmail.com](mailto:jannicefriedman@gmail.com)

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### TempleU PlantReproductiveEvolution

The Spigler Lab at Temple University is seeking applications from highly qualified individuals for a Postdoctoral Fellow position in the Department of Biology. The Postdoctoral Fellow will be involved in an ongoing project on variation in the mating system and phenotypic selection on floral traits across fragmented populations of a native wildflower species. In addition, the Postdoctoral Fellow will be integrally involved in the design and implementation of new field and/or greenhouse studies related to areas that suit the combined interests of the successful candidate and Spigler Lab, such as mating system and floral trait evolution, plant-pollinator interactions, plant-seed predator dynamics, demography, and/or population genetics. There will also be numerous opportunities to mentor undergraduates in research and to participate in outreach efforts. Additional information about the Spigler lab can be found at <http://rachelspigler.weebly.com>. Candidates must have a (1) PhD in Ecology, Evolutionary Biology, Botany, or related field; (2) an interest in plant reproductive ecology and evolutionary biology; (3) experience conducting and managing field and greenhouse studies; and (4) experience with statistics and software packages appropriate for ecological data. Excellent interpersonal, communication, and time-management skills, a strong work ethic, and attention to detail are also essential. Additional preferred qualifications include standard molecular skills (e.g., DNA extraction, PCR, microsatellite genotyping) and related statistical experience.

The position is available immediately and to last for one year, with the possibility of extension based on satisfactory progress and funding. Start date is flexible, but preference will be given to applicants who can start Spring 2015. Generous salary and benefits are provided. Interested applicants should send the following as a SINGLE PDF file by email to Rachel Spigler

([rachel.spigler@temple.edu](mailto:rachel.spigler@temple.edu)): 1) a short statement (one to two pages) on research interests, previous experience, and motivation for applying, 2) your curriculum vitae, and 3) contact information for three references. Informal inquiries about the position are welcome and may also be made to Rachel at [rachel.spigler@temple.edu](mailto:rachel.spigler@temple.edu). Review of applications will begin on February 1, 2015 and continue until the position is filled.

About the Biology Department at Temple University Temple University is a large, comprehensive public research university in Philadelphia, PA, with more than 37,000 undergraduate, graduate, and professional students enrolled in over 400 academic degrees. The Biology Department at Temple University (<https://bio.cst.temple.edu/>) represents an active research community with strengths in ecology, genomics, conservation, and evolutionary biology. The Biology Department is also home to the newly formed Center for Biodiversity (<http://cst.temple.edu/research-centers-and-institutes/center-biodiversity>), Center for Computational Genetics and Genomics (<https://bio.cst.temple.edu/~hey/CCGG/>), and Institute for Genomics and Evolutionary Medicine (<http://igem.temple.edu/>).

Philadelphia is the fifth largest city in the US, rich in history, known for its arts and culture, and is brimming with a vibrant science community. There are approximately 90 colleges and universities in the Greater Philadelphia region, with plenty of opportunities for collaboration. Recreational science activities abound, including 'Science on Tap', a monthly science cafe that features a brief, informal presentation by a scientist or other expert followed by lively conversation, the Academy of Natural Sciences, the Wagner Free Institute of Science, and the annual Philadelphia Science Festival. Philadelphia is also home to Fairmount Park, one of the world's largest city park systems.

Rachel Spigler <[rachel.spigler@temple.edu](mailto:rachel.spigler@temple.edu)>

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### TexasAMU PopulationBehaviourGenomics

A post-doctoral position is available in the Slotman laboratory in the Department of Entomology at Texas A&M University (<http://slotmanlab.tamu.edu/>). Our lab focuses on the evolutionary and behavioral genetics/genomics of disease transmitting mosquitoes. The post-doc will conduct NIH-funded research into the ge-



onomic basis of outdoor feeding preference of the African malaria mosquito *An. gambiae*. This mosquito generally prefers feeding indoors, but after years of indoor-based vector control on Bioko Island has shifted its behavior towards a preference for outdoor feeding. We are taking a whole genome Pool-seq approach to map genetic differences between indoor and outdoor host-seeking *An. gambiae* mosquitoes on Bioko. In addition, the successful candidate will be expected to contribute to ongoing research into the genetic basis of attraction of *An. gambiae* to human hosts.

The ideal candidate will have a background in population genetics, experience with analyzing next-generation sequencing data, and familiarity with R and Python (or Perl).

The Texas A&M System is an Equal Opportunity/Affirmative Action/Veterans/Disability Employer committed to diversity.

The position is available for two years available immediately, but start date is open to negotiation. If you are interested in applying for this position please send a cover letter, CV, PDFs of representative publications, and contact information for three references to [maslotman@tamu.edu](mailto:maslotman@tamu.edu).

[maslotman@ag.tamu.edu](mailto:maslotman@ag.tamu.edu)

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## TrentU 2 ConservationGenomics

Post-Doctoral Fellow (PDF) in Functional Conservation Genomics

A collaborative research program on caribou conservation is seeking a conservation geneticist, molecular ecologist, molecular biologist or bioinformatician with strong quantitative skills for ecotype characterization of Canadian caribou. The relationship among sub-species and ecotypes will be examined in assessing the reconstruction of population histories across Canada. This project is a partnership between academic and provincial government agencies with significant engagement with industrial partners. The PDF will use a large DNA dataset to expand into functional gene characterization and mitogenomics of caribou representative of nationwide sampling efforts. The PDF will be expected to take a leadership role in coordinating a team of graduate and undergraduate students and liaise with project partners. The salary is \$40,000/year and the position will be filled as soon as a suitable candidate is found.

Applicants should submit a CV, a statement of research interests, and the names and contact information for three references.

Please submit applications to:

Dr. Paul J. Wilson Canada Research Chair in DNA Profiling, Forensics & Functional Genomics Trent University, 1600 West Bank Drive, Peterborough, ON, K9J7B8 Phone 705.748.1011 ext. 7259; Fax 705.748.1003 Website: [www.wilsoncrrresearch.ca](http://www.wilsoncrrresearch.ca) [pawilson@trentu.ca](mailto:pawilson@trentu.ca)

or

Dr. Micheline Manseau Natural Resources Institute, University of Manitoba 70 Dysart Road, Winnipeg, MB, R3T 2N2 Phone 204.474.9889; Fax 204.261.0038 Website: [www.lecol-ck.ca](http://www.lecol-ck.ca) [Micheline.Manseau@pc.gc.ca](mailto:Micheline.Manseau@pc.gc.ca)

Post-Doctoral Fellow (PDF) in Landscape Genomics

A collaborative research program on caribou conservation is seeking a researcher with strong quantitative skills to complement a research team examining the spatial genetic/genomic dynamics of Canadian boreal caribou. This project is a partnership between academic, federal and provincial government agencies and the private sector and builds on a multi-year dataset. The PDF will use project data to characterize the spatial genetic structure and landscape/environmental variables influencing caribou herds, ecotypes and associated subspecies based on genetic structure using mitogenomics, SNP analyses and functional gene profiles. The research will assess the potential impacts of anthropogenic activities, e.g. mining and protected areas, on caribou genetic structure by developing predictive genetic structure models within defined conservation units or targeted areas-of-interest for development or protection. The PDF will be expected to take a leadership role in coordinating a team of graduate and undergraduate students and liaise with project partners. The salary is \$40,000/year + benefits and the position will be filled as soon as a suitable candidate is found. Applicants should submit a CV, a statement of research interests, and the names and contact information for three references.

Please submit applications to:

Dr. Paul J. Wilson Canada Research Chair in DNA Profiling, Forensics & Functional Genomics Trent University, 1600 West Bank Drive, Peterborough, ON, K9J7B8 Phone 705.748.1011 ext. 7259; Fax 705.748.1003 Website: [www.wilsoncrrresearch.ca](http://www.wilsoncrrresearch.ca) [pawilson@trentu.ca](mailto:pawilson@trentu.ca)

or

Dr. Micheline Manseau Natural Resources Institute, University of Manitoba 70 Dysart Road, Winnipeg, MB, R3T 2N2 Phone 204.474.9889; Fax 204.261.0038 Website: [www.lecol-ck.ca](http://www.lecol-ck.ca) [Micheline.Manseau@pc.gc.ca](mailto:Micheline.Manseau@pc.gc.ca)

Jill Lalor Research Technician Trent University Genomics Lab A112 and Wilson Lab C254 2140 East Bank Drive Peterborough, ON K9J 7B8 705-748-1011 ext 6657

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## UArizona SimpsonFellowship EvolutionSystematics

G. G. Simpson Postdoctoral Fellowship in Evolution V  
University of Arizona

The Department of Ecology and Evolutionary Biology announces one postdoctoral fellowship position beginning Fall 2015, named in honor of G. G. Simpson's long tenure at the University of Arizona. Simpson Fellows are expected to conduct research in evolutionary biology and/or systematics that includes one or more of the University of Arizona's extensive natural history collections (otherwise the specific research topic and taxonomic focus are open). The EEB vertebrate collections and the University Herbarium have a strong taxonomic focus on the flora and fauna of the southwest United States and adjacent Mexico. The position is part of an ongoing commitment to natural history collections on the University of Arizona campus. Postdoctoral fellows are expected to establish research collaborations with faculty having a primary or joint appointment in the Department of Ecology and Evolutionary Biology and must contact one or more prospective advisers during the application process. Responsibilities of the positions include a modest teaching commitment (e.g., a graduate seminar once per year in the fellows research specialty). Salary is \$40,000 plus benefits (nine-month appointment). A research stipend of \$5000 will also be included. The positions are renewable for a second year contingent on satisfactory performance.

Applicants should submit application materials online at the University of Arizona Human Resources website (<https://www.uacareertrack.com>; look for job #57245), including C.V., statement of research and teaching interests and experience (including a brief description of the specific research project that they are interested in undertaking as a Simpson Fellow and the course they are interested in teaching), and two letters of reference. A brief letter of support from the prospective postdoctoral mentor(s) is also required. Reference letters and the letter of support should be emailed directly to sanderm@email.arizona.edu. Position is open until filled, but we anticipate reviewing applications beginning on February 9, 2015. Contact Dr. Michael Sanderson

(sanderm@email.arizona.edu) for further information.

Michael J. Sanderson, Professor Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721

Office: BSW 412 Phone:520-626-6848  
email:sanderm@email.arizona.edu

lab web site: <http://loco.biosci.arizona.edu> Ceiba phylogenetic tree visualization: <http://sourceforge.net/projects/ceiba> PhyLoTA Browser: <http://phylo.ta.net> r8s software: <http://loco.biosci.arizona.edu/r8s> sanderm@email.arizona.edu

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## UBritishColumbia SingleCellGenomics

Research Associate Position in Single Cell Phylogenomics University of British Columbia Vancouver, Canada The Department of Botany seeks a well-trained highly motivated and enthusiastic individual interested in exploring the evolutionary biology of complex microbial life and their organelles using single cell genomics methods coupled with phylogenomic analyses as a Research Associate. The applicant must have a PhD or equivalent and at least three additional years of research experience. Expertise in eukaryotic biodiversity and evolutionary history, and the application of single cell genomics methods (genomic and transcriptomic datasets) and phylogenetic analyses are essential. The applicant must have excellent written and oral communication skills and be highly organized. Basic molecular biology and analyses techniques are also highly desirable. The candidate must have a proven record of publication in significant journals in the field. The position is available starting May 15 2015 for an initial period of one year with a possibility for extension subject to a satisfactory performance and funding. To apply, please send a cover letter outlining research experience and interest, a curriculum vitae and the names and contact information for 3 referees to Patrick Keeling, Department of Botany, University of British Columbia, 3529-6270 University Boulevard, Vancouver, B. C. V6T 1Z4, Canada. Email [pkeeling@mail.ubc.ca](mailto:pkeeling@mail.ubc.ca). Fax (604) 822-6089. Closing date is Feb. 16, 2015. UBC hires on the basis of merit and is strongly committed to equity and diversity within its community. We especially welcome applications from visible minority group members, women, Aboriginal persons, persons with disabilities, persons of minority sexual orientations and gender identities, and others

with the skills and knowledge to productively engage with diverse communities. Canadians and permanent residents of Canada will be given priority.

pkeeling@mail.ubc.ca

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## UCalifornia Berkeley Evolutionary Physiology

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\*Title: \*Postdoctoral Position Evolutionary Physiology-Integrative Biology

\*Description: \*The Department of Integrative Biology at the University of California, Berkeley invites applications for a Postdoctoral Employee starting in the summer of 2015. The successful candidate will have the opportunity to study the evolution of metabolic physiology of insects using a range of model systems including montane willow leaf beetles (\*Chrysomela aeneicollis\*), wing-polymorphic Florida sand crickets (\*Gryllus firmus\*) or related cricket species, and \*Drosophila\* species. Understanding the potential for evolution of metabolic physiology in response to changing environments is an essential component of predicting organismal responses to climate change. The details of the project are flexible depending on the interests of the successful candidate, but will involve some combination of field work, biochemistry and physiology, molecular biology, and modelling. Please see [cmwilliamslab.com](http://cmwilliamslab.com) for more information.

The Integrative Biology program is ranked in the top 10 biology programs nationwide (National Research Council, 2010). The department and wider campus provide a thriving and exciting intellectual culture with extensive opportunities for collaboration.

\*Responsibilities: \*(1) Perform field work; (2) Insect husbandry; (3) Design and carry out experiments on insects using biochemistry, physiology, and molecular biology; (4) Data analysis and statistical modelling; (5) Preparing and submitting papers for publication; (6) Supervising and mentoring undergraduate students

\*Minimum/Basic Qualifications Required: \*Applicants must complete all degree requirements except the dissertation by the time of application.

\*Additional Required Qualifications: \*The successful

candidate will have a strong publication record in peer-reviewed journals and a background in biochemistry, physiology or molecular biology. Applicants must have PhD or equivalent by the expected start date.

