
E v o l D i r

February 1, 2017

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

Foreword

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

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

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



Foreword	1
Conferences	2
GradStudentPositions	27
Jobs	60
Other	84
PostDocs	98
WorkshopsCourses	123
Instructions	147
Afterword	148

Conferences

Ames Iowa EvolQuantGenet Jun1-3 Registration ... 2	Groningen-Netherlands EvolutionMedicineSociety Aug18-21 16
Austin SMBE AnnualMeeting Jul2-6 3	Hawaii HistoryOfPacificMarineLife May23-25 17
Austin SMBE Behavior Jul2-6 3	Lund SexHermaphrodites Mar9-10 RegistrationOpen 17
Austin SMBE ConvergentEvolution Jul2-6 4	LundU SwedishOikos2017 Feb7-9 RegistrationClosing 18
Austin SMBE EpigeneticsAndEvolution Jul2-6 4	Marseilles 21stEvolutionaryBiol Sep26-29 EarlyDeadline 19
Austin SMBE EvoSysBioOfCells Jul3 5	Marseilles EBM21 Sep26-29 EarlyDeadlineTopics .. 19
Austin SMBE HostParasiteCoevoluton AbstractDeadline 5	Mosocow ICIM Aug18-23 OldSpecimensNewTechnology 19
Austin SMBEIntegratingAncientAndModernDNA Jul2-6 6	NHM London EvolutionColourAndVision Apr27 ... 20
Austin SMBE SymbiosesAndInteractions Jul2-6 7	Paris EvolutionSymbiosis Mar15-17 21
Austin Texas SMBE HostParasiteCoevolution Jul1-6 7	Paris Holobionts Apr19-21 RegistrationExt 21
Barcelona PopulationGenomics Apr3-5 8	PorquerollesIsle France MathEvolBiol Jun12-16 2 .. 21
Beijing FireEcolEvol Aug20-25 8	Portland Evolution ASN SensoryDrive Jun23-27 ... 22
Blossin InsectEvolutionaryImmunity Aug28-Sep1 ... 9	Portland SSE MaleCompSpeciation Jun23-27 22
Chize France EcologyBehaviour Jun19-23 10	Portland SSE SexInTheWild Jun23-27 23
CityULondon MathModelsEvolution Jul10-12 10	Portland SSE Speciation Jun23-27 24
Colombia EvoDevo Oct9-13 10	Shanghai IUFROGeneticsGenomics Nov1-3 24
Edinburgh RNAPathwayEvolution Mar10 12	UExeter FishPopulations Jul3-7 25
Gothenburg BioSyst Aug15-18 13	UFMS Brazil Evol 25
Gothenburg BioSyst Barcoding Aug15-18 13	YosemiteNationalPark Symbiosis May5-7 Registration 26
Groningen ESEB AgeingBiology Aug20-25 13	
Groningen ESEB CytonuclearSpeciation Aug20-25 14	
Groningen ESEB GeneticExchangeMicrobesDisease Aug20-25 15	
Groningen ESEB GenomicsOfAdaptation Aug20-25 15	
Groningen ESEB SexualSelection Aug20-25 16	

Ames Iowa EvolQuantGenet Jun1-3 Registration

Each year, AGA symposia bring together 80-100 participants in a relaxed and collegial setting to share ideas on genetic and genomic research topics.

This year's meeting is AGA2017: Evolutionary Quantitative Genetics in the Wild. Hosted by AGA President Anne Bronikowski, it will be held on the campus of Iowa State University. The opening reception on 1 June will be in the beautiful Reiman Gardens and Butterfly House: <http://www.reimangardens.com/> Registration and student award details will be available soon at <http://www.theaga.org> . CONFIRMED SPEAKERS:

David Coltman, University of Alberta, Canada

Jeff Conner, Michigan State University
Lynda Delph, University of Indiana
Ned Dochtermann, North Dakota State University
Lucia Gutierrez, University of Wisconsin
Fred Janzen, Iowa State University
Adam Jones, Texas A & M University
Emily Josephs, University of California, Davis
Andrew McAdam, University of Guelph, Canada
Joel McGlothlin, Virginia Technical Institute
Mike Morrissey, St Andrews University, UK
Max Rothschild, Iowa State University
Julia Saltz, Rice University
Cynthia Weinig, University of Wyoming
Jason Wolf, University of Bath, UK
Thomas Reed, University College, Cork, Ireland
Anjanette Baker
AGA Manager agajoh@oregonstate.edu
AGAJOH <AGAJOH@oregonstate.edu>

Austin SMBE AnnualMeeting Jul2-6

The Annual Meeting of the Society for Molecular Biology and Evolution will be in downtown Austin Texas July 2-6 2017.

Abstract submissions are due FEB 1.

The scientific program spans a wide variety of cutting edge topics in evolutionary biology. SMBE offers many travel awards and other prizes for students and post-docs, as well as assistance with care of children or other dependents. Please go to <http://www.smbe2017.org/> to submit an abstract and to see the list of plenary speakers and symposium topics.

We hope to see you in Austin! Nancy Moran, Howard Ochman, Claus Wilke

Department of Integrative Biology University of Texas at Austin

nancy.moran@austin.utexas.edu

Austin SMBE Behavior Jul2-6

SMBE 2017 Symposium “Systems approaches to behavior”

We welcome abstract submissions for a symposium on “Systems approaches to behavior” at SMBE 2017 in Austin, TX. The symposium will feature talks by Lauren O’Connell (Harvard University) and Hans Hofmann (UT Austin). The deadline for abstract submissions is February 1: <http://www.smbe2017.org/> If you have any questions, please feel free to contact Julia Saltz (julia.b.saltz@rice.edu)

Symposium summary: Understanding the diversity of animal behaviors and how this diversity evolves is an intricate challenge because behavior uniquely combines inputs across biological scales—from genes, transcripts, and proteins interacting at tissue, organ, and whole organismal levels to environmental factors such as other individuals via social interactions. The goal of our symposium is to bring together researchers working at the interface of multiple levels of behavioral and molecular analysis to highlight how systems-level approaches can lead to new insights about behavioral evolution. Our symposium will be timely because high-dimensional “-omics” data, representing functional information at multiple biological scales, is rapidly becoming available; but the evolutionary relevance of such information, particularly for highly-plastic phenotypes like behavior, remains unclear. Our symposium will contribute to building an integrated conceptual framework for thinking about the causes of variation in behavior at a systems level and how such systems can evolve. Our invited speakers will provide “worked examples” illustrating how different molecular levels, neurobiology, and ecology can be integrated to understand why behavior varies within individuals, among individuals, and among species.

– Julia B. Saltz Assistant Professor Biosciences at Rice University 6100 Main Street, MS-170 Houston, TX 77005 julia.b.saltz@rice.edu Saltzlab.wordpress.com
jbsaltz@gmail.com

Austin SMBE Convergent Evolution Jul2-6

SMBE 2017 Symposium “Convergent evolution”

We are pleased to announce a symposium on “Convergent evolution” at SMBE 2017 in Austin, Texas, this July. Our invited speakers are Jay Storz (University of Nebraska-Lincoln), Matthew Hahn (Indiana University), and Sarah Kocher (Princeton University). Abstract submissions for contributed talks and posters are welcome and due on 1 February 2017. Please use the following link for submission: <http://www.smb2017.org/abstracts/>. Note that abstract submission is possible prior to registration for the conference.

Symposium description:

*** Convergent evolution, wherein species independently evolve substantially similar phenotypes in response to similar selective pressures, is a potentially powerful criterion to identify genotypes underlying adaptive evolution. The on-going boom in comparative genomics has renewed interest in the molecular and genetic basis of convergent phenotypes. Recent progress in the field has demonstrated the extent of convergence in a wide variety of contexts, from microbes to vertebrates, and resulting from conditions including environmental shifts, sensory systems, and biochemical challenges. In addition, whole-population sequencing and in vitro evolution has provided evidence of the dependence of convergence on the nature of the selective pressure. At a higher level, the study of convergence is outlining the constraints on adaptive evolution and deepening our understanding of natural selection. In light of the increasing amount of genomic data available, the field will benefit from a discussion of the challenges in robustly identifying and testing apparent cases of convergence, with one major challenge being distinguishing adaptive convergence at the sequence level from chance events. This symposium will present a balanced program of historical evolution, in vitro evolution, methodology and theory in convergent evolution. Talks will span the full spectrum of potential convergence ranging across molecules, networks, and phenotypes. ***

SMBE 2017 will offer child care support during the conference (<http://www.smb2017.org/destination/-childcare-at-smb2017/>), and you can apply for child care awards as well (<http://www.smb2017.org/smb2017/awards/ChildCareTravelAward>).

SMBE 2017 will take place in Austin, Texas, from 2 to 6 July 2017.

Thanks,

Tim Sackton (tsackton@g.harvard.edu) Nathan Clark (nclark@pitt.edu)

“tsackton@g.harvard.edu” <tsackton@g.harvard.edu>

Austin SMBE EpigeneticsAndEvolution Jul2-6

SMBE 2017 Symposium “Epigenetics and Evolution”

We are pleased to announce a symposium on “Epigenetics and Evolution” at SMBE 2017 in Austin, Texas, this July. Our invited speakers are Isabel Mendizabal (Georgia Institute of Technology) and Damon Lisch (Purdue University). Abstract submissions for contributed talks and posters are welcome and due on 1 February 2017. Please use the following link for submission: <http://www.smb2017.org/abstracts/>. Note that abstract submission is possible prior to registration for the conference.

Symposium description:

*** The quote from Dhobzhansky (“Nothing makes sense in biology except in the light of evolution”) is overused. But there may be no current area of biology to which this quote is more pertinent than epigenetics. In many respects, the study of epigenetics has been a sterling success. Geneticists and molecular biologists have unraveled some of the intricacies of epigenetic pathways and the interplay of epigenetics with development. And yet, without the tools and context of evolutionary biology, it is difficult to put these findings into a proper context. Evolutionary comparisons provide a filter to help determine what phenomena are conserved, general, and important over time. In this symposium, we seek to integrate epigenetic information into an evolutionary framework, including the effects of epigenetics on development, phenotype, and genome evolution. ***

SMBE 2017 will offer child care support during the conference (<http://www.smb2017.org/destination/-childcare-at-smb2017/>), and you can apply for child care awards as well (<http://www.smb2017.org/smb2017/awards/ChildCareTravelAward>).

SMBE 2017 will take place in Austin, Texas, from 2 to 6 July 2017. Thanks,

Thanks,

Alexandros Bousios (alexandros.bousios@gmail.com)
Soojin Yi (soojinyi@gatech.edu) Brandon Gaut
(bgaut@uci.edu)

– Alexandros Bousios, PhD Marie-Curie Research Fellow
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Austin SMBE EvoSysBioOfCells Jul3

SMBE 2017 Symposium: Evolutionary Systems Biology of Cells Please join us for an exciting symposium addressing key challenges at the interface of cell biology, systems biology, and evolution. How do cells evolve so many fascinating forms and functions and which tools can we use to discover more?

Keynote speakers —

- Prof. Michael Lynch (Bloomington): Evolutionary Cell Biology - Prof. Trey Ideker (UCSD): Translation of Genotype to Phenotype by a Hierarchy of Cell Subsystems

We welcome abstract submissions for contributed talks and posters due * Next * Wednesday:

Important dates —

- 1st Feb 2017: SMBE abstract submission deadline, submit here <http://www.smb2017.org/abstracts/> - 1st March 2017: SMBE abstract notification - 29th March 2017: End of reduced registration rates

The Society for Molecular Biology and Evolution Conference will be held in Austin, Texas, from 2 to 6 July 2017. Symposium is on July 3rd.