\*Appointment: \*This position reports to Dr. Caroline Williams. The initial appointment will be at 100% time for 1 year with the expectation of extension based on satisfactory performance and availability of funding. The approximate start date of this position will be July 1, 2015.

\*Salary\*: \$42,000-\$49,128/annually, depending prior postdoctoral experience and qualifications. Generous benefits are included( <http://vspa.berkeley.edu/postdocs>).

\*To Apply\*: <https://aprecruit.berkeley.edu/apply/-JPF00640> Interested individuals should submit (via the website above) application documents as PDFs, which includes (i) an updated curriculum vitae (required), (ii) a cover letter (required), (iii) names with contact information for 3-5 individuals who have agreed to provide a reference (required) for this specific position (contact information includes title, institution, email, basis for this individual's recommendation of the applicant). Letters of reference may be requested of the finalists.

Department Contact: CarolineWilliams, Supervisor, [cmw@berkeley.edu](mailto:cmw@berkeley.edu)

The initial review date for this recruitment is February 17, 2015; please apply by this date to be fully considered for the position. The position will be open until filled.

All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are provided via a third party (i.e., dossier service or career center), to the UC Berkeley statement of confidentiality ( <http://apo.berkeley.edu/evalltr.html>) prior to submitting their letters.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: <http://policy.ucop.edu/doc/4000376/NondiscrimAffirmAct> Caroline Williams, PhD Assistant Professor Valley Life Sciences Building, #5120 Department of Integrative Biology University of California, Berkeley

Office: 510-643-9775 Lab: LSA 535 and 539 Skype: caro\_williams Email: [cmw@berkeley.edu](mailto:cmw@berkeley.edu) Website: [cmwilliamslab.com](http://cmwilliamslab.com)

Mailing address:

Williams Lab University of California, Berkeley Department of Integrative Biology 3040 Valley Life Sciences Building # 3140 Berkeley, CA 94720-3140

cmw@berkeley.edu

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## UGuelph Biodiversity

Postdoctoral Fellowship Opening at the Biodiversity Institute of Ontario

Position description

The Biodiversity Institute of Ontario ([www.biodiversity.ca](http://www.biodiversity.ca)) at the University of Guelph announces an opening for a highly qualified post-doctoral fellow. This position will involve working with large datasets of DNA barcode sequences to address fundamental questions about the evolution and distribution of global biodiversity. For example, how do diversification rates, molecular evolutionary rates, and species ages vary with geography and with biological traits? Funding is available for two years, but renewal after the first year is contingent on adequate progress. The position will be supervised by Drs. Sarah Adamowicz and Paul Hebert and will involve regular collaboration with additional researchers at BIO and beyond. As this research has the potential to result in excellent publications in high impact journals, the position will provide an outstanding opportunity for those pursuing a career in biodiversity science.

Qualifications

A highly motivated individual with strong background and publications in one or preferably more than one of the following areas is sought:

- Macroecology - Macroevolution - Molecular phylogenetics - Population genetics - Molecular evolution - Bioinformatics

Applicants must currently hold their PhD or anticipate earning their PhD prior to May 1, 2015. Applications are welcomed from candidates from any nation. Given equal qualifications, preference will be given to Canadian citizens and permanent residents.

To apply

Send a cover letter, curriculum vitae, up to three reprints, and the names and contact information for three references to Sarah Adamowicz by email

([sadamowi@uoguelph.ca](mailto:sadamowi@uoguelph.ca)). Applications will be considered starting on January 15th, 2015, and will continue until the position is filled. The start date is negotiable; ideally, candidates will be available to take up the position before July 1, 2015.

Sarah J. Adamowicz, Ph.D. Assistant Professor Biodiversity Institute of Ontario & Department of Integrative Biology University of Guelph 579 Gordon Street Guelph, Ontario N1G 2W1 Canada

Email: [sadamowi@uoguelph.ca](mailto:sadamowi@uoguelph.ca) Phone: +1 519 824-4120 ext. 53055 Fax: +1 519 824-5703 <http://www.dnabarcoding.ca/> <http://www.barcodinglife.org/> <http://www.uoguelph.ca/ib/people/faculty/-adamowicz.shtml> [sadamowi@uoguelph.ca](mailto:sadamowi@uoguelph.ca)

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## UHelsinki LifeHistoryEvolution

POST DOC position in genomics and LIFE-HISTORY evolution at the university of helsinki, finland

Applications are invited for 24 month post doc (with a possibility of up to 2 year continuation) in the research group of Marjo Saastamoinen as part of the ERC funded META-STRESS project (Starting Grant scheme). The successful applicant will join the Centre of Excellence in Metapopulation Research at the University of Helsinki.

The project aims to understand the mechanisms that allow organisms in the wild to cope with environmental stress. The large metapopulation of the Glandville fritillary butterfly gives a unique opportunity to study processes operating from genes within individuals all the way to metapopulation-level dynamics (> 20 years of data). In this project ecological studies will be integrated with molecular approaches to unravel the significance of different mechanisms - candidate genes, epigenetic inheritance and intestinal microbial communities - potentially influencing individual responses to environmental challenges. Molecular and genomic tools (including the genome; Ahola et al. 2014, Nat Comm) are available for this species to apply to ecologically relevant traits.

Recent relevant publications include:

Saastamoinen M, Norio H & Van Nouhuys S (2013) Direct and trans-generational responses to food deprivation during development in the Glandville fritillary butterfly. *Oecologia* 171: 93-104.

Saastamoinen M, Ikonen S, Wong SW, Lehtonen R &

Hanski I (2013) Plastic larval development in a butterfly has complex environmental and genetic causes and consequences for population dynamics. *Journal of Animal Ecology* 82: 529-539.

Kvist J., Wheat C. W., Kallioniemi E., Saastamoinen M., Hanski I. & Frilander M. (2013). Temperature treatments during larval development reveal extensive heritable and plastic variation in gene expression and life history traits. *Molecular Ecology* 22: 602-619.

The successful candidate should have PhD / post doctoral experience in evolutionary genetics, bioinformatics, microbiology, evolutionary biology or similar, and a strong interest in working with natural populations. Excellent written and verbal communication skills, and the ability to think independently and creatively are required. You must demonstrate the ability to work as part of a team, and participate in supervision of more junior group members.

More information: <http://www.mv.helsinki.fi/home/-msaastam> ; [www.helsinki.fi/science/metapop](http://www.helsinki.fi/science/metapop) Starting date: April 2015

Application deadline: 13 February 2015

Mail your application with title post-doc META-STRESS (CV with publications included, contact details of two references, and a letter (MAX 1 page) with a description of your research interests and why you would be a suitable candidate for the project) as a single pdf file to [biotiede-mrg@helsinki.fi](mailto:biotiede-mrg@helsinki.fi).

Informal inquires to [marjo.saastamoinen@helsinki.fi](mailto:marjo.saastamoinen@helsinki.fi)

Dr Marjo Saastamoinen

Academy Research Fellow

Center-of-Excellence in Metapopulation Biology

Department of Biosciences

PO Box 65 (Viikinkaari 1)

FI-00014 University of Helsinki

FINLAND

tel. + 358 (0)50 448 4471

<http://www.mv.helsinki.fi/home/msaastam/> Marjo Saastamoinen <[marjo.saastamoinen@helsinki.fi](mailto:marjo.saastamoinen@helsinki.fi)>

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## UJerusalem Evolution MicroRNAs

A postdoc position (funded up to 4 years) and a PhD student position (funded up to 5 years) are available in the Moran lab at Department of Ecology, Evolution and Behavior at the Hebrew University of Jerusalem, Israel (HUJI). These positions will be funded by a new European Research Council (ERC) project aimed to shed new light on the evolution of post-transcriptional regulation by microRNAs. In our lab we use the sea anemone *Nematostella vectensis* as a model and employ various biochemical, genetic, microscopic and computational approaches to answer our questions. The fellowships associated with the project are at the very high end of Israeli standards and the successful candidates will also receive funds for attending relevant international workshops and conferences.

The Hebrew University of Jerusalem (HUJI) is Israel's premier university. HUJI has been ranked among the top universities in the world in two comprehensive surveys conducted by The Times Higher Education Supplement of London and Shanghai University. The host lab is located at the Natural Sciences campus, where a wide range of available technical services and facilities enable the cutting-edge research in various fields of Life Sciences. Our department is highly international and the lab working language is English.

The suitable candidate should have experience in standard biochemical and molecular biology techniques. Having prior experience in microscopy and/or computational analysis of HiSeq data is an advantage.

More details about our research group can be found online at [yehumoran.com](http://yehumoran.com) Interested candidates are welcome to contact Yehu Moran ([yehu.moran@mail.huji.ac.il](mailto:yehu.moran@mail.huji.ac.il)). Please send a CV, list of publications and contact details of 2-3 referees.

Yehu Moran

Yehu Moran <[yehu.moran@mail.huji.ac.il](mailto:yehu.moran@mail.huji.ac.il)>

## UKent Blastocystis adaptations

Postdoctoral Research Associate Position: Revealing the anaerobic adaptations of the mitochondrion-related organelles of Blastocystis.

We are looking to recruit an enthusiastic post-doc with skills in molecular and biochemical parasitology and proteomics.

Applications are invited for a postdoctoral research fellow post at the School of Biosciences, University of Kent, UK. This is a 3-year post, funded by the BBSRC, to work in the Laboratory of Molecular and Evolutionary Parasitology of Dr. Anastasios Tsaousis. The aims of the research are to exploit the anaerobic adaptations of the mitochondrion-related organelles of Blastocystis.

Project: Blastocystis is a human intestinal parasite, recently considered to be a stramenopile, with a controversial pathogenicity, mainly because of lack of knowledge around its life cycle and function of its organelles. Since Blastocystis is a strict anaerobe, it was thought that lacked of canonical mitochondria, and instead it had hydrogenosomes, anaerobic organelles related to mitochondria. Recent genomic and transcriptomic data generated from Blastocystis demonstrated the presence of 700 putative mitochondrial and hydrogenosomal proteins. Amongst these only a few so far have been shown to localise into the organelles. The organelles are predicted to have additional mitochondrial characteristics, including pathways for amino acid metabolism, pyruvate metabolism and an incomplete tricarboxylic acid cycle. The Blastocystis mitochondrion-related organelles (MROs) have metabolic properties that are found in aerobic and anaerobic mitochondria but also in hydrogenosomes. The purpose of this project is to understand the evolutionary adaptations of Blastocystis and especially its mitochondrion-related organelles (MROs) under different environmental conditions. This work will identify the significance of the evolutionary important of mitochondrion-related organelles for the organism, but in addition will discover novel functions that can potentially be used in systems biology, or targeting parasitic and even mitochondrial diseases. The project will involve purifying the MROs under different environmental conditions, followed by proteomic and biochemical analyses of the different novel pathways.

The successful candidate will have a PhD degree in molecular biology/ biochemistry or the related disci-

pline with experience in molecular parasitology and cell culturing of parasites. Experience in mitochondrial biochemistry, good interpersonal skills and ability to communicate technical information is essential.

Closing date for applications is March 01, 2015.

For any questions or clarifications, please contact Dr. Anastasios Tsaousis at: a.tsaousis@kent.ac.uk

Further information about the post and the application procedure can be found at: [https://jobs.kent.ac.uk/fe/tpl\\_kent01.asp?s=-4A515F4E5A565B1A&jobid=39021,2352231265&key=-42702864&c=782372028302&pagestamp=-sewbaadijtuufmxab](https://jobs.kent.ac.uk/fe/tpl_kent01.asp?s=-4A515F4E5A565B1A&jobid=39021,2352231265&key=-42702864&c=782372028302&pagestamp=-sewbaadijtuufmxab) Dr. Anastasios D. Tsaousis (PhD) Lecturer in Biosciences University of Kent, School of Biosciences, Room: Ingram 220 Canterbury, CT2 7NJ, UK tel: +44 (0) 1227 827007

email: [tsaousis.anastasios@gmail.com](mailto:tsaousis.anastasios@gmail.com)  
A.Tsaousis@kent.ac.uk

Webpage: <http://www.kent.ac.uk/bio/profiles/staff/-tsaousis.html> Personal webpage: [www.adtsaousis.com](http://www.adtsaousis.com)  
A.Tsaousis@kent.ac.uk

## ULausanne BarnOwlPolymorphism

1 POST DOCTORAL FELLOWSHIP (minimum 1 year)

Genetic basis of colour variation in the barn owl, *Tyto alba*.

The barn owl varies in the degree of three melanin-based plumage traits. This variation has been shown to strongly heritable and associated with a number of behavioural, physiological and life history traits. In order to understand the underlying genetic basis of colour variation, we intend to run RNAseq analyses, a method that is successfully working for the barn owl.

For this project, the ideal candidate should have a strong background in computational evolutionary biology, experience in analysing next-generation sequencing data and/or in fine-scale mapping of phenotypic variation.

References:

Ducrest A-L, Keller L & Roulin A. 2008. Pleiotropy in the melanocortin system, coloration and behavioural syndromes. *Trends in Ecology and Evolution* 23, 502-510.

Roulin A & Ducrest A-L. 2011. Association between

melanism, physiology and behaviour: a role for the melanocortin system. *European Journal of Pharmacology* 660, 226-233.

Prof. Alexandre Roulin Department of Ecology & Evolution Building Biophore University of Lausanne CH-1015 Lausanne Switzerland

Desk 3202Tel: 0041 21 692 41 89 Mobile: 0041 79 686 08 64 Fax: 0041 21 692 41 65 Website: <http://www.unil.ch/dee/page7006.html> Alexandre Roulin <Alexandre.Roulin@unil.ch>

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## ULund MolecularEvolutionaryEcol

Postdoc position in Molecular Ecology and Evolution at Lund University, Sweden

Research Topic: Sexual Selection and Introgression in Lizards

Background

Gene transfer between species or sub-species via hybridization is increasingly recognized as an important source of diversification and adaptation. However, only rarely are systems sufficiently well understood to predict the degree and direction of hybridization, which makes current studies largely exploratory and reliant on post-hoc explanations. To circumvent this problem we have experimentally established the causes of hybridization between two sub-species of the common wall lizard, *Podarcis muralis*. These studies suggest that introgression in secondary contact will be driven by sexual selection, with a number of predictions regarding the direction, extent, and phenotypic and genomic patterns of introgression. We now wish to test these predictions in independent regions of hybridization using extensive phenotypic data and generation of genome-wide nucleotide markers that can be mapped onto the draft genome of the species.

Job assignment

The tasks involve (i) Planning research; (ii) Generating, processing and analyzing data on single nucleotide polymorphism; (iii) performing analyses to establish genomic and geographic patterns of introgression using sequence and phenotypic data; (iv) field work to collect further samples; and (v) preparation of results for publication. The successful applicant is expected to contribute to the intellectual environment of the host group through active participation in discussion groups, meetings, and other

activities. We encourage maintaining and establishing new collaborations. Co-supervision of MSc students may be part of the assignment. The position is funded by a grant from the Swedish Research Council to Dr Tobias Uller (<http://www.biology.lu.se/tobias-uller>) and is initially for two years, with the possibility of a one-year extension.

Eligibility/ Entry requirements

The applicant must have a PhD in Molecular Ecology, Evolution or associated fields and have extensive experience with analyses of high-throughput sequence data. A background in the application of genome data to non-model organisms is highly meritorious. Applicants must be highly motivated to pursue research in ecology and evolution, show outstanding organizational skills, and have a track record of completed research projects.

Basis for assessment

Applicants are evaluated based on documented ability to develop and carry out high-quality research. Such evidence may include a strong track record of publications in scientific journals, documentation of successful completion of research projects, high intellectual capacity and problem-solving ability, technical and analytical know-how, organizational skills, enthusiasm, dedication, and an ability to work both independently and in a team. Where possible, statements to these effects should be accompanied by objective or independent assessment of the candidate's track record and potential (e.g., via letters of support).

Applicants should follow the instructions on the following webpage when preparing their application: <http://www.lu.se/lediga-anstallningar-availability-jobs?x=3D0&Dnr=3D651840&Type=E> For further details or informal contact, please contact Tobias Uller at [tobias.uller@biol.lu.se](mailto:tobias.uller@biol.lu.se)

Dr Tobias Uller Wallenberg Academy Fellow Department of Biology Lund University

[tobias.uller@zoo.ox.ac.uk](mailto:tobias.uller@zoo.ox.ac.uk)

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## UMichigan ComputationalEvolutionaryBiol

Job title: Postdoctoral position in computational evolutionary biology / phylogenetics

A postdoctoral position in computational evolutionary biology / phylogenetics is available in Dan Rabosky's lab

at the University of Michigan, Ann Arbor. The postdoctoral researcher will be involved the development and application of methods for studying evolutionary dynamics (speciation, extinction, phenotypic evolution) across phylogenetic trees that potentially include many thousands of taxa. The project will involve extensions of the BAMM / BAMMtools software platform developed by the Rabosky lab (see <http://bamm-project.org> for more information).

BAMM is a Bayesian framework for modeling complex mixtures of dynamic evolutionary processes on phylogenetic trees. The postdoctoral researcher will be involved with development and implementation of new methods for modeling evolutionary dynamics from phylogenetic and/or paleontological data. An area of particular interest involves combined analyses of paleontological and neontological data with BAMM. An additional objective involves development of BAMMtools, our R package for analyzing and visualizing evolutionary dynamics from BAMM output.

The ideal candidate will have a background in computational biology and/or quantitative methods in evolutionary biology. Programming experience in C/C++ and/or R is required. Previous experience studying macroevolution dynamics is helpful, but we welcome applications from any area of computational biology, including population genetics, theoretical ecology, and applied mathematics.

The position offers exceptional opportunities for independent research, career development, and quantitative skills training. We have an outstanding group of researchers in quantitative/computational evolutionary biology and biodiversity science in the Department of Ecology and Evolutionary Biology, the UM Museum of Zoology, and the UM Museum of Paleontology.

Applications should be sent to drabosky at umich.edu. Please include a cover letter describing your research interests and background, a C.V., evidence of programming experience, and contact information for three references. Any questions about the position can be directed to Dan Rabosky.

Dan Rabosky Assistant Professor & Curator of Herpetology Museum of Zoology & Department of Ecology and Evolutionary Biology University of Michigan Ann Arbor, MI 48109-1079 USA

<http://bamm-project.org> drabosky@umich.edu

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## UMichigan HostParasiteInteractions

Subject: Postdoc position: ecology and evolution of host-parasite interactions

A postdoctoral position focusing on the evolutionary ecology and/or community ecology of host-parasite interactions is available in the laboratory of Meghan Duffy at the University of Michigan. The successful candidate for this position will be expected to carry out independent research relating to the ongoing research in the Duffy Lab. Some major themes include the evolution of hosts and parasites, eco-evolutionary dynamics in host-parasite systems, and the evolutionary and community ecology of multihost-multiparasite interactions. There will also be the potential to develop additional projects building on the strengths, interests, and expertise of the successful candidate. Research will involve using *Daphnia* and their microparasites as a model system, and will involve a combination of field work and lab experiments. Experience in disease ecology, community ecology, and/or evolutionary ecology is expected. Experience working with *Daphnia* would be beneficial, but is not required.

More information on the Duffy Lab can be found at: <https://duffylab.wordpress.com/> More information on the Department of Ecology and Evolutionary Biology at the University of Michigan can be found at: <http://www.lsa.umich.edu/eeb/> The start date for this position is flexible, but preference will be given to applicants who can start by mid-summer 2015. Funding is available for at least two years, but is contingent on satisfactory progress in year one. Interested individuals should send a CV, a brief description of research and professional goals, and the names and contact information for 3 references to Meghan Duffy by e-mail (duffymeg@umich.edu).

Review of applications will start on 1 February 2015 and will continue until the position is filled. The University of Michigan is an equal opportunity / affirmative action employer.

Meghan Duffy, Ph.D. Associate Professor Department of Ecology & Evolutionary Biology <http://duffylab.wordpress.com/> Office: 1039 Ruthven Museums Building Phone: 734-763-3658

Meghan Duffy <duffymeg@umich.edu>



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## UMinnesota PlantMicrobeEvolution

We seek two postdoctoral research associates to join us in a project on the evolution of plant and microbial species in Minnesota prairies under climate change. Postdocs will investigate the capacity of plant-microbe associations to adapt or acclimate to rapidly changing environment, and to evaluate the current geographic scale of local adaptation. We anticipate that one postdoc will focus on plant genetic variation and questions of local adaptation and adaptive capacity, while the second will focus on plant-associated microbial communities and the potential for microbes to either constrain or accelerate adaptation of plant hosts to changing environment. Postdocs in these positions will be working with a collaborative group of faculty (PI: Ruth Shaw, co-PIs Georgiana May, Donald Wyse), graduate and undergraduate students as well as volunteers. Training opportunities include teaching in graduate seminars, developing citizen-science programs, conservation planning, or interaction with governmental and non-governmental agencies. To apply, please submit a cover letter of application, CV, and names and contact information for three references.

Applicants primarily interested in plant genetic variation should apply at: [employment.umn.edu/applicants/Central?quickFind6037](http://employment.umn.edu/applicants/Central?quickFind6037) (Ruth Shaw, [shawx016@umn.edu](mailto:shawx016@umn.edu)).

Applicants primarily interested in microbial symbionts of plants should apply at: [employment.umn.edu/applicants/Central?quickFind6041](http://employment.umn.edu/applicants/Central?quickFind6041) (Georgiana May, [gmay@umn.edu](mailto:gmay@umn.edu)).

Georgiana May <[gmay@umn.edu](mailto:gmay@umn.edu)>

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## UNatIAutoMexico PlantEvolution

POSTDOCTORAL POSITION IN PLANT EVOLUTIONARY BIOLOGY Research Group of Dr. Susana Magallón ([https://www.researchgate.net/profile/Susana\\_Magallon](https://www.researchgate.net/profile/Susana_Magallon)) Instituto de Biología, Universidad Nacional Autónoma de México (UNAM) Mexico City, Mexico

RESEARCH TOPICS: - Effect of fossil calibrations in molecular clock analyses of flowering plants. - Stochastic local clocks applied to dating seed plants. DATES: - Application deadline: February 23, 2015. - Start of the postdoctoral position: September, 2015. REQUIRED OF CANDIDATES: PhD degree obtained in the 3 years previous to date of hire; 36 years old or younger at the date of hire; research productivity demonstrated through scientific publication record.

APPLICATION MATERIALS: CV; statement of academic interests and goals (1 page max.); PDFs of publications; one academic reference.

FUNDING: The candidate will enter a competitive selection to obtain one of the Postdoctoral Fellowships granted by the Coordination for Scientific Research, UNAM ([http://www.cic-ctic.unam.mx/cic-consejo.tecnico/download/conv\\_bp/gaceta.4575.pdf](http://www.cic-ctic.unam.mx/cic-consejo.tecnico/download/conv_bp/gaceta.4575.pdf)). The position is available for one year, with the possibility to extend to a second year.

PLEASE SUBMIT REQUESTS OF INFORMATION AND APPLICATIONS TO: [s.magallon@ib.unam.mx](mailto:s.magallon@ib.unam.mx)

\* \* \* \* \*

Susana Magallón PhD

Instituto de Biología Universidad Nacional Autónoma de México 3er Circuito de Ciudad Universitaria Del Coyoacán México D.F. 04510 Mexico

Phone: (52-55) 5622-9087 Fax: (55-52) 5550-1760

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## UNotreDame ConservationBiology

\*POSTDOCTORAL POSITION(S) IN CONSERVATION BIOLOGY\*

\*University of Notre Dame\*

At least one postdoctoral research position is available to pursue collaborative projects in conservation biology that would inform the management and policy of aquatic invasive species. The postdoctoral fellow(s) would join an interdisciplinary team of researchers, contribute to multiple projects, and would lead one or more subprojects involving: characterization of aquatic (freshwater and marine) communities with eDNA; quantitative

analysis to forecast species dispersal and range changes caused by shipping and other vectors, and their interaction with other anthropogenic drivers (e.g., climate change); quantification of the ecological and economic impacts of invasions; and management and policy of invasive species at regional or global scales. Intellectual leadership would be expected, with the choice of topic(s) depending on experience and interests. Opportunities for collaborations exist with computer scientists, economists, and policy experts. The postdoc(s) would also assist with the organization and administration of projects, and contribute to on-going publication preparation. Funding is available for at least two years. Applicant screening is rolling; the desired start date is as soon as possible during spring 2015. Salary and benefits will be competitive. The postdoc would be supervised by David Lodge (<http://www3.nd.edu/~lodgelab/>) and would likely collaborate with other researchers at Notre Dame (including Michael Pfrender, <http://www3.nd.edu/~mpfrende/>) and other universities. More information on the context of these projects can be found on the websites for the ND Environmental Change Initiative (<http://environmentalchange.nd.edu/>) and the ND Genomics and Bioinformatics Core Facility (<http://nd.edu/~genomics/index.html>). Applicants should email (in one pdf document) a letter describing prior research experience and current interests, a curriculum vitae, and the names and contact information of three references to David Lodge (dlodge@nd.edu). In the email subject line, please put "Postdoctoral Application for Spring 2015." The University of Notre Dame is an Equal Opportunity/Affirmative Action Employer. cgantz@nd.edu

## UOttawa SingleCellGenomics

One Postdoctoral Position in Single-Cell Genomics/Transcriptomics - University of Ottawa

The Corradi Lab is currently seeking a postdoctoral fellow to work on a research project involving Single-Cell Genomics and Transcriptomics. The research will be supervised by Dr. Nicolas Corradi and carried out in a CIFAR (Canadian Institute for Advanced Research) - affiliated laboratory located in the Department of Biology of the University of Ottawa, Canada. The position is funded for two years. The candidate will contribute to the funded NSF proposal ZygoLife (<http://zygolife.org/home/>). The Postdoctoral Fellow will be using Single-

Cell Transcriptomics and Genomics tools as a mean to gather first-hand, large-scale sequence data from several poorly studied species of Arbuscular Mycorrhizal Fungi (AMF). The resulting data will be analysed using bioinformatics tools, and compared to similar data obtained from other fungal lineages by collaborators within the ZygoLife project to better understand the biology of these essential plant symbionts. Specific enquiries about the project can be sent to Dr. Nicolas Corradi (ncorradi@uottawa.ca).

Applicants are expected to have some background in Comparative Genomics or Molecular Mycology. Preference will be given to candidate with former experience in one or more of the following areas: AMF cultivation, AMF Taxonomy, Phylogenetics, Population Genetics, Environmental Genomics, Metagenomics.

A complete application package includes a CV, a short description of past research accomplishments and future goals, and the names and e-mail addresses of at least 2 references. Evaluation of applications starts immediately and will continue until a suitable candidate is found.

The University of Ottawa is a large, research-intensive university, hosting over 40,000 students and located in the downtown core area of Canada's capital city (<http://www.science.uottawa.ca/fac/welcome.html>). Ottawa is a vibrant, multicultural city with a very high quality of life (<http://www.ottawatourism.ca/fr/>)

Applications can be sent to Dr. Nicolas Corradi (ncorradi@uottawa.ca).