More Details —

The symposium program will also be published at:
- <http://evolutionarysystemsbiology.org/meeting/2017-SMBE/>

SMBE supports the presence of children at the conference: - <http://www.smb2017.org/destination/childcare-at-smb2017/>

Symposium Description —

Cells are the basic units of life. Decades of research

in molecular-, cell-, and systems-biology have accumulated impressive insights into the molecular mechanisms of life, but the biodiversity of cellular systems remain vastly under-explored despite its critical role in evolution. Building on successful models of well-known cells in controlled environments, this symposium aims to bring together cell biologists, systems biologists, evolutionary biologists, and others interested in advancing models of evolution at the cellular level. This focus on cellular systems celebrates the latest advances in the relentless Evolutionary Synthesis that started with Fisher 1918, and has been continuing whenever evolutionary biologists study complex biological systems to achieve an integrative understanding of evolution. Topics of interest include, but are not be limited to:

- Mechanistic simulations predicting distributions of mutational effects on cellular growth or survival
- Mechanisms for establishing, maintaining, and modifying cellular pathways, gene-regulatory sub-networks and genetic subsystems
- Mechanisms for evolving novel cell types
- Methods that help study the above

We will discuss how to integrate recent advances in genome biology, computational molecular systems biology, cell biology and evolutionary biology.

Symposium organizers —

Dr. Laurence Loewe Evolutionary Systems Biology Group Laboratory of Genetics and Wisconsin Institute for Discovery University of Wisconsin-Madison 330 North Orchard Street, Madison, WI, 53715 Tel: +1 (608) 316 4324 Email: loewe@wisc.edu <http://wid.wisc.edu/profile/laurence-loewe/> Prof Anne-Ruxandra Carvunis Department of Computational and Systems Biology University of Pittsburgh 3501 Fifth Avenue, 3064 BST3 Pittsburgh, PA 15260, USA Email: Carvunis@gmail.com <http://carvunislab.csb.pitt.edu/> “ll@evre.de” <ll@evre.de>

Austin SMBE HostParasiteCoevolution AbstractDeadline

We invite you to submit an abstract for the symposium on Host-Parasite Coevolution, at the SMBE meeting in Austin Texas July 2-7. Abstracts for talks or posters are due February 1 2017. The submission website is here: <https://b-com.mci-group.com/AbstractSubmission/SMBE2017.aspx> A description of the symposium below:

The complex dynamics of host-parasite coevolution have infrequently been described as changes in gene, protein, or cell function. But as more researchers delve into diverse host and parasite systems, armed with technological advances and focused on molecular evolution, it is an opportune time to discuss novel findings and compare definitions and questions. This symposium will foster dialogue among ecologists, geneticists, molecular biologists, and immunologists, all united by an interest in the mechanisms that underlie natural host and parasite evolution. Although presentations will cover a wide range of taxa and approaches, speakers will also address unifying concepts, including: Which questions and approaches are likely to scale across many systems, and which are relevant to only subset of taxa? How can molecular data be used to revamp models of host-parasite interactions (or to design new ones), and what previous theoretical predictions demand mechanistic attention? What are the big differences between studying two-species versus multi-species interactions? How is the molecular or cellular biology of immunity different in wild populations (as opposed to lab settings), and how can we best study immunology in the wild? And finally, what advances in other fields of biology should be incorporated into host-parasite studies, and vice versa?

Thanks, Dan Bolnick Jesse Weber Natalie Steinel

Dr. Daniel I. Bolnick

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Austin SMBEIntegratingAncientAndModernDNA Jul2-6

SMBE 2017 Symposium “Integrating Ancient and Modern DNA”

We are pleased to announce a symposium on “Integrating Ancient and Modern DNA” at SMBE 2017 in Austin, Texas, this July. Our invited speakers are Beth Shapiro (UC Santa Cruz) and Stephan Schiffels (Max Planck Institute for the Science of Human History, Jena,

Germany). Abstract submissions for contributed talks and posters are welcome and due on 1 February 2017. Please use the following link for submission: <http://www.smbe2017.org/abstracts/>. Note that abstract submission is possible prior to registration for the conference.

Symposium description:

The study of contemporary whole genomes has greatly improved our understanding of the evolution of populations, but the availability of ancient genomic data should give us a much more detailed comprehension of the evolutionary process. However, the integration of ancient and modern DNA into a coherent inferential framework is challenging notably due to heterogeneous sampling times and locations, differences in coverage, and post-mortem DNA damages. We also lack appropriate theoretical models linking these two types of samples, as one for instance often ignores the diffusion of genes in both space and time and assumes that old and modern samples belong to the same population. The proper integration of old and contemporary samples is essential to e.g. better distinguish genetic drift from selection, follow specific adaptive processes over time, uncover ancestral relationships among populations, distinguish between alternate modes of selection, follow changes in gene flow over time, or probe past population movements. In this symposium, we aim at bringing together empiricists and theoreticians presenting either novel methodological advances or new genomic datasets including a mixture of ancient and modern samples or experimental/natural time series to tackle fundamental problems in evolution.

SMBE 2017 will offer child care support during the conference (<http://www.smbe2017.org/destination-childcare-at-smbe/>), and you can apply for child care awards as well (<http://www.smbe.org/smbe/awards-ChildCareTravelAward>).

SMBE 2017 will take place in Austin, Texas, from 2 to 6 July 2017.

Thanks,

Simon Aeschbacher (simon.aeschbacher@iee.unibe.ch)
Laurent Excoffier (laurent.excoffier@iee.unibe.ch) Anna-Sapfo Malaspinas (anna-sapfo.malaspinas@iee.unibe.ch)

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Austin SMBE SymbiosesAndInteractions Jul2-6

SMBE 2017 Symposium “Symbiosis and Interactions”

We are accepting abstracts for our symposium on “Symbiosis and Interactions” at SMBE 2017 in Austin, Texas, from July 2-6. The symposium features invited speakers Daniel Sloan (Colorado State University) and Teresa Pawlowska (Cornell University). Abstract submissions for contributed talks and posters are due Wed Feb 1 (<http://www.smbe2017.org/abstracts/>).

Symposium summary: Symbiotic interactions between independent organisms play a critical role in providing new ecological niches and promoting biological diversification. Over evolutionary time, hosts and symbionts often enter a permanent co-evolutionary relationship, where proper maintenance and regulation of symbiosis is required for both lineages to survive. Although beneficial, symbiotic partners are also faced with challenges. Symbionts experience rapid evolution due to high levels of genetic drift and potential selection for selfish traits and hosts must evolve to compensate for these factors in order to maintain functional symbiosis. Thus symbioses may be more similar to a coevolutionary arms race rather than a static optimum. Our understanding of coevolutionary interactions largely focuses on organelles (i.e. mitochondria and plastid) and intracellular endosymbionts present within host cells. Examining the role of genetic variation and functional constraints on the evolution of interacting genomes will shed light on how obligate interactions between co-evolving genomes can promote reproductive isolation, thus promoting biological diversification. This symposium highlights work examining coevolutionary interactions involving organelles and endosymbionts and how these interactions may impact the evolutionary trajectory of these lineages. This symposium provides a central opportunity for integrating the advancements in both endosymbiont and organelle evolution as well as symbiosis.

Thanks, Rebecca Chong (becky.chong@utexas.edu)
Chih-Horng Kuo (chk@gate.sinica.edu.tw)

– Rebecca A. Chong Ph.D. Postdoctoral Fellow Department of Integrative Biology University of Texas at Austin

“becky.chong@utexas.edu” <becky.chong@utexas.edu>

Austin Texas SMBE HostParasiteCoevolution Jul1-6

At SMBE in Austin this July, there will be a symposium on Host-Parasite Coevolution, featuring invited speakers Andrea Graham and Deiter Ebert. Abstract submissions for talks or posters for the symposium are welcome and are due February 1 2017. The submission website is here: <https://b-com.mci-group.com/-AbstractSubmission/SMBE2017.aspx> A description of the symposium below:

The complex dynamics of host-parasite coevolution have infrequently been described as changes in gene, protein, or cell function. But as more researchers delve into diverse host and parasite systems, armed with technological advances and focused on molecular evolution, it is an opportune time to discuss novel findings and compare definitions and questions. This symposium will foster dialogue among ecologists, geneticists, molecular biologists, and immunologists, all united by an interest in the mechanisms that underlie natural host and parasite evolution. Although presentations will cover a wide range of taxa and approaches, speakers will also address unifying concepts, including: Which questions and approaches are likely to scale across many systems, and which are relevant to only subset of taxa? How can molecular data be used to revamp models of host-parasite interactions (or to design new ones), and what previous theoretical predictions demand mechanistic attention? What are the big differences between studying two-species versus multi-species interactions? How is the molecular or cellular biology of immunity different in wild populations (as opposed to lab settings), and how can we best study immunology in the wild? And finally, what advances in other fields of biology should be incorporated into host-parasite studies, and vice versa?

Thanks, Dan Bolnick Jesse Weber Natalie Steinel

Dr. Daniel I. Bolnick Professor Department of Integrative Biology Chair, Graduate Program in Ecology Evolution and Behavior One University Station C0990 University of Texas at Austin Austin, TX 78712

512-471-2824 fax 512-471-3878 danbolnick@austin.utexas.edu

Lab website: <https://bolnicklab.wordpress.com> danbolnick@austin.utexas.edu

Barcelona Population Genomics Apr3-5

NGS'17: Structural Variation and Population Genomics, 3-5 April 2017, Barcelona, Spain

Hosted by the International Society for Computational Biology (ISCB) and the Centre for Genomic Regulation (CRG), the Next-generation sequencing conference covers a broad range of topics in genome sequencing and analysis. Our particular focus areas in 2017 are structural variation and population genomics.

New sequencing technologies have opened up the possibility to sequence genomes at a previously unprecedented scale. The sequencing of whole genomes from large number of individuals representing multiple populations allows the extent of genetic diversity, of both at the single nucleotide level, and of larger structural variants, to be catalogued. Using such data the genetic basis of evolutionary and disease processes can be explored. The meeting will draw together researchers from diverse backgrounds who develop and apply novel tools to sequencing data. Topics covered will include, but are not limited to, genome assembly, variant characterization and analysis, gene expression, population history, disease, and more!

The conference program will be a combination of keynote talks from renown scientists with research focusing on structural variation and population genomics, a selection of thought-provoking submitted abstract talks, technology and applications talks, as well as posters.

Laura Prat Busquets <laura.prat@crg.eu>

Beijing FireEcolEvol Aug20-25

Dear Colleagues,

We are excited to invite you to submit abstracts and attend our upcoming symposium on

“ Wildfire Ecology and Life Evolution: From Ancient Time to Present”

which will be part of the 2017 International Congress of Ecology (INTECOL 2017). The conference will be

taking place from August 20th - August 25th, 2017 in Beijing, China.