Representative publications:

- Riley R. et al. 2014. Extreme Diversification of the MATA-HMG Gene Family in the Plant - Associated Arbuscular Mycorrhizal Fungi. *New Phytologist*. 201: 254-268
- James T.Y et al. 2013. Shared signatures of parasitism and phylogenomics unite the Cryptomycota and Microsporidia. *Current Biology*. 23 (16), 1548-1553
- Tisserant E. et al. The arbuscular mycorrhizal Glomus genome provides insights into the evolution of the oldest plant symbiosis. *Proceedings of the National Academy of Sciences - USA*. 110 (50), 20117-20122R576-R577
- Pombert J.F. et al. 2012. Gain and loss of multiple functionally-related horizontally transferred genes in the reduced genomes of two microsporidian parasites. *Proceedings of the National Academy of Sciences - USA* 109(31):12638-43
- Selman M. et al. 2011. Acquisition of an animal gene by two microsporidia. 2011. *Current Biology* 21: R576-R577

Nicolas Corradi Professeur Agrégé / Associate Professor Boursier de l'Institut canadien en recherches avancées / Fellow of the Canadian Institute for Advanced Research Université d'Ottawa / University of Ottawa Département de biologie / Department of Biology Pavillon Gendron / Gendron Hall Bureau 257 / Room 257 30 Marie Curie Priv. Ottawa ON Canada K1N 6N5 Tel. +1 (613) 5625800 # 6563 Website:<http://mysite.science.uottawa.ca/ncorradi/index.html> Nicolas Corradi <[ncorradi@uottawa.ca](mailto:ncorradi@uottawa.ca)>

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## UPittsburgh PlantEvolGenomicsEcophysiology

Postdoc in Plant Evolutionary Genomics & Ecophysiology at the University of Pittsburgh

Postdoctoral fellow to join a collaborative project examining functional, population genetic and ecophysiological mechanisms underlying success of polyploid plants.

The work aims to predict the effect of whole genome duplication on ecological and evolutionary responses to environmental change. The postdoc will identify the ecological, population genetic and genomic factors that underlie functional trait (e.g., associated with drought and freeze tolerance) variation, ecological amplitude and gene expression diversity using the wild strawberry (*Fragaria*) as a model system (see Liston et al 2014. *AJB*101:1686-1699; Johnson et al 2014 *Bot J Linn Soc* 176:99-114). The specific goals are to 1) analyze gene expression (transcriptomes) and physiological traits of natural and synthetic polyploids and their diploid progenitors in the greenhouse and common gardens at climatically diverse sites, 2) use NGS of target-captured sequence from natural populations of plants to identify patterns of genetic diversity and signatures of selection, reconstruct phylogenetic relationships and generate high density linkage maps (Tenneson et al 2014 *GBE* 6:3295-331 3).

Responsibilities include the establishment and monitoring of experiments in the field and under controlled conditions in the lab, collection and analysis of population genetic/genomic, phenotypic and physiological data, and the preparation of manuscripts for publication. The project affords opportunities for international travel and training as part of an US-China international research collaboration. There is also the opportunity to design and implement additional allied projects tailored to the skills and interests of the postdoc.

We are looking for an evolutionary-minded candidate with a genomics, ecophysiological and/or population ecology background interested in a combination of field work and genomic work. Candidates that have demonstrated experience in transcriptome analysis, genetic linkage mapping, and/or population and comparative genomics are preferred. Ability to travel between field sites in Oregon and laboratory in Pennsylvania is required.

The postdoc position is for two years, renewable up to two additional years. Start date is negotiable, but June 2015 is preferred.

The project is collaboration among the labs of Dr. Tia-Lynn Ashman, Department of Biological Sciences at the University of Pittsburgh and Dr. Aaron Liston, Department of Botany and Plant Pathology, and Dr. Richard Cronn US Forest Service at Oregon State University.

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 (e.g., plant ecophysiology, transcriptome analysis, NGS library prep, statistics, bioinformatics).

Deadline for application materials is February 28, 2015.

For informal enquiries, please contact Tia-Lynn Ashman [tia1@pitt.edu](mailto:tia1@pitt.edu)

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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## UppsalaU EvolPlantGeneticsGenomics

Apologies for double-posting, but the link in the original ad sent a week ago appears broken. Please use this link <http://www.uu.se/en/about-uu/join-us/details/?positionId=49550> to find the ad and the link for application.

Best wishes,

Jon

Position for one Postdoc in Evolutionary Plant Genetics/Genomics at Uppsala University, Sweden

We seek a Postdoc to join a project examining the ge-

netic and ecological mechanisms underlying adaptive differentiation among natural populations of the plant model organism *Arabidopsis thaliana*. The research will be conducted within the framework of an international research collaboration. The goals are to identify QTL (quantitative trait loci) contributing to local adaptation and to key traits involved in adaptation, to characterize the effects of individual QTL, to examine whether adaptive evolution is constrained by trade-offs and pleiotropy, and to explore the molecular basis of the detected QTL, and their geographic distribution. Focus will be on the genetic basis and adaptive significance of variation in flowering time. Duties include the establishment and monitoring of experiments in the field and under controlled conditions in the lab, QTL-mapping, data analysis, and the preparation of manuscripts for publication. Specific subprojects can be tailored to the skills and interests of the successful candidate.

The project is a collaboration between the labs of prof Jon Agren at the Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, and prof Doug Schemske at the Department of Plant Biology, Michigan State University.

We are looking for a candidate with a keen interest in population genetics, genomics, QTL-mapping, evolutionary ecology and/or ecophysiology. Proficiency in English is a requirement.

The successful postdoc candidate should have a PhD completed within 3 years of the application deadline (reasons such as prolonged periods of illness and parental leave can motivate a longer period). The postdoc position lasts for two years, and can be extended for up to two more years

Deadline for application is 26 January 2015

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

<http://www.uu.se/en/about-uu/join-us/details/?positionId=3D49550> For informal enquiries, please contact prof Jon Agren, jon.agren@ebc.uu.se, +46-18-471 2860.

Jon Agren Plant Ecology and Evolution Department of Ecology and Genetics, EBC Uppsala University Norbyvägen 18 D SE-752 36 Uppsala Sweden

jon.agren@ebc.uu.se

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## UppsalaU EvolutionaryPlantGenomics

Position for one Postdoc in Evolutionary Plant Genetics/Genomics at Uppsala University, Sweden

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<http://www.uu.se/en/about-uu/join-us/details/?positionId=49550> For informal enquiries, please contact prof Jon Agren, jon.agren@ebc.uu.se, +46-18-

471 2860.

Jon Agren Plant Ecology and Evolution Department of Ecology and Genetics, EBC Uppsala University Norbyvagen 18 D SE-752 36 Uppsala Sweden

jon.agren@ebc.uu.se

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## UToledo FishGenomicsGenetics

Postdoctoral Researcher in Fish Genomics and Genetics Great Lakes Genetics/Genomics Laboratory, University of Toledo Lake Erie Center, Toledo, OH Closing Date: February 28, 2015 Web Address: <http://www.utoledo.edu/nsm/lec/research/ggl/index.html>  
Description The research project is to help 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 postdoctoral research associate will organize large DNA sequence databases, train and co-supervise students and technicians, and be thoroughly competent and experienced in bioinformatics, DNA extraction, PCR, DNA sequencing, and population genetic and systematic evolutionary data analyses.

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. Grant funding record preferred. Data management experience, bioinformatics, and data analysis experience in molecular phylogenetics and population genetics required. DNA extraction, PCR, DNA Sequencing (both Sanger and Illumina MiSeq), sequence alignment and GenBank experience required. Familiarity with QIIME, Unix/Linux operating systems and writing script in Perl is a plus. Strong communication (written, oral) skills required. Experience in working with fishes strongly preferred. Strong personnel interaction skills and experience in training others required. Oral research presentation experience at national or international scientific conferences required. Fish specimen collection experience Vstrongly preferred.

How to Apply Send (1) cover letter, (2) CV, (3) 2 letters of reference, (4) copies of graduate and undergraduate transcripts via .pdf to Dr. Stepien at carol.stepien@utoledo.edu. Competitive salary, full benefits. Beautiful well-funded lab (by NSF, USEPA, ARS, Sea Grant) on Lake Erie (with view) at Lake Erie Cen-

ter field station 20-25 minutes from main University of Toledo campus. The Great Lakes Genetics Laboratory currently has another post-doc, 3 Ph.D. students, a full-time technician, and 2 undergraduate researchers. 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.

Contact Carol Stepien Distinguished University Professor and Director Lake Erie Center and Dept. Environmental Sciences 6200 Bayshore Rd. Toledo, OH 43615 Phone: 4195308362 Fax: 4195308399 carol.stepien@utoledo.edu

“Klymus, Katy Elizabeth”  
<Katy.Klymus@UToledo.Edu>

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## UUtah HerbivoreMicrobiomeBiodiversity

\*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 through January 30, 2015\*. The preferred start date is March 15, 2015. Please send a 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, care of Dr. Jael Malenke <jaelmalenke@gmail.com>; please put 'Microbiome Postdoctoral Applicant' in the Subject Line.

jaelmalenke@gmail.com

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## UZurich GeneticsMaternalEffects

Postdoc position in Evolutionary Genetics of Maternal Effects University of Zurich, Switzerland

My group combines complementary approaches from evolutionary ecology, ecophysiology and genetics/genomics to understand the evolution and evolutionary consequences of prenatal maternal effects in different bird systems. Within this project, I have a postdoc position available to investigate the genetic basis of prenatal maternal investment using established, replicated Japanese quail selection lines for high and low maternal egg investment.

Goal of the project is to identify genomic regions associated with differential maternal investment, and to link DNA sequence variation with the physiological and ecological phenotype of mothers from high and low investment lines. Thereby this project can provide an integrative understanding of the molecular and physiological architecture underlying variation in maternal reproductive strategies.

The ideal candidate for this position has a strong interest in evolutionary biology, a can-do attitude and good writing and organisational skills. Given the large amount of data and the nature of the analyses involved (e.g. handling of SNP data, QTL mapping), expertise in evolutionary genetics, quantitative genetics, and/or bioinformatics is essential.

The postdoc will be based at the Institute of Evolutionary Biology and Environmental Studies of the University of Zurich, providing ample opportunities for collaborations and interactions with researchers working in related and complementary fields (<http://www.ieu.uzh.ch>).

[/www.ieu.uzh.ch](http://www.ieu.uzh.ch)). The institute is very international and the working language is English.

The position is funded by the Swiss National Science Foundation for the duration of 18 months (gross salary CHF / Euro 94'000 per annum). The ideal starting date is May 1st 2015, or as soon as possible afterwards.

Applications should include 1) a cover letter outlining your motivation to work on this project, as well as relevant experience, 2) a detailed curriculum vitae, and 3) the contact details of three academic referees. Send the above as a single .pdf file to [barbara.tschirren@ieu.uzh.ch](mailto:barbara.tschirren@ieu.uzh.ch)

Review of applications will start on February 26th 2015. For more information, feel free to contact me!

Prof. Dr. Barbara Tschirren Institute of Evolutionary Biology and Environmental Studies University of Zurich Winterthurerstrasse 190 8057 Zurich - Switzerland

Email: [barbara.tschirren@ieu.uzh.ch](mailto:barbara.tschirren@ieu.uzh.ch) <http://www.ieu.uzh.ch/staff/professors/tschirren.html>  
[barbara.tschirren@ieu.uzh.ch](mailto:barbara.tschirren@ieu.uzh.ch)

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## Vienna DrosophilaThermalAdaptation

Postdoctoral position: functional genetics of thermal adaptation in *Drosophila*

A postdoctoral position is available at the Institute of Population Genetics, Vetmeduni Vienna (Austria). The research focus of the Institute of Population Genetics is on understanding the genetics of adaptation. In the framework of an ERC funded project we are using experimental evolution and whole genome re-sequencing of pooled individuals to identify genes involved in the adaptation to new thermal environments. We are searching for a talented postdoc to experimentally validate the identified candidates using state of the art genome editing in *Drosophila simulans*.

The successful candidate will have experience with genome editing in *Drosophila* as well as *Drosophila* genetics. A background in evolutionary biology or population genetics is not needed, but it is expected that the future post holder will be interested to expand her/his research interest to this major research focus of the institute.

Vienna is home to the VDRC Stock Center, and a high-profile *Drosophila* research community, most notably

at the IMP (<http://www.imp.ac.at/>) and the IMBA (<http://www.imba.oeaw.ac.at/>). In addition to a stimulating scientific environment, Vienna also offers an extraordinarily high quality of life. Affordable housing, excellent public transport, great restaurants, a range of international schools, two operas, two music centers, many theaters and museums in combination with a pleasant climate make Vienna one of the most attractive cities in Europe.

The position is available from March 2015 for up to three years. The application should be emailed to christian.schloetterer@vetmeduni.ac.at as a single pdf containing CV, list of publications, a statement of research interests, and the names of three references with contact details. While the search will continue until the position is filled, applications should be received by February 15, 2015 to ensure full consideration.

julia.hosp@gmail.com

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## VirginiaTech ComparativeGenomics

**\*Postdoc\*\*toral Associate\*\*** Position in Computational Biology at Virginia Tech\*

\*Description: \*

The laboratory of Dr. Song Li invites applications for a post-doc position in the College of Agriculture and Life Sciences at Virginia Tech. Li lab focuses on developing computational algorithms that integrate large-scale data to address key questions in comparative genomics. The lab has the following ongoing projects: 1) Understanding the evolution of alternative splicing and antisense transcripts using RNA-seq data in diverse species. 2) Identifying active regulatory networks controlling cell type- or condition-specific gene expression. Understanding the evolutionary dynamics of gene regulatory networks. 3) Developing Hidden Markov Model (HMM) based gene prediction method that incorporates diverse genomic data and evolutionary conservation to improve gene and splicing variant discovery and annotation.

\*Qualifications\*\*:

Ph.D in Bioinformatics, Computational Biology, Computer Science, Applied Mathematics or other related field.