<http://www.intecol2017.org/en/index.asp> Symposium description

[T11-01] Wildfire Ecology and Life Evolution: From Ancient Time to Present

Wildfires have been a significant evolutionary factor shaping the ecology of flora from ancient time to the present. This symposium synthesise research from on how has shaping ecology and evolution of terrestrial ecosystems from ancient time to the present, and how current knowledge can be translated into better fire management. “ Wildfires are common and widespread in the modern world, with about 60% of the Earth’s land surface being burnt over a 15-year period. The fossils provide strong evidence in support of hypotheses of great antiquity for fire. Charcoals as evidence of presence of ancient wildfire first appeared from the late Silurian, 410 Ma. However, ecologists and paleo-botanists have long believed that climate and soils controlled the distribution of ecosystems, the role of wildfire was largely overlooked. The strong focus on the negative impact of wildfires on life and property has historically hindered our understanding of fire ecology. Only very recently, evidence become emerging that wildfire played an important role throughout the history of life on the Earth. Wildfire influences on global ecosystem patterns and processes, and has had a pronounced effect on the evolution of biotas, and distribution of ecosystem.

In view of the limited fossil evidence for fire being a significant ecological and evolutionary factor, a major breakthrough in determining the origin of fire-related lineages has occurred over the last seven years. There is accumulating molecular evidence that fire-adapted lineages go back many tens of millions of years. These dates have been largely reconciled with fossil evidence. Humans and our ancestors are the only fire-making species. As we have expanded their use of fire, our actions have come to dominate some ecosystems and change natural processes in ways that threaten the sustainability of some landscapes. Moreover, the interaction between fires and climate change add to the future uncertainty. We need to learn more about how wildfire interacts with a multitude of ecosystem processes. Particularly, we need better data on past and current human influences on fire regimes, and a greater understanding of different cultural traditions of landscape burning and their positive and negative social, economic and ecological effects.

This symposium intends to bring together ecologists, public educator, practitioners and policy-makers who have common interest on wildfire, synthesise research

from global fire-prone ecosystems on how wildfire as ecological and evolutionary factor shaping terrestrial ecosystem from ancient time to the present, so that current knowledge can be translated into better fire management.

We are looking forward to many exciting contributions and to a stimulating discussion with you! The deadline for ABSTRACT SUBMISSION is February 10, 2017.

To submit abstracts online, please go to:

<http://www.intecol2017.org/en/index.asp> Meanwhile, participants of this symposium are encouraged to submit the same abstract to Proceedings of the symposium 'Wildfire Ecology and Life Evolution: From Ancient Time to Present' of the International Congress of Ecology (INTECOL 2017 Beijing). See <http://journal.frontiersin.org/researchtopic/5544/-proceedings-of-the-symposium-wildfire-ecology-and-life-evolution-from-ancient-time-to-present-of-the-for-details>. So that Proceedings (of abstracts) will be published by Frontiers in Plant Sciences free of charge.

For those participants who wish to publish their presented work (or any fire-related work) in a full paper, please consider submitting the full paper to a special issue of Frontiers in Plant Science before September 1 2017. This invitation is extended to anyone, including those are not able attend the symposium, wish to publish a manuscript related to wildfire ecology and life evolution). Frontiers in Plant Science is an open access journal, indexed by ISI (with an impact factor of 4.5 in 2016) and Scopus. The journal however charges an article process fee but discount may apply. See <http://journal.frontiersin.org/researchtopic/5544/-proceedings-of-the-symposium-wildfire-ecology-and-life-evolution-from-ancient-time-to-present-of-the>.

— / —

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>

Blossin Insect Evolutionary Immunity Aug28-Sep1

REGISTRATION IS NOW OPEN FOR THE:
Ecological Immunology Workshop 2017 on:

'Insect immunity: genomics, microbiome, applications'

28th August to 1st September 2017 in Blossin (close to Berlin), Germany.

This workshop will bring together researchers interested in ecological immunology with a focus on insects, and with diverse scientific backgrounds ranging from molecular biology to ecology. The hallmark of these workshops, started in 2001, is the open atmosphere fostering free exchange by keeping it an affordable, small conference (100 participants). The format consists of eighteen invited speakers, contributed talks and a dedicated poster. Long breaks provide plenty of opportunity for informal exchange. Past workshops have initiated new collaborations and ideas focusing on frontier research that has not been published. The premises are basic but in a beautiful location conducive to the success of the meeting. We will be located at a lakeside, which at this time of the year offers great swimming and canoeing, and a small private bar at the harbour [<http://www.blossin.de>]. ****OUR WEBSITE**** <http://rolffeolution.net/-ecological-immunology-workshop-2017/> Registration fee includes accommodation and catering (all meals)

Important dates The deadline for abstract submission of oral and poster presentations is 28th February 2017 Registration closes at the latest on 31st March 2017 or when the maximum number or possible participants is reached, i.e. 100 persons. Final programme announcement is 31st July 2017.

Program and invited speakers

Genomics and functional work in the wild Seth Barribeau, University of Liverpool Nicole Gerardo, Emory University Brian Lazzaro, Cornell University Hinrich Schulenburg, University of Kiel Ann Tate, University of Texas Lumi Viljakainen, University of Oulu Chris Wheat, University of Stockholm

Host-symbiont interactions affecting host immunity Nichole Broderick, University of Connecticut Ewa Chrostek, MPI Infection Biology Ellen Decaestecker, University of Leuven Abdelaziz Heddi, INSA-Lyon Martin Kaltenpoth, University of Mainz David Schneider, Stanford University

Applying ecological immunology Lena Bayer-Wilfert, University of Essex Astrid Groot, University of Amsterdam Dino McMahon, Free University Berlin Brian Weiss, Yale University Ken Wilson, University of Lancaster

We are looking forward to welcoming you at the Ecological Immunology Workshop 2017.

Kind regards,

Organizing Committee Jens Rolff, Free University of Berlin Oliver Otti, University of Bayreuth Paul Schmid-Hempel, ETH Zurich Magdalena Nagel, Free University

of Berlin

If you have any questions concerning the meeting please do not hesitate to e-mail us: oliver.otti@uni-bayreuth.de (program) magdalena.nagel@fu-berlin.de (travel and registration)

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

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

web: Otti's homepage < http://www.bayceer.uni-bayreuth.de/toek1/de/mitarbeiter/mit/mitarbeiter_detail.php?id_obj=106154 >

Ecological Immunology Meeting 2017 in Blossin < <http://rolffevolution.net/ecological-immunology-workshop-2017/> >

Oliver Otti <oliver.otti@uni-bayreuth.de>

Chize France EcologyBehaviour Jun19-23

The “Rencontres Ecology & Behaviour” Association is glad to announce the 13 th edition of the international « Ecology & Behaviour » meeting, from 19th to 23rd June 2017 in the “Centre d’Etudes Biologiques de Chizé”, France.

This is a week conference for international early career scientists in animal ecology and behaviour (only PhD students and post-docs can apply).

If you are interested, submission of applications is opening until the 19th March 2017 on the website: <https://eb2017.sciencesconf.org> < <https://eb2017.sciencesconf.org> >

Regards,

Sophie Dupont - Communication Manager for the “Rencontres Ecology & Behaviour” Association sophie.dupont@cebc.cnrs.fr

sophie.dupont93@gmail.com

CityULondon MathModelsEvolution Jul10-12

Mathematical Models in Ecology and Evolution 10th - 12th July 2017: CALL FOR ABSTRACTS AND REGISTRATION IS OPEN

City, University of London will be hosting the 6th conference in the bi-annual series on Mathematical Models in Ecology and Evolution. Mathematical Modelling plays a central and increasingly important role in ecology and evolution. The object of this conference is to showcase the latest developments of mathematical models in ecology and evolution and to demonstrate its important role to a new generation of researchers.

The Organising Committee are calling for both talk and poster abstracts. Submissions should be no more than 150 words and should include a topic title, along with a full description. Submissions should be made using the online submission form by 15th March 2017.

Registration for the conference is also now open. Early bird tickets for the conference are available until 1st June 2017.

For abstract submission, registration and other information please visit the conference website <http://www.city.ac.uk/MMEE2017> “Broom, Mark” <Mark.Broom.1@city.ac.uk>

Colombia EvoDevo Oct9-13

On behalf of the organizing committee of the Latin American Society of Developmental Biology (LASDB) Meeting it is our pleasure to invite you to the IX LASDB meeting to be held in Medellín, Colombia from October 9th - 13th, 2017. The Meeting will convene in Colombia for the first time, a megabiodiverse country at the core of the Americas.

Abstract submission deadline and early bird registration: May 3 2017

Topics in the plenary sessions include:

- Animal and plant developmental biology
- Stem cells, Neurobiology, Medicine and Development

- Post-embryonic development and regeneration
- Evo-Devo and Next Generation Sequencing
- Confirmed speakers include:
- Nobel Awardee
- Sir John Gurdon, Gurdon Institute, UK; University of Cambridge
- The stability and reversal of cell differentiation
- Karen Sears, University of Illinois, USA
- >From genome to phenome: The developmental basis of mammalian variation
- Enrique Amaya, The University of Manchester, UK
- Reactive oxygen species as facilitators of embryonic development and appendage regeneration
- Maria Barna, Stanford University, USA
- Bio-imaging of tissue patterning and cellular communication during embryonic development
- Jeremiah Smith, University of Kentucky, USA
- Developmentally programmed rearrangement of the lamprey genome
- Sylvain Marcellini, Universidad de Concepción, Chile
- Evolution of the vertebrate skeletogenic programme
- Siobhan Brady University of California Davis, USA
- Spatiotemporal regulation of root development
- Fernando Camargo, Boston Children's Hospital, USA
- Adult stem cell biology, organ size regulation and cancer
- Joseph Arboleda-Velasquez, Schepens Eye Research Institute, USA
- Molecular methods for the diagnosis and treatment of cerebral Ischemic Small-Vessel Disease
- Jesus Chimal-Monroy, Universidad Nacional Autónoma de México
- Digit patterning is controlled by an antagonism between retinoic acid and TGF beta
- Miltos Tsiantis, Max Planck Institute for Plant Breeding Research, Germany
- How crucifer leaves got their leaflets
- Karen Echeverri, University of Minnesota, USA
- Molecular mechanisms of regeneration in axolotls
- Randall Voss, University of Kentucky, USA.
- Genetic and Genomic Analyses of Tissue Regeneration Using a Model Salamander (*Ambystoma mexicanum*)
- Rodrigo Nunes da Fonseca, Universidade Federal do Rio de Janeiro, Brazil
- Evolution of early embryonic patterning in arthropods
- Miguel Concha, Laboratory of Experimental Ontogeny, Chile
- Novel roles for extra-embryonic tissue in directing early embryo morphogenesis in vertebrates.
- Patrizia Ferretti, University College London, Institute of Child Health, UK
- Regeneration of complex body structures in vertebrates.
- Robb Krumlauf, Stowers Institute for Medical Research, USA
- Hox genes: Regulating the balance between pluripotency and differentiation
- Veronica Di Stilio, University of Washington, USA
- The ABC model of flower Development in non-core eudicots
- Brigitte Galliot, Université de Genève, Switzerland
- Hydra, a model for regenerative and aging studies
- Marianne Bronner, Caltech, USA
- Gene regulatory control of neural crest development
- Vivian Irish, Yale University, USA
- Petal development: a twist in fate
- Hernan Lopez Shier Helmholtz Zentrum München
- Multicellular self-organisation during organ repair
- Luis Alfredo Cruz Ramirez, CINVESTAV. Langedio, Mexico
- Molecular circuits controlling plant stem cell niches
- Igor Schneider, Universidade Federal de Pará, Brazil
- Evolutionary origins of vertebrate appendage regeneration program
- Lee Niswander, University of Colorado, USA
- Visualizing neural tube closure and uncovering the causes of neural tube defects
- Carole La Bonne, Northwestern University, USA
- Stem Cells, Gene Regulatory Networks and the Evolution of Vertebrates
- Robert Reed, Cornell University, USA
- Developmental genetic basis of butterfly wing pattern evolution
- Robert Sablowski, John Innes Centre, UK
- Coordination between cell growth, cell cycle and organo-

genesis in plants

Maria Angela Nieto, Instituto de Neurociencias, Alicante, Spain

Epithelial plasticity in health and disease

Jose Garcia-Aranda, University of Puerto Rico, Rio Piedras

Understanding regeneration; a visceral reaction

Cristina Ferrandiz Instituto de Biología Molecular y Celular de Plantas, UPV, CSIC, Spain

A stylish story of carpel evolution

Claudia Torres Farfán, Universidad Austral de Chile

Development and Chronobiology

Roberto Mayor, University College London, UK

Integrating physical and molecular forces during collective cell migration

Katia del Rio-Tsonis, Miami University, USA

Epigenetic signatures during chick retina regeneration

Alejandro Sanchez Alvarado, Stowers Institute for Medical Research, USA

The Developmental plasticity of planarians

Joachim Wittbrodt, Centre for Organismal Studies Heidelberg, Germany

Vertebrate eye and brain development and regeneration

— / —

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>

Edinburgh RNApathwayEvolution Mar10

Dear Evoldir,

I think this symposium will be of interest to some of you (and registration is free!)

*** Information transmission in small RNA pathways: Mechanisms and consequences ***

When: Friday 10 March 2017 Where: Royal Society of Edinburgh, George Street, Edinburgh

Registration: <https://small-rna-pathways.eventbrite.co.uk> This one-day symposium aims to stimulate discussion between researchers working on different aspects of small-RNA biology. This includes both molecular biologists and evolutionary biologists interested in small-RNA mechanisms in disease and life-history contexts.

The theme of “information transmission” has been chosen to include the transmission of information through the pathways themselves (interaction or coevolution between small RNAs and their targets, target recognition), transmission in space by small-RNA transport (between tissues or between hosts and parasites), or transmission of information in time, either within-individuals (‘memory’) or between individuals (mother to offspring).

Plenary Speakers: * Prof. Shou-Wei Ding * Prof. Sir David Baulcombe FRS

Confirmed Speakers: * Antony Jose (University of Maryland) * Peter Sarkies (MRC London Institute of Medical Sciences) * Maria Carla Saleh (Institut Pasteur, Paris) * Carine Meignin (IBMC, Strasbourg) * Herve Vaucheret (INRA) * Friedrich Kragler (Max Planck Institute of Molecular Plant Physiology)

The meeting will be held at the Royal Society of Edinburgh on 10 March 2017

Registration will open at 9 am, and the opening plenary will start at 9.30 am. The meeting will close with an informal buffet and drinks starting at 5.50pm.

The meeting is free to attend, including lunch and coffee, but please register at <https://small-rna-pathways.eventbrite.co.uk> There will be poster sessions during the breaks and lunch, and if you wish to bring a poster (A0 portrait) please include the poster title and a brief (50 word) summary when you register.

On behalf of the organisers: Amy Buck and Darren Obbard

a.buck@ed.ac.uk; darren.obbard@ed.ac.uk

Centre for Immunity, Infection and Evolution University of Edinburgh Ashworth Laboratories Charlotte Auerbach Road Edinburgh EH9 3FL 0131 651 3688

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

“darren.obbard@ed.ac.uk” <darren.obbard@ed.ac.uk>

Gothenburg BioSyst Aug15-18

BioSyst.EU represents European scientists dealing with topics of systematic biology.

The third meeting of the BioSyst.EU will be organised by the Swedish Systematics Association in corporation with the University of Gothenburg and will be held August 15-18, 2017 at the Wallenberg Conference Centre, Gothenburg, Sweden.

The meeting will feature half-day symposia held by member societies of BioSyst.EU and external organisations as well as open sessions with mixed presentations.

More information on the meeting, and registration forms, are available at the following sites:

www.biosyst.eu www.conferencemanager.se/-BiosystEU2017
 “Catarina.Rydin@su.se”
 <Catarina.Rydin@su.se>

Gothenburg BioSyst Barcoding Aug15-18

Dear colleagues,

I would like to draw your attention to the upcoming BioSyst.EU conference in August 2017 in Sweden, Gothenburg, where we will organize a half-day symposium on “DNA-barcoding and the future of biodiversity monitoring”, with a special focus on metabarcoding approaches for biodiversity monitoring.

We are aiming at bringing together the experts on this topic and would like to cover as many aspects as possible in a balanced fashion - given the time limitation for approx. 1 plenary talk and 8 regular talks. There is of course room for poster contributions as well.

Registration for presentations closes at February 1st. It would be great if you let us know if you are interested in bringing the audience up to date with the latest findings from your field of research.

Application for presenters is done by sending an e-mail to

BioSyst2017abstracts@gmail.com.

The e-mail should contain the following information:
 -Which symposium you would prefer to be assigned to
 -The title of your presentation
 -If it is an Oral presentation or Poster
 -An abstract in either doc/pdf/txt-format.

Please find further details on the conference here:

<http://www.conferencemanager.se/BiosystEU2017/-start.html> <http://www.conferencemanager.se/-BiosystEU2017/speakers-and-symposia.html> Please apologize any cross-postings.

best, Matthias Geiger

Matthias Geiger <geiger@daad-alumni.de>

Groningen ESEB AgeingBiology Aug20-25

Dear Colleagues,

We are excited to invite you to submit abstracts and attend our ESEB2017 symposium [S5] on “*Evolutionary Biology of Ageing: integrating function and mechanism*”.

The symposium will take place at the 16th Congress of the European Society for Evolutionary Biology (ESEB), in Groningen, Netherlands, 20-25 August 2017. The deadline for abstract submission is *_January 10, 2017*_.

Less than a week left for abstract submission!!

To submit abstracts online, please go to: <http://www.eseb2017.nl/call-for-abstracts/> SYMPOSIUM DESCRIPTION: Ageing is an almost ubiquitous feature of living organisms but its evolution and mechanistic basis are still poorly understood. The rapid advances in our understanding of the molecular biology of ageing pose new challenges for our understanding of ageing evolution, and have created an urgent need for the integration of recent empirical insights with an evolutionary framework of senescence and lifespan. Thus the ambition of this symposium is to address the integration of function and mechanism in our understanding of the process and evolution of senescence, both from an empirical and a theoretical point of view. In addition, we aim for a perspectives paper by the organizers together with the speakers. Questions of interest include: Does the evolution of ageing depend on the mechanisms mediating senescence and death, and if so - how? Is the trade-off between reproduction and survival indispensable for our understanding of the biology of ageing? How important

are condition-dependent and true extrinsic mortality rates for the evolution of ageing? How and why do developmental processes and growth affect the evolution of senescence? What do state-dependent (i.e. sex-specific or caste-specific) ageing patterns tell us about ageing in general?

INVITED SPEAKERS (both confirmed): Russell Bonduriansky (UNSW, Sydney, Australia) Thomas Flatt (University of Lausanne, Switzerland)

ORGANIZERS: Alexei Maklakov (Uppsala) Ido Pen (Groningen) Simon Verhulst (Groningen)

Alexei A. Maklakov Associate Professor Animal Ecology/Department of Ecology and Genetics Evolutionary Biology Centre Uppsala University Norbyvägen 18D Uppsala, SE-752 36 Sweden

Tel: +46 18 471 2672 Fax: +46 18 471 6484

University lab page: <http://www.ieg.uu.se/animal-ecology/Research+groups/maklakov-lab> Our

Lab page: <http://alexeimaklakov.com> Google

Scholar: <http://scholar.google.com/citations?user=8aCng7oAAAAJ&hl=en&oi=ao> Research Gate:

https://www.researchgate.net/profile/Alexei_Maklakov

Alexei.Maklakov@ebc.uu.se

Groningen ESEB Cytonuclear Speciation Aug20-25

Dear Colleagues,

We encourage you to submit abstracts and attend our ESEB2017 symposium [S28] on “Intragenomic conflicts and cytonuclear incompatibilities as engines of speciation”

The symposium will take place at the XVI Congress of the European Society for Evolutionary Biology (ESEB), in Groningen, Netherlands, 20-25 August 2017. The deadline for abstract submission is January 10, 2017.

For abstract guidelines, please visit <http://www.eseb2017.nl/call-for-abstracts/abstract-guidelines>

SYMPOSIUM DESCRIPTION: This symposium is the result of merging two former independent proposals, “Intragenomic conflicts and speciation” and “The impact of mitonuclear incompatibilities on animal speciation”.

Conflicts between genetic elements within an individual for transmission into the next generation are increasingly

recognized as powerful drivers of evolutionary change. A by-product of the conflicts and their differential resolution can be negative epistatic interactions causing reduced fitness of hybrids and thus paving the way to speciation. Multiple genes involved in postzygotic reproductive isolation between recently diverged species have experienced bouts of adaptive evolution which cannot be easily linked to ecological selection, but which could result from intragenomic conflict (IC) and selection for its resolution. Also phenotypes of interspecific crosses experiencing asymmetric hybrid breakdown can often be linked to ICs. A major unresolved question is the relative role of ecologically based selection and selection due to ICs in the early stages of speciation. In this symposium we would like to bring together diverse experimental, comparative and theoretical perspectives on the subject.

Many different and essential molecular factories within the cell combine units contributed both by nuclear and organelle genomes. Notwithstanding the functional constraints that operate on those complexes, the independent control of the replication of those genomes anticipates challenging scenarios for the interplay of genetic conflicts, compensatory changes and molecular drive. Mitochondrial and plastid genome variation in natural populations have been traditionally considered as essentially neutral, and accordingly used during the last three decades to reconstruct the history of genetic lineages in a huge number of animal and plant species. Direct evidence of cytonuclear incompatibilities in wild populations is relatively common in plants, but definitely not in animals, which could be particularly hard to analyze in this respect. If mitonuclear incompatibilities in wild animal populations were finally unveiled, it would be necessary to revise the main conclusions of hundreds of papers dealing with phylogeographic patterns in animal species, published in the last 30 years, and the general role of the coevolution of nuclear and organelle genomes in speciation.

Organizers: Wieslaw Babik, Tracey Chapman, Radwan Jacek, Horacio Naveira, Antón Vila-Sanjurjo

Invited speakers: Daven Presgraves, Dan Mishmar —

Dr. Horacio F. Naveira Professor of Genetics GIBE (<http://www.udc.gal/grupos/gibe/index.html>) Center of Advanced Scientific Research (CICA) Department of Molecular and Cellular Biology Faculty of Sciences University of A Coruña Ro da Fraga 10 (Campus Zapateira) 15008 A Coruña, SPAIN

Tel. (34)881012047

horaci@udc.es

Groningen ESEB
GeneticExchangeMicrobesDisease
Aug20-25

Dear Colleagues,

We are excited to invite you to submit abstracts and attend our ESEB2017 symposium [S21] on “Genetic exchange in microbial adaptation and infectious disease”².

The symposium will take place at the 16th Congress of the European Society for Evolutionary Biology (ESEB), in Groningen, Netherlands, 20-25 August 2017. The deadline for abstract submission is January 10, 2017.