Track record of publications in bioinformatics, computational biology or comparative genomics.

Strong programming skills in Python, Perl, Java, C++,

R or other language.

Experience with Linux and high performance computing environment.

Demonstrated ability in developing novel statistical or machine learning methods in computational biology.

Experience in genome scale data analysis such as analysis of microarray, ChIP-Seq and RNA-Seq data, network analysis, biological sequence analysis or other relevant computational genomics experience.

Highly motivated for interdisciplinary research, excellent communication skills, and the ability to work independently as well as within a research group

Initial appointment is one year, with possible extension depending on performance. The interested applicants should send their C.V., available date, and names of three references to [songli\(at\)vt.edu](mailto:songli(at)vt.edu). Review of applications will begin January 31th 2015.

\*Faculty Profile\*: <http://www.cses.vt.edu/people/-tenure/songli.html> \*Lab Website\*: <http://tinyurl.com/-LiLabAtVT> Song Li <[songli@vt.edu](mailto:songli@vt.edu)>

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## YaleU 2 EvolutionaryBiol

Two Postdoctoral Positions Available at the Caccone Lab at Yale University

The Caccone laboratory associated with the Yale Institute for Biospheric Studies (YIBS), the department of Ecology and Evolutionary Biology (EEB) and the School of Public Health (EPH) invites applications for two post-doctoral positions.

The first position involves supporting the Center for Systematics and Conservation Genetics within the YIBS Institute. This center mission is to support research and education in evolutionary and ecological genetics at Yale University. Thus, the optimal candidate should have a strong collaborative personality and like to train undergraduate and graduate students in a variety of DNA based techniques. The postdoc will be involved in several research projects carried out within this YIBS center. One long-running project is on Giant Galapagos tortoises evolutionary, ecological, and conservation genetics. One project key to this position is using genomic tools to identify hybrid tortoises with ancestry in extinct species using hybrid capture approaches and high-throughput sequencing. There are several other large genomic datasets available and extensive samples

from across the Galapagos tortoise radiation providing scope for the postdoc to develop evolutionary and population genomic projects with these and additional data in line with their independent interests. Interest in applying genomic tools to conservation questions is essential, as is experience with both the lab work and bioinformatic analysis of large genomic-scale datasets for population genetic/genomic questions. Field work experience is also preferred, but not required. The preferred start date for this position is 1st April 2015.

The second position is funded by an NIH based program project with the overall goal of understanding the transmission epidemiology of tsetse transmitted diseases in East Africa. This particular position involves studying the population genetics and genomics of tsetse flies in East Africa (*Glossina fuscipes* and *Glossina pallidipes*) to assess their population structure to aid in their monitoring and control. The project involves collecting and analyzing microsatellite and SNP markers to understand patterns and levels of genetic diversity, as well as understand the possible drivers that are shaping the observed patterns. This will also include analysis of environmental and microbial (*Wolbachia* and others components of the microbial community) data. The optimal candidate should have previous experience in analyzing population genetic data (DNA sequence and microsatellites), preferably have worked with environmental data, be familiar with population genomic analyses, and in general have some bioinformatics expertise to be able to analyze large datasets. This project is part of a long-term collaboration with Dr Aksoy (Yale School of Public Health) and several scientists and Institutions in East Africa. As this project has a strong field component, the postdoc will be expected to participate in the field-based activities and be involved in its coordination and progress. We study the tsetse fly (*Glossina* sp.) to investigate the physiological, molecular and genetic mechanisms that underlie 1) vector population structures in east-Africa (Uganda and Kenya), 2) tsetse host-African trypanosome interactions, 3) tsetse host-endosymbiotic bacteria interactions, and 4) tsetse unique viviparous reproductive biology. The genome sequence of tsetse and all of its associated microbial partners are now available, making the system highly tractable. The position is available immediately.

Yale University offers exciting opportunities for academic achievement and professional growth. New Haven, which is conveniently located between Boston and New York City, is a dynamic city with cultural resources that include world-renowned museums, theatres, concert halls and fine dining establishments.

Salary and benefits are according to Yale and NIH guidelines. Candidates should provide their CV and a short research interest statement to Adalgisa Caccone (Adal-

gisa.Caccone@yale.edu).

Adalgisa Caccone Senior Research Scientist ESC 140 Ecology and Evolutionary Biology Yale University 21 Sachem St. New Haven, CT 06520 Tel 203-432-5259 fax 203-432-7394

“Caccone, Gisella” <adalgisa.caccone@yale.edu>

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## YaleU PrimateGenetics

\*Post-Doctoral Associate to research primate socio-endocrinology and genetics at Yale Anthropology \*

The Department of Anthropology and the School of Forestry & Environmental Studies at Yale University invite applications for a full-time, two-year Postdoctoral Associate position in biological anthropology and/or primatology during academic years 2015-17. The post-doctoral position is offered within the Owl Monkey Project directed by Dr. Eduardo Fernandez-Duque ([owlmonkeyproject.wordpress.com](http://owlmonkeyproject.wordpress.com)).

The successful applicant will collaborate on research projects related to the socio-endocrinology and genetics of captive and wild owl monkey populations. The applicant will participate in the analyses of hormonal samples collected as part of an ongoing NSF project on the energetics of biparental care in owl monkeys. The applicant will also be responsible for data analysis and manuscript preparation using data from multi-year behavioral and demographic datasets. The position will include some field work in Argentina and/or in one of two captive colonies of owl monkeys where research is conducted.

A Ph.D. degree in animal behavior, biological/evolutionary anthropology, ecology, conservation, or related field is required. The position will remain open until filled, but applicants are advised to submit their applications by February 15, 2015 for primary consideration since some interviews will take place at the AAPA Meetings (St. Louis, Missouri, March 25-29). Applicants must have a demonstrated record of publication in peer-reviewed journals and/or successful grant writing.

Please email the following documents to both of these email addresses:

[owlmonkeyproject@gmail.com](mailto:owlmonkeyproject@gmail.com) and [eduardo.fernandez-duque@yale.edu](mailto:eduardo.fernandez-duque@yale.edu):

1. A cover letter indicating your interest in the position.



2. A CV with names and email addresses of three referees.
3. A 1-2 page research experience and future goals statement.
4. pdf samples of publications (submitted, in press, or

published).

Yale University is an Equal Opportunity/Affirmative Action Employer.

Ben Finkel <benjfinkel@gmail.com>

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## Workshops Courses

<p>Barcelona Cladistics Jun29-Jul3 ..... 145</p> <p>Barcelona PhylogeneticAnalysisUsingR May4-8 ... 146</p> <p>BodegaBay AppliedPhylogenetics Mar7-14 ..... 147</p> <p>Erasmus MasterProgram EvolutionaryBiology .... 147</p> <p>Glasgow StableIsotopeMixingModels Jul27-30 .... 148</p> <p>Guarda Switzerland EvolutionaryBiol Jun13-20 .. 149</p> <p>HarvardU PhenotypicPlasticity May1-5 ..... 149</p> <p>Munich InvertGenomics Mar22-24 Registration ... 150</p> <p>Panama Workshops Jan15 DeadlineReminder .... 151</p> <p>Portal Arizona AntEvolution Aug6-16 ..... 151</p> <p>Portugal IntraSppDiversityNGS Jul27-31 ..... 152</p>	<p>SCENE Glasgow AdvancingInR 2 Nov30-Dec4 ... 152</p> <p>SCENE Glasgow GISforEvolBiol Aug11-13 ..... 153</p> <p>SCENE Glasgow RGeneticDataAnalysis Aug3-7 .. 154</p> <p>SCENE Glasgow SpatialEcolR Nov16-20 ..... 155</p> <p>Swiss Alps EvolutionaryBiology June19-25 ..... 156</p> <p>Tubingen OriginsHumanCooperation Jun22-26 ... 156</p> <p>UCalifornia LosAngeles ConsGenomics Mar22-27 .. 157</p> <p>ULeipzig ProgrammingForEvolutionaryBiology Mar17-Apr2 ..... 158</p>
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### Barcelona Cladistics Jun29-Jul3

Dear colleague,

there are some places available for the workshop “QUANTITATIVE CLADISTICS AND USE OF TNT - 2nd Edition”, June 29 - July 3, 2015.

Instructors: Dr. Goloboff and Dr. Szumik (Conicet, Argentina).

PLACE: Facilities of the Centre de Restauraci i Interpretaci Paleontologica, Els Hostalets de Pierola, Barcelona (Spain).

WEBPAGE: <http://www.transmittingscience.org/>-

[courses/phylo/cladistics/](#) PROGRAM:

- Intro and Basics. Parsimony and phylogenetic systematics. Character optimisation and mapping. Most parsimonious reconstructions and specific changes. Input/output in TNT. Dataset formats. Using GB->TNT to create matrices. Instruction files. Options for graphic output (SVG, metafiles). Creation of batch± files. Editing trees. Handling tree files. Groups of trees, characters and taxa.
- Tree calculation. Tree searches. Exact solutions, Wagner trees, branch-swapping. Local and global optima. Use of multiple addition sequences. Improving search strategies. Factors which affect the efficiency of tree searches. Constraints and timeouts±.
- Ambiguity and consensus; summarizing results. Zero-length branches and collapsing rules. Types of consen-

sus and their use; improving consensus trees; supertrees. Pruned consensus. Comparison of tree-topologies; SPR distances.

- Character weighting. Successive and implied weighting. Auto-weighted optimization. Refining character weighting with blocks; taking into account missing entries. User-defined weighting functions.

- Group supports. Concept of group support. Bremer supports; how to calculate them; search of suboptimal trees. Problems with Bremer supports; absolute and relative Bremer support. Partitioned Bremer support and individual Bremer supports. Measures based on resampling; effect of search strategies and collapsing rules. Problems with resampling methods.

- Tree search in large and difficult data sets. Special search algorithms. Sectorial searches. Ratchet and drifting. Tree fusing. Combining different algorithms. Driven searches and stabilization of consensus.

- Scripting. Automation of decisions to go beyond simple commands. Flow control. Decisions. Expressions, user variables, and internal variables. Design of simple scripts.

This course is co-organized by Transmitting Science, the Institut Catal de Paleontologia M. Crusafont and the Centre de Restauraci i Interpretaci Paleontologica. Places are limited and will be covered by strict registration order.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Soledad De Esteban-Trivigno, Ph.D.

Soledad De Esteban Trivigno  
<soledad.esteban@transmittingscience.org>

Klaus Schliep (Universidad de Vigo, Spain).

DATES: May 4-8, 2015

More information: <http://www.transmittingscience.org/courses/phylo/phylogeny-with-r/> or wrting to courses@transmittingscience.org.

This course is for biologists dealing with the analysis of multiple molecular sequences at several levels: Populations, species, clades, communities. These biologists address questions relative to the evolutionary relationships among these sequences, as well as the evolutionary forces structuring biodiversity at different scales. The objectives are: (i) to learn the theoretical bases phylogenetic analysis, (ii) to know how to choose a strategy of molecular data analysis at the interâ or intraspecific levels, (iii) to be able to initiate a phylogenetic analysis starting from the files of molecular sequences until the interpretation of the results and the graphics. The software used for this course will be centered on the R language for statistics. This will include the use of specialized packages particularly ape, phangorn, and adegenet.

PLACE: Facilities of the Centre of Restauraci i Interpretaci Paleontologica, Els Hostalets de Pierola, Barcelona (Spain).

Organized by: Transmitting Science, the Institut Catal de Paleontologia M. Crusafont and the Centre de Restauraci i Interpretaci Paleontologica de Els Hostalets de Pierola.

Places are limited and will be covered by strict registration order.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Dr. Soledad De Esteban-Trivigno

soledad.esteban@transmittingscience.org

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## Barcelona Phylogenetic Analysis Using R May 4-8

Dear Colleagues,

There are some places left for this course that can be of interest for people in this list: "AN INTRODUCTION TO PHYLOGENETIC ANALYSIS USING R - Second Edition".

INSTRUCTORS: Dr. Emmanuel Paradis (Institut de Recherche pour le Développement, France) and Dr.

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## BodegaBay AppliedPhylogenetics Mar7-14

[FINAL NOTICE]

UC Davis

### WORKSHOP IN APPLIED PHYLOGENETICS

at Bodega Marine Laboratory, Bodega Bay, California

March 7V14, 2015

Sponsored by the

University of California, Davis and Bodega Marine Laboratory

<http://treethinkers.org> Introduction Phylogenetic methods have revolutionized modern systematics and become indispensable tools in evolution, ecology and comparative biology, playing an increasingly important role in analyses of biological data at levels of organization ranging from molecules to ecological communities. The estimation of phylogenetic trees is now a formalized statistical problem with general agreement on the central issues and questions. A nearly standard set of topics is now taught as part of the curriculum at many colleges and universities. On the other hand, application of phylogenetic methods to novel problems outside systematics is an area of special excitement, innovation, and controversy, and perspectives vary widely.

This Spring, for the sixteenth consecutive year, we will teach a workshop for graduate students interested in applying phylogenetic methods to diverse topics in biology. The one-week course is an intensive exploration of problems to which modern phylogenetic approaches are being applied and the most current statistical tools and approaches that are used to solve those problems. We cover a wide range of topics in comparative phylogenetics. The course starts with recent advances in phylogenetic inference, and then focuses on methods for making inferences from phylogenies.

The course will be held at the Bodega Marine Laboratory on the Northern California coast, which has on-site housing. The course format will involve equal parts of lecture, discussion, and hands-on software training. One afternoon during the week will be left free for field trips to local natural areas.