To submit abstracts online, please go to: <http://www.eseb2017.nl/call-for-abstracts/> SYMPOSIUM DESCRIPTION: Horizontal gene transfer (genetic exchange) plays a key role in microbial evolution. New insights into mechanisms and consequences of gene exchange, such as the contribution of phage-encoded genes to bacterial adaptation in the gut and CRISPR systems for bacterial immunity, are fundamentally changing our understanding of how the genetic variation that fuels evolution is created. Moreover, genetic exchange is central to the evolutionary biology of infectious disease. For example, antibiotic resistance alleles and virulence factors are often encoded on mobile elements such as plasmids. This symposium aims to bridge the gap between research on the basic evolutionary biology of genetic exchange and consequences for understanding the evolution and epidemiology of infectious diseases. We think this will make an exciting ESEB symposium because genetic exchange is a highly active field among theoretical and experimental evolutionary biologists, and its role in pathogen evolution is a clear example of how evolutionary biology can inform public health and medicine. The invited speakers are at the forefront of research on horizontal gene transfer, its role in evolution in general and in key contexts like antibiotic resistance. To minimize implicit bias in reviewing submitted abstracts we will use a blinding procedure.

INVITED SPEAKERS (both confirmed): Didier Mazel (Institut Pasteur, Paris, France) Alvaro San Millan (University of Oxford, UK)

ORGANIZERS: Jan Engelstädter (U Queensland) Alex Hall (ETH Zurich) Ellie Harrison (U York)

If you have any questions, please don't hesi-

tate to contact one of us (j.engelstaedter@uq.edu.au, alex.hall@env.ethz.ch or ellie.harrison@york.ac.uk). We hope to see you in Groningen later this year!

— Jan Engelstädter The University of Queensland School of Biological Sciences Brisbane, QLD 4072 Australia

phone: +61 7 336 57959
www.engelstaedterlab.org ”j.engelstaedter@uq.edu.au“
 <j.engelstaedter@uq.edu.au>

Groningen ESEB
GenomicsOfAdaptation Aug20-25

Abstract submission deadline: **Next Tuesday Jan 10**

Dear All,

We would like to invite abstract submissions for our upcoming symposium on the Genomics of Adaptation that will take place as part of the 16th Congress of the European Society for Evolutionary Biology (ESEB). The conference will take place from August 20th - August 25th, 2017 in Groningen, the Netherlands.

SYMPOSIUM DESCRIPTION: Genomics of Adaptation [S16] Model organisms for life-history research are mainly studied in the lab where functional genetics is assessable. In general, however, knowledge about their eco-evolutionary dynamics, such as biotic interactions, is rare. By contrast, in organisms for which the ecology and adaptation strategies in the field are well known, we typically lack the appropriate genetic tools to investigate functionality. Advances in genomics and statistics as well as investments in evolutionary model organisms are now providing access to putatively adaptive genome-wide variation within species from across the tree of life. In this symposium, we focus on integrating life-history biology, genetics and evolutionary ecology in the genomics era. We wish to (1) highlight the role of genetic architecture of complex traits, such as adaptations to biotic interactions or life-history traits; (2) contrast this to morphological traits which are generally thought to have a less complex genetic architecture; and (3) discuss the opportunities and drawbacks of specific model systems.

INVITED SPEAKERS (**updated**): Susan Johnston, University of Edinburgh (<https://susanejohnston.wordpress.com>) Peter Tiffin, University of Minnesota (<http://cbs.umn.edu/tiffin-lab/>)

ABSTRACT SUBMISSION The deadline for abstract

submission is this coming Tuesday January 10, 2017. For more information and to submit abstracts online, please visit: <http://www.eseb2017.nl/call-for-abstracts/> We look forward to an exciting symposium and seeing you all in Groningen!

Sincerely, Ben Blackman, UC Berkeley Maaïke de Jong, University of Bristol Bart Pannebakker, Wageningen University Noah Whiteman, UC Berkeley Jelle Zandveld, Wageningen University

Benjamin Blackman Department of Plant and Microbial Biology University of California, Berkeley 361 Koshland Hall Berkeley, CA 94720

Phone: 510.664.7807 E-mail: bkblackman@berkeley.edu Web: <http://nature.berkeley.edu/blackmanlab> "bkblackman@berkeley.edu" <bkblackman@berkeley.edu>

Groningen ESEB SexualSelection Aug20-25

Dear Colleagues,

We are excited to invite you to submit abstracts for ORAL and POSTER presentations and attend our ESEB2017 symposium [S12] on "Environmental effects on sexual selection".

<http://www.eseb2017.nl/sub/s12-environmental-effects-on-sexual/> The symposium will take place at the 16th Congress of the European Society for Evolutionary Biology (ESEB), in Groningen, Netherlands, 20-25 August 2017. <http://www.eseb2017.nl/home/> The deadline for abstract submission is January 10, 2017. To submit abstracts online, please go to: <http://www.eseb2017.nl/call-for-abstracts/> SYMPOSIUM DESCRIPTION [S12] Environmental effects on sexual selection

Sexual selection plays an important role in the evolution of novel traits and can both enhance and delay the rate of adaptation to changing environments. As for all other traits, the evolution of sexual traits depends on three factors: variation in trait expression, heritability of this variation, and the association of traits with reproductive output. However, specifically in the case of sexual selection environmental variation and selection pressures (mate choice and competition) can interact to shape the evolutionary dynamics of secondary sexual traits. It is currently widely debated how environmental change will affect sexual selection and, inversely, what the role

of sexual selection is in adaptation to a new environment. In a time of major environmental change, these questions are particularly important. We encourage submission of a diversity of studies (descriptive, experimental, theoretical) that address the influence of spatial or temporal variation of environmental conditions on the expression of sexual traits, their heritability, or their selective advantage. We aim to cover a wide range of methodological approaches, systems and modalities to facilitate a lively exchange about how to study and understand the magnitude of environmental effects on sexual selection.

INVITED SPEAKERS: Ulrika Candolin (Helsinki), Erik Svensson (Lund)

ORGANIZERS: Carlos Camacho, Karen de Jong, Katja Heubel, Jes os Martinez-Padilla, Jaime Potti

If you have any questions, please don't hesitate contacting one of us (jmartinezpadilla12@gmail.com, katja.heubel@uni-koeln.de, kjong@uni-koeln.de). We hope to see you in Groningen later this year!

Katja, Karen & Jes os

Dr. Katja Heubel, docent University of Cologne Institute for Zoology General Ecology Ecological Research Station Grietherbusch Grietherbusch 3a 46459 Rees-Grietherbusch phone: +49 2851-8130 GSM +49 173-8215997 email: katja.heubel@uni-koeln.de

"katja.heubel@uni-koeln.de" <katja.heubel@uni-koeln.de>

Groningen-Netherlands EvolutionMedicineSociety Aug18-21

February 15 is the deadline for abstract submission for The International Society for Evolution, Medicine & Public Health Third Annual Meeting August 18-21, 2017 in Groningen, Netherlands, in conjunction with the European Society for Evolutionary Biology (ESEB) meeting August 21-25.

Registration for both meetings will open in February.

Keynote speakers include Svante P  abo, Linda Partridge, Stephen Stearns, Marian Joels, Mervyn Singer, Sylvia Cremer, Francisco Ubeda, and Peer Bork.

Full information at <http://evolutionarymedicine.org> rmesse@gmail.com

Hawaii HistoryOfPacificMarineLife May23-25

Dear List

We invite abstract submissions for the GSA 2017 113th Annual meeting held at the Hawaiian Convention Center < <https://www.meethawaii.com/convention-center/> > in Honolulu. After the great success of ICRS 2016, we hope that you will come and share your research with us again on the beautiful island of O'ahu and enjoy the variety of activities including fieldtrips < <http://www.geosociety.org/GSA/Events/Section.Meetings/GSA/Sections/cd/-2017mtg/fieldtrips.aspx> > and courses < <http://www.geosociety.org/GSA/Events/Section.Meetings/GSA/Sections/cd/2017mtg/courses.aspx> > available.

Abstract Submission Deadline: 14th February 2017

Student travel grants and registration waivers are available.

*Theme Session T22: *Cenozoic Paleogeography, Paleogeography, and Evolutionary History of Pacific Marine Life < <https://gsa.confex.com/gsa/2017CD/top/-index.epl> >

This session will focus on all environmental and evolutionary aspects of the Cenozoic (66-0 Ma) history of marine life in the Pacific Ocean at all temporal and spatial scales. It will include studies employing evidence from paleoceanography as well as studies employing evidence from the modern fauna. Of particular interest are studies on the phylogeny of major taxa, paleoecological or evolutionary adaptations in a changing marine environment, and the influence of changes in seawater chemistry and temperature throughout the Cenozoic. Among other things, we welcome studies that include the reconstruction of the history or coral reef or molluscan communities. Paleobotany, molecular studies, and micropaleontology are all meant to be included.

Registration and abstract submission: Here! < <https://gsa.confex.com/gsa/2017CD/top/-papers/index.cgi?sessionid=42156&username=-291968&password=367139> >

23-25 May 2017 - Honolulu, Hawai'i USA

Hawai'i Convention Center, Honolulu, Hawai'i < <https://www.meethawaii.com/convention-center/> >

Important Deadlines

Abstracts Submission 14 February

Early Registration 17 April

Student Travel Application 17 April

Student Volunteer for Registration Waiver 17 April

Registration Cancellation 24 April

Hotel Reservation Rate 1 May

Please contact Steve or Sonia for further details about this session:

Principal organizer: Dr. Steven M. Stanley, stevenst@hawaii.edu

Co-organizer Dr. Sonia J. Rowley, srowley@hawaii.edu

Feel free to forward the following information to colleagues or students who might have an interest in participating in this session.

We look forward to seeing you there

Aloha

– Sonia J. Rowley PhD Postdoctoral Research Fellow University of Hawai'i at Manoa POST 713, 1680 East-West Road Honolulu, HI 96822 +1 808 348 6224

Research Affiliate - Bishop Museum Chief Science Officer - Assoc. Marine Exploration

Sonia Rowley <srowley@hawaii.edu>

Lund SexHermaphrodites Mar9-10 RegistrationOpen

Dear all,

We are happy to announce that 2017 SHOW meeting will be held in Lund, Sweden during 9 - 10th of March!

The meeting will take place in the Ecology building (Sölvegatan 37) which is located northeast of the city centre. It takes between 10-15 minutes to get there by bus from the centre, or 30 minutes by walking. The preliminary schedule for the meeting is:

Wednesday, 8th March: Informal meet-up at restaurant Inferno in downtown Lund
Thursday, 9th March: 9-12: talks 13-16: talks 16-17: poster presentations Evening: conference dinner at restaurant Hardings in Marieholm (town located close to Lund)
Friday, 10th March: 9-12: talks 13-15: workshop/group discussion 16: meeting closes

As usual, we will reserve the last session on Friday for discussion/workshop and we are grateful for suggestions and ideas for discussion topics, and thoughts on what the meeting should focus on.

The dinner venue is Hardings in Marieholm, a small town in the countryside, less than 20 minutes train ride from Lund. Since this involves additional travel expense (approximately 100 SEK return fee), we have decided to make the dinner optional. Thus, the registration fee without the conference dinner will be slightly less expensive (300 SEK) than with (450 SEK). Alcohol with dinner is purchased separately by cash or card - Hardings sells wine, cocktails, locally brewed beer, and has a decent selection of whiskey and rum. Tickets to and from Marieholm can easily be purchased at the time of travel or in advance through the SkÅ¥netrafiken app (Android: <https://play.google.com/store/apps/details?id=se.fskab.android.reseplaneraren&hl=en>, iPhone: <https://itunes.apple.com/se/app/skanetrafiken/-id310917083?l=en&mt=8>).

Travelling to Lund by airport is very convenient, since Kastrup airport (in Copenhagen, Denmark) is just across the bridge. Trains from Kastrup airport to Sweden depart every 20 minutes and takes around 40-50 minutes to Lund.

There are several places to stay in Lund, and most of them are located in the city center, like for example these two hotels: <http://www.concordia.se/en.aspx> <https://www.elite.se/en/hotels/lund/hotel-bishops-arms> and this hostel: <http://www.winstruphostel.se/>. Another option would be to stay closer to the Ecology building where the meeting is held, at Hotel Ideon: <https://www.elite.se/en/hotels/lund/hotel-ideon/>. Please make your own reservation at your preferred hotel/hostel.

If you like to attend, please reply with the information in the registration form below. The deadline registration is February The small registration fee (450 SEK with conference dinner, 300 SEK without) can be paid in cash on arrival or by bank transfer to Jessica Abbott, and will cover food and drinks during the meeting.

SHOW 2017 REGISTRATION

First name: Last name: Institutional address: Email: Tel:

Do you want to give a talk? YES / NO If yes, please provide a preliminary title:

Do you want to bring a poster? YES / NO If yes, please provide a preliminary title:

I would like to attend the conference dinner: YES / NO

If yes, meal preference: Pork / Chicken / Vegetarian

Special dietary requirements:

Preferred method of payment: Cash / Bank transfer

Finally, please feel free to forward this email to others not on the email list who you feel might be interested in attending the SHOW.

We look forward to seeing you in Lund soon!

All the best,

Jessica, Åsa and Anna

- Dr. Jessica K. Abbott Department of Biology Section for Evolutionary Ecology Lund University Sölvegatan 37 223 62 Lund, Sweden Phone: 046 222 9304 Website: <http://jessicakabbott.com> "It is those who know little, and not those who know much, who so positively assert that this or that problem will never be solved by science." - Charles Darwin, Descent of Man

Jessica Abbott <jessica.abbott@biol.lu.se>

LundU SwedishOikos2017 Feb7-9 RegistrationClosing

The last day to register for Oikos 2017 is Monday January 16th. Don't miss this opportunity to meet ecologists and evolutionary biologists from throughout Sweden!

Register here: <http://oikos2017.event.lu.se/registration>

The Swedish Oikos Congress 2017 will take place 7th - 9th February 2017 in Lund. Venue for the meeting will be Paleastra, in the heart of the city. A conference dinner will be held on the evening of February 8th, and there will be pre-congress workshops on Monday February 6th. The meeting is open to all ecologists and evolutionary biologists regardless of subdiscipline, and we have a wide breadth of talks and plenaries!

- Dr. Jessica K. Abbott Senior University Lecturer Department of Biology Section for Evolutionary Ecology Lund University Sölvegatan 37 223 62 Lund, Sweden Phone: 046 222 9304 Website: <http://jessicakabbott.com> "It is those who know little, and not those who know much, who so positively assert that this or that problem will never be solved by science." - Charles Darwin, Descent of Man

Jessica Abbott <jessica.abbott@biol.lu.se>

**Marseilles 21st Evolutionary Biol
Sep26-29 EarlyDeadLine**

Dear all , the early dead line for the 21st evolutionary biology meeting at Marseilles (September 26-29 2017) is January 31.

more info :aeeb.fr

best regards

Pierre

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

**Marseilles EBM21 Sep26-29
EarlyDeadlineTopics**

Dear all , the early dead line for the 21st evolutionary biology meeting at Marseilles (September 26-29 2017) is January 31.

The following subjects will be discussed:

* Evolutionary biology concepts and modeling; * Biodiversity and Systematics; * Comparative genomics and post-genomics (at all taxonomic levels); * Self non Self Evolution * Holobiome evolution * Environment and biological evolution; * Origin of life and exobiology; * Non-adaptative versus adaptative evolution; * The « minor » phyla: their usefulness in evolutionary biology knowledge; * Convergent evolution * Evolution of complex traits (Evo-Devo)

more info :aeeb.fr

best regards

Pierre

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

**Moscow ICIM Aug18-23
OldSpecimensNewTechnology**

Dear colleagues,

We welcome contributed talks in our symposium “Morphological Lazarisation: when new technology brings life to historical specimens” at the International Congress on Invertebrate Morphology in Moscow this August, 18th-23rd. Museum specimens remain an invaluable part of our work and are often of stunning quality, even in comparison with more recently obtained material. We want to celebrate this, and the development of modern techniques which help us bring these specimens back to new life.

We realise that there may be certain political and personal concerns associated with attending this year’s conference, and we want to reassure you that we understand these concerns. Your support of science without borders is very important to us and the International Society for Invertebrate Morphology, to our host committee in Moscow and to the wider community, so we hope that you will join us this summer to celebrate research with our colleagues in Russia. Registration and abstract submission are now open! Please do register when possible - there are just two weeks left before the early bird deadline.

All presenting authors can submit one oral and one poster abstract. Please do encourage others in your labs and networks to submit content for the symposium - we would be delighted to have other researchers, at any career stage, join us.

A quick breakdown of the various upcoming deadlines: www.icim4.com 1st February = Early bird registration deadline. Early bird registration is 250 EUR, increasing to 280 EUR. Note that to request an invitation letter for your visa application, you will need to complete the necessary boxes in the registration form (marked ‘for visa support’).

31st March = Manuscript deadline for publication in Invertebrate Zoology. If you wish to submit a manuscript related to the symposium, the deadline for submissions is coming up at the end of March. See here for more information.

30th April = Abstract and registration deadline. Note that to request an invitation letter for your visa application, you will need to complete the necessary boxes

in the registration form (marked 'for visa support').

Regarding visas, we recommend that all speakers complete their applications as soon as possible after receiving their letter of invitation. There are further guidelines available here on the ICIM website. www.icim4.com Finally, we are collecting examples of new discoveries made using historic specimens. If you have or know of a particularly interesting example, we would love to hear about it!

Best wishes for the coming months,

Lauren Sumner-Rooney and Julia Sigwart

"j.sigwart@qub.ac.uk"

NHM London Evolution Colour And Vision Apr27

Dear Colleagues,

The Natural History Museum (London, UK) together with the Malacological Society of London is hosting a symposium, "Molluscan Colour and Vision" to be held on the 27th of April 2017 at the Natural History Museum.

The phylum Mollusca is highly speciose and is the largest phylum in the marine realm. Many species are brightly coloured and patterned and yet nearly all molluscs are thought to be colour blind. Despite their limitations with colour vision, molluscs showcase a myriad of different eye types, many of which are unique in the animal kingdom. In this symposium speakers will cover a range of topics that highlight the extraordinary nature of colour and vision in molluscs.

Schedule 1030-1100: Registration 1100-1110: Introduction and welcome 1110-1130: Jakob Vinther: Fossil colour and molluscan evolution. 1130-1220: Daniel Speiser: The function and evolution of highly-dispersed visual systems in molluscs. 1220-1240: Trevor Wardill: Neural control of squid skin iridescence and its potential role for communication. 1240-1400: MSL AGM 1400-1450: Sönke Johnsen: Tricks of light, mirror, and color: The beautiful camouflage of pelagic cephalopods. 1450-1510: Lauren Sumner-Rooney: The repeated evolution of eye loss in deep-sea solariellid gastropods. 1510-1530: Marcel Koken: New lights on biodiversity: natural fluorescence. 1530-1600: Tea and coffee. 1600-1620: Suzanne Williams: Identification of pigments and genes contributing to shell colour in a marine snail. 1620-

1640: Nick Roberts: Seeing the world in a different light - polarization vision in cephalopods. 1640-1700: Angus Davison: Cepaea colour polymorphism - why and how do snails vary in their shell colour and banding? 1700-1720: Alexander Arkhipkin: Coevolution in body coloration and camouflage in cephalopods and fish. 1720-1730: Wrap up and thanks 1730-1900: Wine reception

Registration The meeting is free but registration is necessary.

Please register by sending an email to the automated account MSL-events@nhm.ac.uk. You will receive a bounce back message to say that you have successfully registered. Please do not send queries to this account. Each participant must register in a separate email.

Speakers Daniel Speiser, University of South Carolina <http://www.biol.sc.edu/daniel-speiser> Sönke Johnsen, Duke University <http://sites.biology.duke.edu/-johnsenlab/> Jakob Vinther, University of Bristol http://www.jakobvinther.com/Front_page.html Lauren Sumner-Rooney, Museum für Naturkunde, Berlin https://www.researchgate.net/profile/Lauren_Sumner-Rooney Nick Roberts, Bristol University <http://www.ecologyofvision.com/> Trevor Wardill, University of Cambridge <http://www.pdn.cam.ac.uk/directory/-trevor-wardill> Angus Davison, University of Nottingham <http://www.angusdavison.org/> Alexander Arkhipkin, Falkland Islands Fisheries Department <http://south-atlantic-research.org/our-people/research-fellows/66-sashaarkh> ipkin

Marcel Koken, Centre National de la Recherche Scientifique https://www.researchgate.net/profile/-Marcel_Koken Suzanne Williams, Natural History Museum <http://www.nhm.ac.uk/our-science/departments-and-staff/staff-directory/suzanne-williams.html>

Dr Suzanne Williams Dept of Life Sciences Natural History Museum Cromwell Rd London SW7 5BD United Kingdom Tel: + 44 (0) 207 942 5351

<http://www.nhm.ac.uk/research-curation/staff-directory/zoology/s-williams/index.html>

"s.williams@nhm.ac.uk" <s.williams@nhm.ac.uk>

Paris EvolutionSymbiosis Mar15-17

The Institute of Biology Paris-Seine (IBPS, Université Pierre et Marie Curie, Paris) is organizing its annual international symposium on the biology of symbiosis.

During the three days of the conference, 18 French, European and North-American scientists will present their work in four main sessions:

§Symbiosis in our environment and within several species (gorilla, chimp, worm...) §Symbiotic interactions during the immune response in infectious diseases (malaria, dengue virus...) §Evolution, modelling and biology of symbiosis §The importance of the microbiota in human health (metabolic diseases, neurologic troubles, obesity...)

Speakers : Antoine Danchin - ICAN, Paris, France à Nicole Dubilier - MPI -Bremen, Germany à Colombar de Vargas - Roscoff Station, France à Eric Baptiste - IBPS, Paris, France à Howard Ochman - Texas University, Austin, USA à Marc-André Sélosse - MNHN, Paris, France à Bruno Lemaître - EPFL, Lausanne, Switzerland à Georges Dimopoulos - Johns Hopkins University, Baltimore, USA à Louis Lambrechts - Pasteur Institute, Paris, France à Philippe Sansonetti - Pasteur Institute, Paris, France à Jan Sapp - York University, Toronto, Canada à Jeroen Raes - Catholic University of Leuven, Belgium à Nancy Moran - Texas University, Austin, USA à Jens Nielsen - Gothenburg University, Sweden à Karine Clément - ICAN, Paris, France à Sven Pettersson - Karolinska Institute, Stockholm, Sweden - Nanyang Tech. University, Singapore à Michel Neunlist - Nantes University, France

Venue: March 15-17, 2017 Amphitheater Durand, Esclançon building, Jussieu Campus, 4 place Jussieu, 75005, Paris

Registration open here on November 15th: <https://symbiosis.sciencesconf.org> Symposium announcement page: <http://www.ibps.upmc.fr/en/news-events/events/ibps-symposium-symbiosis> Contact: ibps.comm@upmc.fr

Philippe Lopez <philippe.lopez@upmc.fr>

Paris Holobionts Apr19-21 RegistrationExt

Dear colleagues,

Registration for the International Conference on Holobionts, Paris April 19-21, 2017 is extended to Feb. 15th.