Topics Covered \* Estimating, evaluating and interpreting phylogenetic trees \* Recent advances in Bayesian

inference of phylogeny \* Model specification issues: model selection, adequacy and uncertainty \* Diagnosing MCMC performance \* Divergence-time estimation: relaxed clocks, fossil calibration \* Species-tree estimation \* Character evolution: ancestral-state estimation, rates of trait evolution \* Lineage diversification: detecting rate shifts, testing key innovation hypotheses

Instructors for the 2015 workshop \* Jonathan Eisen \* Rich Glor \* Tracy Heath \* Sebastian Hohna \* John Huelsenbeck \* Michael Landis \* Sarah Longo \* Mike May \* Brian Moore \* Samantha Price \* Bruce Rannala \* Bob Thomson \* Peter Wainwright

Prerequisites Available housing limits course enrollment to ~30 students. Preference is given to doctoral candidates who are in the early to middle stages of their thesis research, and who have completed sufficient prerequisites (through previous coursework or research experience) to provide some familiarity with phylogenetic methods. Unfortunately, because of limits on class size, postdocs and faculty are discouraged from applying.

Admission and Fees Students will be admitted based on academic qualifications and appropriateness of research interests. The course fee is \$750. This includes room and board at BML for duration of the course (arriving March 7, leaving March 14) and return transportation from Davis to the Bodega Marine Labs.

Application Deadline Applications are due by January 10, 2015. Please send a completed application form and one letter of recommendation from your major advisor. Applications should be sent via email as PDFs to [mikeryanmay@gmail.com](mailto:mikeryanmay@gmail.com). Students will be notified via e-mail by January 13, 2015 of acceptance.

Application Forms and Information Visit the Bodega website for additional information and to download an application form.

Send all application materials to:

Mike May Department of Evolution and Ecology 5343 Storer Hall University of California Davis Davis, CA 95616 email: [mikeryanmay@gmail.com](mailto:mikeryanmay@gmail.com)

“Brian R. Moore” <[brianmoore@ucdavis.edu](mailto:brianmoore@ucdavis.edu)>

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## Erasmus MasterProgram EvolutionaryBiology

Erasmus+ Master Program in Evolutionary Biology (MEME)

MEME is a two-year research oriented master program for talented and motivated students who are interested in understanding evolution in all its facets. It intends to provide an optimal preparation for subsequent doctoral studies and eventually a career in academic research.

The MEME program addresses the driving forces of evolution at all levels of organismal organization (from cells and individuals to populations and ecosystems), and allows students to study all kinds of organisms (microorganisms, plants, animals) in all kinds of habitats (marine as well as terrestrial) with a diversity of approaches (field, lab, theory). The focus of the program is not only on how evolution shaped life on our planet in the past, but also on how understanding the principles underlying evolution can provide new insights and help to cope with present-day challenges in a variety of fields, including ecology, epidemiology, physiology, immunology, genetics/genomics, bioinformatics, economics and the social sciences.

To offer a program of such broad scope, four European universities (University of Groningen, Netherlands; University of Montpellier II, France; Ludwig Maximilians University of Munich, Germany; Uppsala University, Sweden), have joined forces with Harvard University (USA). Together, this consortium has put together an attractive multidisciplinary program that meets highest standards. All students have to study at (at least) two partner universities, and they will receive a double degree from two partner universities they have attended.

Being financed by the European Community, MEME has to satisfy the high quality standards imposed by the prestigious Erasmus+ Program. A limited number of full scholarships is available for European and non-European students and these will be awarded in a selective procedure. Details on the program and the selection procedure can be found on [www.evobio.eu](http://www.evobio.eu). Starting date: 15 August 2015 Application deadline: 1 February 2015

Please alert your students to this great opportunity!

More information and how to apply - please see [www.evobio.eu](http://www.evobio.eu) Questions about the contents of the program: Franjo Weissing ([f.j.weissing@rug.nl](mailto:f.j.weissing@rug.nl))

Questions about the requirements and the application procedure: Irma Knevel ([i.c.knevel@rug.nl](mailto:i.c.knevel@rug.nl))

[maartje.giesbers@gmail.com](mailto:maartje.giesbers@gmail.com)

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**Glasgow**  
**StableIsotopeMixingModels**  
**Jul27-30**

Statistics course: Stable Isotope Mixing Models (SIMMs) using SIAR, SIBER and MixSIAR (July 27th - 30th 2015)

Recently SIMMs have become a very popular tool for quantifying the foraging ecology of organisms within an ecosystem. This analysis can be particularly useful to evolutionary biologists that study environmental and ecologically driven evolution and speciation for example resource polymorphisms, sympatric speciation, adaptive radiation, etc. This course will cover the concepts, technical background and use of stable isotope mixing models (SIMMs) with a particular focus on running them in R.

Course content is as follows;

Day 1: Basic concepts Module 1: Introduction; why use a SIMM? Module 2: An introduction to Bayesian Statistics. Module 3: Differences between regression models and SIMMs. Practical: Revision on using R to load data, create plots and fit statistical models. Round table discussion: understanding the output from a Bayesian model

Day 2: Understanding and using SIAR Module 4: Do's and Don'ts of using SIAR Module 5: The statistical model behind SIAR Practical: Using SIAR for real-world data sets; reporting output; creating richer summaries and plots of the results Round table discussion: Issues when using simple SIMMs

Day 3: SIBER and MixSIAR Module 6: Creating and understanding Stable Isotope Bayesian Ellipses (SIBER) Module 7: What are the differences between SIAR and MixSIAR? Practical: Using MixSIAR on real world data sets; benefits over SIAR Round table discussion: When to use which type of SIMM

Day 4: Advanced SIMMs Module 8: Using MixSIAR for complex data sets: time series and mixed effects models Module 9: Source grouping: when and how? Module 10: Building your own SIMM with JAGS Practical: Running advanced SIMMs with JAGS Round table discussion: Bring your own data set

Cost is £450 for the 4 days including lunches and refreshments or £625 for an all-inclusive option which in-

cludes the addition of accommodation, breakfast, lunch, dinner and refreshments. This course will be held at SCENE (Scottish Centre for Ecology and the Natural Environment), Glasgow, United Kingdom from July 27th - 30th 2015. There is also the possibility to have discussions regarding your own research so you are encouraged to bring your own data with you.

For further details or questions or to register please email [oliverhooker@prstatistics.co.uk](mailto:oliverhooker@prstatistics.co.uk) or visit [www.prstatistics.co.uk](http://www.prstatistics.co.uk) Please feel free to distribute this among colleagues if you think it is suitable

Additional upcoming courses; AN INTRODUCTION TO USING GIS IN ECOLOGICAL FIELD STUDIES; APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS; SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R; ADVANCING IN R;

Oliver Hooker PhD research student University of Glasgow

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Oliver Hooker <o.hooker.1@research.gla.ac.uk>

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### Guarda Switzerland EvolutionaryBiol Jun13-20

RE: PhD and master students workshop: Guarda summer school in evolutionary biology 2015, Switzerland

It my pleasure to announce this year's Guarda summer school in Evolutionary Biology for master and PhD students. The main aim of the course is to develop the skills to produce an independent research project in evolutionary biology.

The summer school takes place 13. - 20. June 2015 in the Swiss mountain village Guarda. Faculty includes Rosemary and Peter Grant (Princeton University, USA), Richard Lenski (Michigan State University, USA), Sebastian Bonhoeffer (ETH-Zurich, Switzerland) and Dieter Ebert (Basel University, Switzerland)(organizer).

The course is intended for master students and early PhD students with a keen interest in evolutionary biology.

The web page with all details can be found under: <http://www.evolution.unibas.ch/teaching/guarda/index.htm> Application is open now. Deadline is 12. February 2014.

Please communicate this information to interested students.

With best wishes,  
dieter ebert

Dieter Ebert University of Basel, Zoological Institute, Vesalgasse 1, 4051 Basel, Switzerland Tel. +41 (0)61 267 03 60 Email: [dieter.ebert@unibas.ch](mailto:dieter.ebert@unibas.ch)

[dieter.ebert@unibas.ch](mailto:dieter.ebert@unibas.ch)

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### HarvardU PhenotypicPlasticity May1-5

Dear Colleagues,

microMORPH is pleased to announce our third interdisciplinary workshop, Phenotypic Plasticity: Evolution at the Intersection of Ecology, Genetics, and Development, to be held at the Arnold Arboretum of Harvard University in Boston, MA on May 1st - 3rd, 2015.

We are inviting graduate students and postdoctorals interested in exploring phenotypic plasticity from the perspective of development and microevolution to participate in this workshop (details below, or see attached flyer).

microMOPRH is an NSF funded Research Coordination Network (RCN). The goal of this RCN is to promote interdisciplinary interactions in evolutionary developmental biology at the emerging interface between developmental biology and the study of intraspecific and interspecific variation.

microMORPH INTERDISCIPLINARY WORKSHOPS bring together small groups of graduate students, postdoctorals, and faculty with diverse interests and expertise to interact and discuss critical concepts, intellectual objectives, emerging technologies, and analytical approaches that have the potential to advance our understanding of the evolution of plant form. All participants give presentations on their research and there is extensive discussion following each presentation. These workshops provide students, postdoctorals, and faculty with unique opportunities to explore new and challenging frontiers of knowledge.

FACULTY PARTICIPANTS INCLUDE: Sally Assmann (Pennsylvania State University), Ben Blackman (University of Virginia), David Des Marais (Harvard University), Michael Donoghue (Yale University), Lisa Donovan (Uni-

versity of Georgia), Andrew Doust (Oklahoma State University), Cynthia Jones (University of Connecticut), Neelima Sinha (University of California, Davis), Mark van Kleunen (Universitat Konstanz), John Stinchcombe (University of Toronto), Sonia Sultan (Wesleyan University), William (Ned) Friedman (Harvard University), and Pamela Diggle (University of Connecticut).

**APPLICANT INFORMATION:** We encourage applications from graduate students (at all stages of their dissertation research) and postdoctoral researchers now through February 28th, 2015. Eight student/postdoctoral participants will be chosen to attend, give presentations on their research and engage in the discussions. microMORPH will fund travel, accommodations, and meals for selected participants who are U.S.-citizens or currently based at a U.S. institution. Non-U.S. citizens not currently associated with a U.S. institution are encouraged to apply, but funding cannot be awarded from this NSF grant.

**HOW TO APPLY:** Please visit the microMORPH website (<http://projects.iq.harvard.edu/micromorph>) for full instructions on how to submit applications. Applicants are asked to submit a CV, research statement that includes a description of the proposed talk, and letter of endorsement from their major advisor or supervising principle investigator.

For additional information, contact Becky Povilus at (RCNmicromorph@gmail.com)

Sincerely,

Pamela Diggle (University of Connecticut) - microMORPH CO-PI

William (Ned) Friedman (Harvard University) - microMORPH CO-PI

Becky Povilus (Ph.D. Candidate, Harvard University) - microMORPH RA

microMORPH Contact information: email: RCNmicromorph@gmail.com website: <http://projects.iq.harvard.edu/micromorph> "Diggle, Pamela" <pamela.diggle@uconn.edu>

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## Munich InvertGenomics Mar22-24 Registration

Dear colleagues,

the Global Invertebrate Genome Alliance (GIGA) (<http://giga-cos.org>) consists of over 150 researchers from multiple countries who are committed to building an integrated, international, multidisciplinary community for invertebrate genomic studies. We have proposed a concentrated effort to sequence non-insect/non-nematode invertebrate genomes and transcriptomes for thousands of species, develop new informatics tools and provide substantial genomics and bioinformatics resources to the invertebrate research community.

Invertebrates comprise over 95% of all animal species and are grouped into ~35 distinct phyla, yet only very limited genomic and transcriptomic data are currently available and primarily focus on a few model species. GIGA will target 7,000 non-insect/non-nematode species, with an emphasis on marine taxa because of the unrivaled phyletic diversity in the oceans. Target species will be selected based on their phylogenetic placement, relevance to organismal, ecological, and conservation research and their importance to fisheries and human health.

The GIGA initiative has gained momentum after an inaugural workshop at Nova Southeastern University in March 2013, resulting in the joint publication of a white paper (< <http://m.jhered.oxfordjournals.org/content/105/1/1.full> >). Recently GIGA held a symposium with a broad audience at the 2014 Annual meeting of the Society of Molecular Biology and Evolution in San Juan, Puerto Rico.

The \*2<sup>nd</sup> \*Global Invertebrate Genomics Alliance (GIGA) workshop\*\* will now take place from the 22.-24. March 2015 at the Department of Earth and Environmental Sciences, Ludwig-Maximilians-Universität München, Germany.

We believe that this second GIGA will be vital to keep the GIGA community and goals on track. We would greatly appreciate your attendance as your insight and experience will assist the further development and progress of the GIGA community.

Due to generous support by the German Research Foundation (DFG) we were able to assemble an excellent set of invited speakers (< <http://bit.ly/1BSbl6f> >) and

keep registration costs low (100 Euros).

Attendance is currently limited to 75 participants to keep the workshop at a manageable size. A few seats are still available.

Registration is now open through the GIGA II workshop website < <http://www.palmuc.de/GIGAI> >.

Remaining seats will be given on a first-come, first-serve basis with respect to payment of the registration fees. Registration will close on 15 February 2015, but might be closed earlier if maximum capacity is reached so be quick!

Please direct enquiries about the workshop only to the email address given on the workshop website <[giga2@lrz.uni-muenchen.de](mailto:giga2@lrz.uni-muenchen.de)>.