For more information and details about this event, please visit the conference website at <https://-symposium.inra.fr/holobiont-paris2017/>. Please, do not hesitate to diffuse this announcement to interested colleagues. Thanks. Best regards

Jean-Christophe SIMON

Please note my new email address: jean-christophe.simon@inra.fr

Jean-Christophe SIMON UMR 1349 INRA/Agrocampus Ouest/Université Rennes 1 Institut de Génétique, Environnement et Protection des Plantes (IGEPP) Domaine de la Motte - 35653 Le Rheu Cedex - France

phone: +33 (0)2 23 48 51 54 fax: 33 (0)2 23 48 51 50 web site IGEPP : <http://www6.rennes.inra.fr/igepp> Jean-Christophe Simon <jean-christophe.simon@inra.fr>

PorquerollesIsle France MathEvolBiol Jun12-16 2

MCEB - Mathematical and Computational Evolutionary Biology 12-16 June 2017 - Porquerolles Island, South of France.

Webpage: <http://www.lirmm.fr/mceb2017/> Pre-registration deadline: February 26th

Notification to applicants: March 17th

Final list of attendees: April 17th

Registration page : <http://www.lirmm.fr/mceb2017/-register.php> Scope: Mathematical and computational tools and concepts form an essential basis for modern evolutionary studies. The goal of the MCEB conference (at its 9th 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 "Methods for integrative evolutionary biology: various sources of data, various scales of evolution", which includes the analysis of heterogeneous data (molecular, phenotypic, ecological...), different time scales (from recent times to the origin of life), different spatial scales (from local to worldwide range), the combination of phylogenetics and population genetics, multidisciplinary approaches, etc.. 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 Hyeres, in the South of France, 12-16 June 2017.

Cost: Conference fees including accommodation for four nights, meals, coffee breaks, etc., will be around 450euro, all inclusive. PhD students and postdocs would benefit of financial support.

Keynote speakers:

Elizabeth Allman (Department of Mathematics and Statistics, University of Alaska Fairbanks) <http://www.dms.uaf.edu/%7Eeallman/> Guy Baele (Rega Institute / KU Leuven - Evolutionary and Computational Virology Section) <https://rega.kuleuven.be/cev/ecv/lab-members/GuyBaele.html> Stephane Dray (Laboratoire de Biometrie et Biologie Evolutive (LBBE), Lyon) <http://pbil.univ-lyon1.fr/members/dray/cv.php>

Barbara Holland (Theoretical Phylogenetics Group, School of Mathematics and Physics, University of Tasmania) <http://www.maths.utas.edu.au/People/Holland/> Anna-Sapfo Malaspinas (Institute of Ecology and Evolution, University of Bern) http://www.cmpg.iew.unibe.ch/about_us/team/researchers/-ass_prof_dr_mala spinas_anna_sapfo/index_eng.html

Yun Song (Calabi-Simons Chair in Mathematics and Biology, Departments of Mathematics and Biology, University of Pennsylvania) <http://www.sas.upenn.edu/~yss/>

Marc Suchard (David Geffen School of Medicine at UCLA, Departments of Biomathematics, Biostatistics and Human Genetics) <http://faculty.biomath.ucla.edu/~msuchard/> For more information, visit the website at: <http://www.lirmm.fr/mceb2017/> Please forward this announcement!

Olivier GASCUEL <olivier.gascuel@pasteur.fr>

Portland Evolution ASN SensoryDrive Jun23-27

The American Society of Naturalists is seeking 5-minute lightning talks for a Spotlight Session at the Evolution2017 meetings dedicated to the topic of '25 Years of Sensory Drive?'. In 1992, the American Naturalist published a supplemental issue on the topic of 'Sensory Drive' organized by John Endler.? This issue featured a number of influential papers that emphasized the role of the environment, phylogenetic history, and development on the evolution and functioning of sensory systems. This supplement introduced many ecologists and evolutionary biologists to the intriguing and well-developed topic of sensory ecology.? In this spotlight session, we will consider the role of sensory drive as a guiding framework in ecological and evolutionary studies of communication systems over the past 25 years, and the extent to which it serves as a useful framework going forward.

The format of Spotlight Sessions is the following: 1 15-minute talk 3 5-minute lightning talks 1 15-minute talk 3 5-minute lightning talks 1 15-minute talk

Confirmed Speakers include Molly Cummings (University of Texas at Austin) and Leo Fleishman (Union College). People who give 5-minute lightning talks may also give a 15-minute talk in a regular session. We seek speakers from a diversity of institutions and career stages (including graduate students).

Those interested in participating should e-mail Becky Fuller (fuller@life.uiuc.edu) by February 1, 2017.

"fuller@life.illinois.edu" <fuller@life.illinois.edu>

Portland SSE MaleCompSpeciation Jun23-27

Spotlight Symposium - Evolution Portland 2017

Conference: Portland.SSE_MaleComp&Speciation.Jun23-27

Sexual selection via male competition and the process of speciation

I am organizing a special Spotlight Symposium for this year's Evolution meeting in Portland, focused on the role of male competition in speciation. The meeting takes place June 23-27, 2017 in Portland Oregon.

The role of sexual selection in speciation remains controversial, despite the last two decades of intensive work. The importance of male competition has been almost entirely ignored, as nearly all the work focuses exclusively on how female preferences generate sexual selection in ways that hinder gene flow. This is despite that ecological competition over resources plays a central role in speciation via natural selection, and that male competition can generate very strong selection. However, recent work suggests that incorporating both male competition and female choice into research on speciation can help resolve the controversy over whether and when sexual selection causes speciation, prevents it, or has no real effect. Male competition sometimes complements and other times opposes female choice, which can either accelerate or put a brake on the speciation process, or lead to asymmetries in gene flow. Another complexity is that males compete both before and after copulation through sperm competition or the analogous pollen competition in plants; including this component can draw interesting parallels between animal and plant speciation.

I invite submissions for 5 minute 'Lightning Talks' that present perspectives from behavior, ecology, and evolution in an explicitly evolutionary framework with direct connections to speciation research.

Here's the low-down on Spotlight Sessions from the meeting organizers:

"Spotlight Sessions are more focused than a typical session and have a different format. First, the talks are solicited in advance. Second, each of the six Spotlight Sessions will consist of 3 standard 15-minute talks interspersed with sets of lightning (5-min) talks. We chose this format by the logic that having several high-profile researchers "anchoring" a session on a specific topic with a 15-minute talk will make it more valuable for relatively junior researchers to give a 5-minute talk in a focused session with the right target audience and other relevant and well-known speakers rather than giving a 15-minute talk in a regular session."

Being part of this symposium can highlight your work in this up-and-coming field in context with others interested in similar topics. You get to help pave the way for this new type of symposium at an awesome meeting in the fun city of Portland. Unfortunately, the society cannot compensate your expenses for participating in this symposium.

Please contact me at boughman@msu.edu before Jan-

uary 31, 2017 to indicate your interest in the symposium and send an abstract. Also feel free to contact me if you have questions. I will let you know whether you're selected by March 15, well in advance of the April 15, 2017 early registration discount application deadline. If selected for this Spotlight Session, you will register accordingly on the website. Best wishes to you!

Jenny Boughman

Janette Boughman

Integrative Biology Ecology, Evolutionary Biology & Behavior Program BEACON Center for the Study of Evolution in Action Michigan State University East Lansing MI 48824

boughman@msu.edu

<https://www.msu.edu/~user/boughman/index.html>

<https://www.msu.edu/~user/boughman/index.html>

Jenny Boughman

<boughman@msu.edu>

Portland SSE SexInTheWild Jun23-27

Hi everyone,

I am writing to solicit applications from junior researchers for a 5-minute talk in a "Spotlight Symposium" that, as an Associate Editor at *Evolution*, I am organizing on a topic of my choice for the Society for the Study of Evolution meetings in Portland, OR, June 23-27, 2017. Here is how Spotlight Sessions are described by the meeting organizers:

"Spotlight Sessions are more focused than a typical session and have a different format. First, the talks are solicited in advance. Second, each of the six Spotlight Sessions will consist of 3 standard 15-minute talks interspersed with sets of lightning (5-min) talks. We chose this format by the logic that having several high-profile researchers "anchoring" a session on a specific topic with a 15-minute talk will make it more valuable for relatively junior researchers to give a 5-minute talk in a focused session with the right target audience and other relevant and well-known speakers rather than giving a 15-minute talk in a regular session."

My topic idea is "Sex in the Wild", which will focus on exciting work relevant to the evolution/maintenance of reproductive mode polymorphism in non-model organisms and/or using field-based approaches to study sex (and its alternatives) in natural populations. It seems like a great opportunity to highlight this rela-

tively rare type of research, which is absolutely critical to the study of sex but is often neglected in favor of laboratory and/or model organism-focused studies.

The only problem is that we have no means to offset travel or meeting costs, so I can't offer anything to the speakers besides a spot in an exciting new type of symposium featuring awesome speakers at a great meeting in a very fun city.

Please contact me (maurine-neiman@uiowa.edu) by Jan. 31, 2017 if you're interested in being considered for a 5-minute talk and/or if you have any questions. I will let you know whether you're selected by March 15, well in advance of the April 15, 2017 early registration discount application deadline. If selected for this Spotlight Session, you will register accordingly on the website. You can also sign up for a regular talk, along with your Spotlight talk, if you'd like to do so.

All best wishes for 2017! Maurine Neiman

Maurine Neiman Associate Professor Department of Biology University of Iowa 143 BB, Iowa City IA, 52242, USA maurine-neiman@uiowa.edu <http://www.biology.uiowa.edu/neiman/> "Neiman, Maurine" <maurine-neiman@uiowa.edu>

Portland SSE Speciation Jun23-27

I am excited to solicit applications for 5-minute "lightning talks" for a Spotlight Session on "Speciation with and without sex chromosomes" to be held at the upcoming SSE conference in Portland OR, June 23-27, 2017.

Session description: Studies of the genetics of speciation frequently focus on sex chromosomes. In fact, the "two rules of speciation" (Coyne & Orr 1989) are both based on sex chromosomes. In this symposium we address how sex chromosomes affect speciation and explore how speciation mechanisms may be different in the wide diversity of taxa lacking sex chromosomes.

This is a new format for SSE and each Spotlight Session will include three standard 15-minute talks interspersed with six 5-minute talks. Unfortunately, there are no funds to offset travel or meeting costs. Those who give 5-minute Spotlight talks will also be permitted to register for a 15-minute talk in a regular session.

Confirmed 15-minute spotlight speakers: Suzanne Edmands (University of Southern California), Norman

Johnson (University of Massachusetts, Amherst), Nicole Valenzuela (Iowa State University)

If you are potentially interested in giving a 5-minute talk in this session, please contact me (sedmands@usc.edu) by Jan 31, 2017. I will let you know if you are selected by March 15 and you would then register on the SSE website (early registration deadline is April 15, 2017).

All the best,

Suzanne Edmands

– Suzanne Edmands Professor Department of Biological Sciences 3616 Trousdale Parkway, AHF 316 University of Southern California Los Angeles, CA 90089 (213)740-5548 <http://dornsife.usc.edu/labs/edmands/edmandss@gmail.com>

Shanghai IUFROGeneticsGenomics Nov1-3

We are pleased to invite you to join us November 1-3, 2017 at the IUFRO special working group on Fagaceae and Nothofagaceae genetics and genomics to be held at the beautiful ChenShan Botanical Garden in Shanghai, China. —Mark your calendars and make plans to participate as this exciting meeting will bring together the latest results and insights from several large collaborative genomic studies led by teams on several different continents!