On behalf of the scientific committee of GIGA II

Sincerely,

Gert Wörheide

Prof. Dr. Gert Wörheide Department of Earth and Environmental Sciences, Division of Paleontology & Geobiology & GeoBio-CenterLMU Ludwig-Maximilians-Universität München, and Director, Bavarian State Collections of Palaeontology and Geology Richard-Wagner-Straße 10 80333 München Germany

Phone: +49 (89) 2180-6718 Fax: +49 (89) 2180-6601 E-Mail: [woerheide@lmu.de](mailto:woerheide@lmu.de) [www.palmuc.de](http://www.palmuc.de) | [www.geobiology.eu](http://www.geobiology.eu) Labnews: [www.facebook.com/molpalaeo](http://www.facebook.com/molpalaeo) Tweets: [twitter.com/gwoerhe](https://twitter.com/gwoerhe)

Lab publications: [www.molecularpalaeobiology.eu](http://www.molecularpalaeobiology.eu) [orcid.org/0000-0002-6380-7421](https://orcid.org/0000-0002-6380-7421)

[woerheide@lmu.de](mailto:woerheide@lmu.de)

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### Panama Workshops Jan15 DeadlineReminder

Dear Colleagues,

Don't forget the application deadline for the course "Systematics and Biology of Hydrozoa" is this week.

The 2-week workshop held in Panama is aimed for at a graduate student level, but is open to any researcher wishing to learn more about hydrozoa, including collection managers, people involved in bioinventories and surveys and advanced undergraduates with appropriate preparation.

Find out more at: <http://www.stri.si.edu/sites/->

[taxonomy\\_training/future\\_courses/2015/2015\\_Biology\\_Tropical\\_Hydrozoa.html](http://www.stri.si.edu/sites/-taxonomy_training/future_courses/2015/2015_Biology_Tropical_Hydrozoa.html)

Or Contact one of us

Dr. Rachel Collin [CollinR@si.edu](mailto:CollinR@si.edu) Dr. MariaPia Miglietta [miglietm@tamug.edu](mailto:miglietm@tamug.edu)

Dear Colleagues,

Don't forget the application deadline for the course "Tropical Field Phycology" is this week.

The 2-week workshop held in Panama is aimed for at a graduate student level, but is open to any researcher wishing to learn more about hydrozoa, including collection managers, people involved in bioinventories and surveys and advanced undergraduates with appropriate preparation.

Find out more at: [http://www.stri.si.edu/sites/-taxonomy\\_training/future\\_courses/index.html](http://www.stri.si.edu/sites/-taxonomy_training/future_courses/index.html) Or Contact one of us

Dr. Rachel Collin [CollinR@si.edu](mailto:CollinR@si.edu) Dr. Suzanne Fredericq [sfredericq@yahoo.com](mailto:sfredericq@yahoo.com)

Dear Colleagues,

Don't forget the application deadline for the course "Taxonomy and Biology of Sea Slugs" is this week.

The 2-week workshop held in Panama is aimed for at a graduate student level, but is open to any researcher wishing to learn more about hydrozoa, including collection managers, people involved in bioinventories and surveys and advanced undergraduates with appropriate preparation.

Find out more at: [http://www.stri.si.edu/sites/-taxonomy\\_training/future\\_courses/index.html](http://www.stri.si.edu/sites/-taxonomy_training/future_courses/index.html) Or Contact one of us

Dr. Rachel Collin [CollinR@si.edu](mailto:CollinR@si.edu) Dr. Ángel A. Valdés [aavaldes@csupomona.edu](mailto:aavaldes@csupomona.edu)

"Collin, Rachel" <[CollinR@si.edu](mailto:CollinR@si.edu)>

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### Portal Arizona AntEvolution Aug6-16

ANT COURSE 2015 August 6-16, 2015 Southwestern Research Station (SWRS), Portal, AZ, USA <http://www.calacademy.org/scientists/ant-course>

DEADLINE FOR APPLICATION: April 1, 2015. Application form: <https://docs.google.com/forms/d/1Z5Fu8DHxqW5EGFkiLbxi4mHWpnc2Tn0vzmN5ctvXj1g/viewform?c=0&w=1>. ANT COURSE will be taught at the Southwestern Research Station (SWRS) in Portal Arizona (<http://research.amnh.org/swrs/>). The Station is centered amid the richest ant fauna in North America.

PARTICIPANT ACCEPTANCE CRITERIA. - ANT COURSE is open to all interested individuals. Priority will be given to those students for whom the course will have a significant impact on their research with ants. An entomological background is not required. We aim to include students with a diverse interest in biology, including ant systematics, ecology, behavioral biology, genetics, and conservation. The high instructor to student ratio will allow students to receive individual attention. ANT COURSE is presented in English and limited to 30 participants.

COSTS. - Tuition for the 10-day COURSE is \$475 for current students and \$675 for non-students (including postdocs). In addition, the Southwestern Research Station (SWRS) fee for this period, covering dormitory room and board, is \$670. Transportation costs between home and Tucson (air) or SWRS (auto) are to be borne by all participants.

SPONSORS. - California Academy of Sciences and Museum of Comparative Zoology.

2015 INSTRUCTORS: Brian Fisher (Coordinator), California Academy of Sciences; Stefan Cover, Museum of Comparative Zoology; Bob Johnson, Arizona State University, Tempe; Josh King, University of Central Florida; John LaPolla, Towson University; Jack Longino, University of Utah; Corrie Moreau, Field Museum of Natural History; Scott Powell, George Washington University; Andrew Suarez, University of Illinois; James Trager, Shaw Nature Reserve; Walter Tschinkel Florida State University Tallahassee; Phil Ward, University of California Davis; Special Guests: Raymond Mendez, Howard Topoff.

bpescador@gmail.com

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### Portugal IntraSppDiversityNGS Jul27-31

Dear EvolDir members,  
Happy 2015!

I'm organizing an EMBO practical course that will occur next summer (27-31 July 2015) at the Instituto Gulbenkian de Ciência (Oeiras, Portugal): <http://events.embo.org/15-htp-sequencing/> "This EMBO Practical Course aims to show evolutionary biologists and population geneticists the potentials and perils of using high throughput sequencing to estimate intra-specific genetic diversity, from individuals to populations. Participants will have the opportunity to interact with experienced researchers that have successfully applied the technology in a wide variety of high impact studies, and learn from their successes as well as from their failures. Participants will not only listen to theoretical lectures, but will also practice some of the techniques used in those high impact studies. Participants are strongly encouraged to bring their own projects for discussion and experiment novel techniques with their data."

The deadline for registration is March 31st!

Do share this with anyone for which you think this may be of potential interest.

Thank you.

Kind Regards, Daniel

Daniel Sobral, PhD Head of Bioinformatics Unit Instituto Gulbenkian de Ciência +351214407964

lilia.perfeito@gmail.com

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### SCENE Glasgow AdvancingInR 2 Nov30-Dec4

STATS COURSE 'ADVANCING IN R'

A repeat of the course titled 'ADVANCING IN R' has been arranged for 30th November - 4th December 2015

The content designed to bridge the gap between basic R coding and more advanced statistical modelling.

The course is aimed at PhD students and post docs (although people at any stage of their career are welcome) with basic to moderate knowledge in R.

It will be held at SCENE (Scottish Centre for Ecology and the Natural Environment), Glasgow, United Kingdom.

Course content is as follows and will be delivered by two evolutionary biologists and based on biological/ecological data thus highly relevant to evolutionary biologists.



Module 1 Data manipulation & visualization using {dplyr} and {ggplot} Module 2 Univariate regression, diagnostics & plotting fits Module 3 Adding additional continuous predictors (multiple regression); scaling & collinearity Module 4 Adding factorial (categorical) predictors & incorporating interactions (ANCOVA) Module 5 Model selection & simplification (likelihood ratio tests, AIC) Module 6 Predicting on the basis of coefficients Module 7 Mixed effects model in theory and in practice Module 8 Generalised linear models in theory and practice Module 9 Nonlinear models (polynomial & mechanistic models) Module 10 More advanced topics & combining methods (e.g. nonlinear mixed effect models (NLME) & generalised linear mixed effects models (GLMM)).

Cost is £460 for the 5 days including lunches and refreshments or £635 for an all-inclusive option which includes the addition of accommodation, all meals and refreshments.

There is also the possibility (depending on time) to have casual one to one discussion regarding your own research so you are encouraged to bring data with you however this cannot be guaranteed.

For further details or questions please email [oliverhooker@prstatistics.co.uk](mailto:oliverhooker@prstatistics.co.uk) or visit [www.prstatistics.co.uk](http://www.prstatistics.co.uk) - upcoming courses; ANALYSIS OF STABLE ISOTOPE DATA USING SIA-R; AN INTRODUCTION TO USING GIS IN ECOLOGICAL FIELD STUDIES; APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS; SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R

Oliver Hooker PhD research student University of Glasgow +44 (0) 1360 870 510 +44 (0) 7966 500 340 [o.hooker.1@research.gla.ac.uk](mailto:o.hooker.1@research.gla.ac.uk)

Oliver Hooker <[o.hooker.1@research.gla.ac.uk](mailto:o.hooker.1@research.gla.ac.uk)>

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## SCENE Glasgow GISforEvolBiol Aug11-13

The following course will take place at SCENE (Scottish Center for Ecology and the Natural Environment), Glasgow, United Kingdom. in from August 11th - 13th 2015 - An introduction to using GIS in ecological field studies

GIS is an important tool that can be used to incorporate environmental and biological data to help look for patterns or causes in the spatial distribution of organisms. This course would most likely suite evolutionary biologists that study how the environment may influence how populations behave or distribute themselves in response to environmental drivers such as habitat type, precipitation, temperature, altitude etc and is most suitable to people in the field of ecological speciation, sympatric divergence or adaptive radiation etc.

This course is aimed at biologists and ecologists who are just starting to use GIS in their ecological data collection and analysis and who have little or no existing knowledge of this subject area.

There are only 12 places available in total and last time this course filled very quickly!

For further details or questions please email [oliverhooker@prstatistics.co.uk](mailto:oliverhooker@prstatistics.co.uk) or visit [www.prstatistics.co.uk](http://www.prstatistics.co.uk)

Course details: The course will consist of a mix of background talks, practical sessions based around ArcGIS software and field sessions conducted in the local oak woodland. The field sessions will provide experience in how to collect data in a manner that is GIS-compatible.

The course will cover areas such as making a map for a paper or a report, extracting information from Google Earth for use in a GIS project, collecting GIS-compatible data using a GPS receiver, transferring data between a GPS and a GIS project, creating raster data layers of environmental information, importing data to a GIS project from a spreadsheet and linking species records to environmental information. All the practical exercises will be done using a standard data set so you do not need to have your own data to do this course.

Day 1 - Morning: Background Session: Introduction To GIS Practical Session: Making A Map For Study Area In GIS; Setting the projection, coordinate system and datum for your data frame; Adding existing data layers to your GIS project; Creating a map of a local

region; Plotting nest box locations as a point data layer  
 Creating new data layers in ArcGIS  
 Creating new data layers through Google Earth; Creating a fine-scale map of a study area

Day 1 - Afternoon: Background Session: Collecting Data For Use In A GIS  
 Practical Session: Collecting GIS-Compatible Data In The Field; Converting GIS data layers into GPS-compatible files; Setting up a GPS to record GIS-compatible data; Creating a data sheet to record your data  
 Recording GIS-compatible data along a transect

Day 2 - Morning: Background Session: The Importance Of Error-Checking Your Spatial Data  
 Practical Session: Entering Field Data Into A GIS; Transferring data between a GPS and a GIS project; Creating and entering data into a GIS-compatible spreadsheet; Creating a position validator spreadsheet for a GIS project; Converting latitude and longitude coordinates into decimal degrees; Estimating positions from distance and bearing information

Day 2 - Afternoon: Background Session: Incorporating Environmental Information Into Your GIS  
 Practical Session: Incorporating Environmental Information Into Your GIS; Collecting environmental information in the field; Extracting environmental information from existing data sets

Day 3 - Morning: Background Session: Linking Data Together Based On Spatial Relationships.  
 Practical Session: Investigating Spatial Relationships; Linking the supplied data set to habitat variables; Joining information from an external spreadsheet to a GIS data layer; Analysing spatial relationships using a GAM

Day 3 - Afternoon: Background session: Translating biological tasks into the language of GIS  
 Practical Session: Translating biological tasks into the language of GIS; Creating a summary flow diagram for your GIS project; Collating flow diagrams for the individual steps for a summary flow diagram

At the end of the course, all attendees will receive a certificate of attendance and completion. Each certificate is embossed with the GIS In Ecology official stamp to prevent its fraudulent reproduction. In addition, each certificate has its own unique identification number that we will record, along with your name, meaning that we can verify the authenticity of the certificates we issue (and the course you have completed) on request.

Cost is £425 for the 3 days including lunches and refreshments or £525 for an all inclusive option which includes the addition of accommodation, all meals and refreshments.

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## SCENE Glasgow RGeneticDataAnalysis Aug3-7

Genetic data analysis in R (statistics course)

Overview: This course is ideal for evolutionary biologists that deal with various types of genetic data. The course will provide an extensive overview of exploratory methods for the analysis of genetic data using the R software. It will address a number of key problems in population genetics, such as: How to examine genetic diversity using phylogenetic trees as well as multivariate methods, identify genetic clusters, and unravel spatial genetic patterns. Participants will be provided with the theoretical background and statistical methodology necessary to approach each problem from a number of different angles. Hands-on practical sessions will then provide an opportunity to highlight the pros and cons of methods introduced by the lectures, while conferring to participants advanced knowledge of the R packages *adegenet*, *ape*, and *phangorn*.

The course will run from 3rd - 7th of August 2015 at SCENE (the Scottish Centre for Ecology and the Natural Environment), Glasgow. The cost is £490 including lunches and course materials. An all-inclusive option is also available at £665; this includes breakfast, lunch, dinner, refreshments, accommodation, and course materials.

The course is being delivered by Dr. Thibaut Jombart who has contributed towards a number of R packages (*adegenet*, *adephylo*, *geography*, *outbreaker*, *Outbreaker-tools*, *bmmix*, *epiServe* (author) and *ade4* and *phylobase* (contributor) and Caitlin Collins (Imperial College London) who also contributes to the R packages *adegenet*, *Outbreakertools* and *epiServe*)

Curriculum is as follows;

Day 1: Intro to phylogenetic reconstruction  
 Lecture 1a: Reconstructing phylogenies from genetic sequence data. Three main approaches covered: distance-based phylogenies; maximum parsimony; and likelihood-based approaches. Lecture 1b: Short R refresher. Practical

1: Phylogenetic reconstruction using R. Three main approaches plus rooting a tree; assessing/testing for a molecular clock; and bootstrapping. Main packages: ape, phangorn.

Day 2: Intro to multivariate analysis of genetic data  
Lecture 2: Key concepts in multivariate analysis. Focus on using factorial methods for genetic data analysis. Practical 2: Basics of multivariate analysis of genetic data in R. Topics include: data handling, population genetic tests of population structure (PCA, PCoA). Main packages: adegenet, ade4, ape.

Day 3: Exploring group diversity  
Lecture 3: Approaches to identifying and describing genetic clusters. Topics include: hierarchical clustering, K-means, population-level multivariate analysis (between-group-PCA, DA, DAPC). Practical 3: Applying the approaches covered in morning lecture and emphasising their strengths and weaknesses. Main packages: adegenet, ade4.

Day 4: Genome-Wide Association Studies (GWAS)  
Lecture 4: Intro to GWAS study design and statistical approaches: univariate, regression-based and multivariate analysis. Practical 4: Applying each class of methods covered in morning lecture, with emphasis on their strengths and weaknesses. Main packages: adegenet, glmnet.

Day 5: Spatial genetic structures  
Class 1: Discussing the origin and significance of spatial genetic patterns, and how to test for them. Practical: Visualising and analysing spatial genetic data. Topics: spatial density estimates, Moran/Mantel tests, mapping principal components in PCA, spatial PCA. Main packages: adegenet, adehabitat, ade4.

Please send inquiries to [oliverhooker@prstatistics.co.uk](mailto:oliverhooker@prstatistics.co.uk)  
[oliverhooker@prstatistics.co.uk](mailto:oliverhooker@prstatistics.co.uk)

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**SCENE Glasgow SpatialEcolR**  
**Nov16-20**

STATS COURSE 'SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R'

A repeat of the course titled 'SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R' has been arranged for 16th - 20th November 2015

This course will cover the concepts and R tools that can be used to analyse spatial data in ecology covering elementary and advanced spatial analysis techniques

applicable to both plants and animals.

The course is aimed at PhD students and post docs (although people at any stage of their career are welcome) with basic to moderate knowledge in R.

It will be held at SCENE (Scottish Centre for Ecology and the Natural Environment), Glasgow, United Kingdom.

Course content is as follows and will be based on biological/ecological data and relevant to evolutionary biologists particularly those studying behavior, habitat use and ecological speciation.

Module 1 Introductory lectures; key questions in spatial ecology, the main types of data on species distributions, concepts, challenges and different types of environmental data; useful concepts from statistics; GLM's

Module 2 Density estimation, spatial autocorrelation, Smoothing, Kernel Smoothers, Kriging, Trend-fitting (linear, generalised linear, generalised additive models)

Module 3 Habitat preference, Resource selection functions, MaxEnt: What's it all about? Overview and caveats related to Niche models

Module 4 Analysing grid data, Poisson processes, Occupancy models, Use-availability designs

Module 5 Analysing telemetry data, Presence-only data, Spatial and serial autocorrelation, partitioning variation by mixed effects models

Module 6 Analysing transect data, Detection functions for point and line transects, Using covariates in transect models

Module 7 Advanced methods, Generalised Estimation Equations for difficult survey designs, GAM's for habitat preference, Dealing with boundary effects using soap smoothers, Spatial point processes with INLA

Module 8 Prediction, Validation by resampling, Generalised Functional Responses for species distribution, quantifying uncertainty, dealing with the effects of population density

Module 9 Applications, Designing protected areas, thinking about critical habitat, representing uncertainty

Module 10 Round-table discussions about the analysis requirements of attendees (option for them to bring their own data).

Cost is £475 for the 5 days including lunches and refreshments or £675 for an all-inclusive option which includes the addition of accommodation, all meals and refreshments.

For further details or questions please email [oliverhooker@prstatistics.co.uk](mailto:oliverhooker@prstatistics.co.uk) or visit [www.prstatistics.co.uk](http://www.prstatistics.co.uk)

- upcoming courses; ANALYSIS OF STABLE ISOTOPE DATA USING SIA-R; AN INTRODUCTION TO USING GIS IN ECOLOGICAL FIELD STUDIES; APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS; ADVANCING IN R

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Oliver Hooker <o.hooker.1@research.gla.ac.uk>

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### Swiss Alps EvolutionaryBiology June19-25

Evolutionary Biology Workshop in the Alps

19-25 June 2015, Riederalp, Switzerland

Application Deadline: February 15.

Target participants: PhD students, advanced Master students

The main goals of this annual workshop, based on a concept developed by Stephen Stearns and John Maynard Smith, are to develop the following skills: - developing your scientific ideas through discussions in groups; - thinking critically and expressing oneself clearly; - turning a general idea into a research project; - writing a research proposal and defending it.

Faculty: Judith Mank (University College London) Andrew Read (Pennsylvania State University) Tanja Schwander (University of Lausanne) John Pannell (University of Lausanne) Tadeusz Kawecki (University of Lausanne)

It is you, the students, who will be in charge in this course. You will be divided in groups of 4-5 students. In those groups, you will work on your ideas. You, as a group, will decide what the important open questions in broadly defined evolutionary biology are, you will choose one, and attempt to develop a proposal for a research project that will address it. The faculty will visit the groups during the discussions to answer your questions, provide coaching and give you feedback on your projects, but they will generally take the back seat. Additionally, the faculty will give talks about their research and be available for informal discussion with individual students. At the end you will present your projects to other participants, and we will party.

The workshop will take place in Villa Cassel ([http://-](http://www.pronatura-aletsch.ch/home-en)

[www.pronatura-aletsch.ch/home-en](http://www.pronatura-aletsch.ch/home-en)), at 2000 m of altitude, a >100 year old villa where Winston Churchill once stayed, amid the magnificent mountain landscape of a UNESCO World Heritage Site, walking distance from the largest glacier of the Alps. This isolated site will help you to concentrate on the course while giving you also the chance to enjoy the views and the alpine flora.

Costs: CHF 530.- for room and board. 3 ETSC credit points

To apply, send a single file (pdf or rtf) containing a short motivation letter including a brief summary of your research interest, a cv, and the name of your scientific advisor to Caroline Betto-Colliard <ecologie-evolution@cuso.ch>, with Cc to tadeusz.kawecki@unil.ch .

- Tadeusz J. Kawecki Department of Ecology and Evolution University of Lausanne Biophore, office 3111 CH 1015 Lausanne, Switzerland

tadeusz.kawecki@unil.ch

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### Tubingen OriginsHumanCooperation Jun22-26

Interdisciplinary summer school with Prof. Michael Tomasello about "the origins of human cooperation" in Tübingen, Germany.

Date: June 22nd through June 26th, 2015.

There is a more specific Call for Papers, see here: <http://www.forum-scientiarum.uni-tuebingen.de/-veranstaltungen/unseld-lectures/cfa.html> Application Procedure

Applicants have to send in a completed application form downloadable from our website ([www.unseld-lectures.de/cfa](http://www.unseld-lectures.de/cfa)).

Deadline: February 15th, 2015. A letter of admission will reach successful applicants by March 6th.

There is no program fee. The Forum Scientiarum seeks to facilitate the participation of competent students from all over the world, and as the Forum Scientiarum is provided a limited fund.

Applications should be sent to [unseld@fsci.uni-tuebingen.de](mailto:unseld@fsci.uni-tuebingen.de) or to our postal address: FORUM SCIEN TIARUM Doblerstr. 33 72074 Tuebingen

Michael Herrmann <michael.herrmann@fsci.uni-

tuebingen.de>

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## UCalifornia LosAngeles ConsGenomics Mar22-27

Each year, the La Kretz Center sponsors this hands-on workshop, held jointly at our Field Station and Stunt Ranch. Our goal is to provide training and access to the most current issues and techniques in population genomics, and how these tools can be applied to pressing conservation problems.

Conservation biology and genetics have had a long and intimate relationship, and constitute one of the key applications of evolutionary analysis to real-world biological problems. The impacts of population genetics, phylogenetics and phylogeography have been particularly striking for conservation biology, and have helped solve some of the most pressing problems in biological conservation. As the field of landscape-based genetics continues to grow and mature, the increasing availability of genomic-level data, analytical models and methods stand to make profound new contributions to our ability to identify and protect at-risk populations and recover those that are most endangered. However, genomic level analyses also carry a heavy burden—data sets are enormous, often requiring diverse computational approaches for assembly, quality control and analysis.

This annual workshop will provide a comfortable, informal training environment for a small group of motivated graduate students to explore how conservation problems can best be addressed with genomic-level data. Our goal is to provide hands-on experience on the efficient collection, troubleshooting, and analysis of large data sets for conservation-relevant problems. One of the highlights of our workshop is active participation from members of several US government agencies who are at the forefront of endangered species protection and management, providing a forum for exploring the most relevant aspects of conservation genomics to managers.

The UCLA/La Kretz workshop will be held at the La Kretz Field Station (<http://www.environment.ucla.edu/lakretz/fieldstation/>) and Stunt Ranch Reserve (<http://stuntranch.ucnrs.org>) in the heart of the Santa Monica Mountains. Only 30 miles from UCLA (and LAX airport), but nestled in the relatively undeveloped 160,000 acre Santa Monica Mountains National Recreation Area, the Field Station provides an ideal location that brings exciting new

developments in genomic science and pressing needs in conservation and management together in a single setting.

Our current instructor list, drawn from UCLA faculty and several other southern California partners, includes:

Jonathon Chang Ben Fitzpatrick Paul Gugger Kirk Lohmueller Evan McCartney-Melstad Mark Phuong Peter Ralph Brad Shaffer Victoria Sork Phil Spinks Bob Wayne Ying Zhen (Additional instructors may be added)

Topics covered include:

Overview of traditional conservation genetics  
Next generation platforms: the best tool for the job  
Data management pipelines: Quality Control  
Data storage  
Data organization  
Data types and analyses: SNPs  
Sequences  
Exploring very large data sets  
Functional genomic data  
Genomic data and GIS  
Visualizing geographic structure and demographic history  
Conservation phylogenomics  
Prerequisites

Available housing limits course enrollment to ~20 students. Preference is given to doctoral candidates who are in the early to middle stages of their thesis research, and who have completed sufficient prerequisites (through previous coursework or research experience) to have some familiarity with using a command line interface or programming languages (i.e. Perl, python etc.). Postdocs, faculty, and government researchers may also apply, but preference will be given to graduate students.

### Admission and Fees

Applicants will be admitted based on academic qualifications and appropriateness of research interests. The course fee is \$425. This includes food and lodging at the La Kretz Field Station, as well as any incidental fees, for the duration of the course (arriving Sunday March 22, departing Friday March 27). In addition, course participants who would like to extend their stay at the field station for the remainder of the weekend may do so for no extra charge. For those opting to stay the weekend, departure time will be by 5:00 pm on Sunday March 29.

### Application Forms and Information

Visit the UCLA/La Kretz Center for California Conservation Science website for additional information and to download an application form:

<http://www.environment.ucla.edu/perch/resources/-2015-la-kretz-conservation-genomics-application-4.docx>  
Application Deadline

Applications are due by February 2, 2015. Please send a completed application form and one letter of recommendation from your major advisor. Students will be notified via e-mail by February 9, 2015 of acceptance.

Applications should be emailed as PDFs to: Phil Spinks; email:

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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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## ULeipzig ProgrammingForEvolutionaryBiology Mar17-Apr2

Course on Programming for Evolutionary Biology

When: March 17th - April 2nd 2015

Location: Leipzig, Germany

Application deadline: January 15th 2015

Detailed information about the course content and how to apply: <http://evop.bioinf.uni-leipzig.de/> “Nothing in Biology Makes Sense Except in the Light of Evolution” (Dobzhansky, 1973). Today, evolutionary biology often involves the analysis of an unprecedented amount of information and supports many other disciplines, such as medicine (evolutionary medicine), behavioral biology (evolutionary psychology), ecology, and information transfer. Scientists have to analyze large datasets, which

requires computational programming skills to design and apply own ideas into customized algorithms.

In this intensive 17 days course, students will learn how to survive in a Linux environment, get hands-on experience in two widely used programming languages (Perl and R), and statistical data analysis. The classes will be given by experts in the field and consist of lectures and exercises with the computer. The aim of the course is to provide the students with the necessary background and skills to perform computational analyses with a focus on solving research questions related to genomics and evolution. The philosophy of the course will be “learning by doing”, which means that the computational skills will be taught using examples and real data from evolutionary biology for the exercises. During the course, students will also propose projects of their own interest and perform them as final projects in small groups under the supervision of a teaching assistant. This summer school is open for students from all countries and targeted toward PhD students and postdocs of evolutionary biology or related research fields with no or little programming experience who want to become proficient in computational evolutionary biology in a couple of weeks.

The course takes place at the University of Leipzig.

Dr. Katja Nowick

Group Leader “TFome and Transcriptome Evolution”  
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Katja Nowick <[nowick@bioinf.uni-leipzig.de](mailto:nowick@bioinf.uni-leipzig.de)>

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## Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral

positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvoDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvoDir direct them to the email `evodir@evol.biology.McMaster.CA`. Do not include encoded attachments and do not send it as Word files, as HTML files, as  $\text{\LaTeX}$  files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

## Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by  $\text{\LaTeX}$  do not try to embed  $\text{\LaTeX}$  or  $\text{\TeX}$  in your message (or other formats) since my program will strip these from the message.