Meeting dates: Nov 1-3, 2017.— We will be scheduling pre and post-meeting tours locally in Shanghai and in the surrounding provinces as well as in Yunnan, satisfying both cultural and fagaceous interests.— We will also be organizing genomic analysis and ex-situ conservation workshops associated with the meeting.— This meeting is being jointly organized by the Chen Shan Botanical Garden and The Morton Arboretum's Center for Tree Science.

Venue: ChenShan Botanical Garden, Shanghai, China.—The CSBG is a comprehensive botanical garden with strong scientific content and beautiful garden landscapes, integrating scientific research, popularization of science, landscape and leisure, co-constructed by Shanghai Municipal People's Government, the Chinese Academy of Sciences and the State Forestry Administration.— Officially launched in March 2007, the Garden was fully open on January 23, 2011.— More information about the CSBG can be found at the following link: —<https://www.bgci.org/garden.php?id=4544> . Confirmed speakers

ers: Christophe Plomion (NRA), Antoine Kremer (INRA), Jeannine Cavender-Barres (U Minnesota), Victoria Sork (UCLA), Jeanne Romero-Severson (Notre Dame), Andrew Hipp (Morton), Chuck Cannon (Morton), Sean Hoban (Morton), Xiao-Yong Chen (East China Normal Univ), Ye Sun (South China Ag Univ).

Website for registration and abstract submission will be active by Feb 15, 2017 and a subsequent announcement will be made inviting you to visit the site.

lscher@mortonarb.org

UExeter FishPopulations Jul3-7

The FSBI celebrates its 50th Anniversary in 2017, and to commemorate this landmark we are delighted to announce an International Symposium covering many aspects of fish biology under the broad theme of Understanding Fish Populations, to be hosted at the University of Exeter, UK, 3-7 July 2017.

Included under this broad and diverse overarching subject are multiple sub-themes relating to the fields of evolutionary biology, and we welcome you to join us in presenting research on:

1. Biology of Fish: from the Individual to Populations + Genes, genomes and epigenomes
2. Fish in a Changing World + Evolutionary adaptations
3. Tools for Understanding and Managing Fish Populations + Genetics, genomics and eDNA

The Call for Abstracts for FSBI17, to be held in Exeter (UK) on 3-7 July 2017, are open:

<http://www.exeter.ac.uk/fsbi17/> We look forward to welcoming you to Exeter next summer!

Steve Simpson, Iain Barber & the local organising committee

“Paris, Josie” <J.R.Paris@exeter.ac.uk>

UFMS Brazil Evol

Symposium and Workshop on Ecology and Evolution of Plant Reproduction, 24 - 30 April 2017

Greetings All!

We are pleased to welcome you to the international *Symposium and Workshop on Ecology and Evolution of Plant Reproduction*, at Universidade Federal de Mato Grosso do Sul (UFMS), supported by the European Society for Evolutionary Biology (ESEB).

The *symposium* will be held on *April 24 and 25, 2017* at UFMS in Campo Grande. It is open for presentation of recent studies by researchers and students in all fields of evolution and ecology of plant reproduction. The meeting will be composed of 4 sessions each with a 40-minute plenary and 6-8 contributed 15-20 minute talks per session. The sessions are:

Session I - Pollination, mating and floral evolution,

Plenary speaker Lawrence Harder (Univ. of Calgary)

Session II - Gender strategies and the evolution of plant sexual systems,

Plenary speaker John Pannell (Univ. of Lausanne)

Session III - Genetics and genomics of plant reproduction,

Plenary speaker Stephen Wright (Univ. of Toronto)

Session IV - Applied reproductive biology,

Plenary speaker Marcelo Aizen (Conicet)

Abstracts for talks and posters should be submitted via the conference website (<http://plantevol.sites.ufms.br/>) by March 15.

The *workshop* will follow from *April 26 to 30, 2017* at the UFMS field station in the Pantanal wetland, a spectacular location with a diverse flora and fauna. The main goal of the workshop is to address a general lack of expertise in many approaches central to future progress in plant evolutionary biology, by teaching techniques for problem solving and new skill sets used in innovative research in evolutionary ecology, genomics and applied ecology and evolution. It is intended for graduate students and post-doctoral fellows working on the ecology and evolution of plant reproduction. Five distinguished faculty with diverse backgrounds in plant ecology and evolutionary biology will teach the workshop:

Spencer Barrett (Univ. of Toronto)

Lawrence Harder (Univ. of Calgary)

John Pannell (Univ. of Lausanne)

Marcelo Aizen (Conicet)

Stephen Wright (Univ. of Toronto)

Available housing limits course enrollment to ~20 students.

For application forms and more detailed information, please visit the official website of the event: <http://plantevol.sites.ufms.br/> or get in contact by [*plantevol2017@gmail.com*](mailto:*plantevol2017@gmail.com)

We believe that both the symposium and workshop will offer great opportunities for graduate students and faculty members to meet one another, exchange ideas, learn new approaches and collaborate. We are confident that your support will promote the success of this initiative and the growth of plant evolutionary biology in Brazil and other Latin American countries.

We look forward to meeting you at UFMS, Brazil in April 2017

Yours Sincerely

Nicolay Leme da Cunha PhD

Chair of the Organizing Committee

Ecology and Evolution of Plant Reproduction

(nicolaycunha@gmail.com)

Nicolay Cunha <nicolaycunha@gmail.com>

YosemiteNationalPark Symbiosis May5-7 Registration

Yosemite Symbiosis Workshop - Registration Now Open:

Dear Colleagues,

The Seventh annual Yosemite Symbiosis Workshop will take place on May 5th-7th, 2017 at the Sierra Nevada Research Institute, Yosemite National Park. This has become a great venue for a diversity of symbiosis researchers. We hope to continue to attract a diverse group in 2017!

Keynote speaker 2017: Dr. Corrie Moreau from the Field Museum of Natural History.

Information about our meeting:

Why: Our continuing goal is to better integrate the broad groups of scientists that focus on symbiosis re-

search. Yosemite serves as an ideal site as it is both beautiful and secluded. This will be our 7th annual meeting and we have been consistently attracting scientists from all over the country and overseas.

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

When: The talks and formal meeting will be held May 6-7, 2017, though we make accommodation arrangements available for attendees to arrive on Friday the 5th to provide opportunities to enjoy the park. Since time at the conference is limited, we ask attendees to submit an abstract and a preference (talk versus poster). Priority will be given to those presenting.

Abstract and early bird registration are due on March 6th, 2017.

Where: SNRS has a set of cabins in Wawona and all within a short walk of the conference room.

Costs: See details in the registration page. We will only be able to accept credit card payments this year. Your registration is not activated until you have completed the payment process. NOTE that the payment link is at the top of the registration page. The registration fee includes room and board.

The registration form for the 2017 Symbiosis Workshop is active: <http://snri.ucmerced.edu/symbiosis>
Please direct any questions to the organizers: Joel Sachs joels@ucr.edu A. Carolin Frank cfrank3@ucmerced.edu

*Joel L. Sachs**, Associate Professor* 5406 Boyce Hall
Department of Biology University of California Riverside, CA 92521

Mailing Address: Sachs Lab UC Riverside 3401
Watkins Dr. 1229 Spieth Hall Riverside, CA 92521

Office (951) 827-6357 Fax (951) 827-4286 www.sachslab.com <http://www.biology.ucr.edu/people/faculty/-Sachs.html> "joels@ucr.edu" <joels@ucr.edu>

GradStudentPositions

Auckland OriginInsectReceptors	27	UHongKong ConservationGenetics	45
CaliforniaStateU Northridge CoevolutionPopGenomics	28	UHull UK EvolParentalCare	45
ClemsonU	29	ULeeds UK SeychellesWarblersFitness	46
DurhamU AncientDNA DeadlineExt	29	ULeicester GreatApeGenomicDiversity	47
Glasgow ViralGenomicsBioinformatics	29	ULeicester HumanAncientDNAModernDNAAnalyses	48
GriffithU BioinformaticsGenomics 2	30	ULethbridge AvianEvolution	49
Helsinki MathematicalEcolEvolution	31	ULondon EvolutionaryTheory	50
ImperialC London 2 EvolutionInsectPollinators . . .	31	UManchester PopulationGenomics	50
LundU EvolutionaryEcol	32	UNamur Belgium RotiferEvolution 2	51
MNHN Paris FunctionalMorphology	33	UNamur Belgium RotiferEvolution 3	52
MonashU FairyWrenEvolution	34	UOsnabruck IPK Gatersleben SteppePlantPhylogeogra-	53
MPI Cologne PopulationGeneticModeling	35	phy	53
MPI Jena EvolutionInsectImmunity	35	UPlymouth AdaptationMechanisms ExtDeadline . .	53
MPIO Seewiesen EvolutionCognition	36	UPortsmouth EvolutionFlowering	53
QueensU AdaptationAtSpeciesRangeLimits	36	UPoznan EvolutionSpecialization	54
QueensU SeabirdPopGenomics	37	UppsalaU Metagenomics	55
RHUL London EvolutionInsectCognition	38	UppsalaU Sweden Systematic Biology	55
SimonFraserU 2 EvolutionaryGenetics	39	UQuebecEnOutaouais VernalPoolBiodiversity	55
Spain EvolutionSpeciation	40	URochester MolluscShellEvoDevo	56
Sydney AssistedMigration	40	UtrechtU EvolutionAntimicrobialResistance	57
UColoradoDenver PhysiologicalGenomics	41	UWindsor SalomEvolutionaryGenetics	58
UGreifswald AnimalAdaptation	42	UZurich MatingSystemEvolution	58
UGroningen AvianBehaviour	42	Vienna PopulationGenetics	59
UGroningen EvolutionaryBiology	43	WesternWashingtonU EvolutionaryBiol	59
UHannover MadagascarDemographics	44		

Auckland OriginInsectReceptors

PhD student position

Plant & Food Research, Auckland, NEW ZEALAND

Professor Richard Newcomb
(Richard.Newcomb@plantandfood.co.nz)

Assoc. Professor Thomas Buckley (BuckleyT@landcareresearch.co.nz)

The origin of odorant receptors in insects

A PhD position is available to study the origins of a unique family of receptors for odorants and pheromones that arose early in the evolution of insects. Supported from a grant from the prestigious Marsden Fund, the

PhD project will address the timing and role of the first insect odorant receptors. Our hypothesis is that they appeared just before the origin of insect flight and expanded to fill roles in detecting food, predators and/or mates in this new three dimensional environment. The research will involve the isolation of candidate odorant receptors from the transcriptomes and genomes of early insects and their deorphaning in surrogate cell systems.

<http://www.royalsociety.org.nz/2015/11/05/was-the-first-smell-of-a-meal-or-a-mate/>

The successful candidate will conduct their research within the Auckland laboratories of Plant and Food Research, while being enrolled through the School of Biological Sciences at the University of Auckland. Support includes a \$27k p.a. three year stipend with university fees paid. You will work alongside postdoctoral fellows also working on the problem and other members of the Molecular Sensing team within Plant & Food Research,

together with collaborators from Landcare Research in New Zealand and the Max Planck Institute for Chemical Ecology in Germany. Candidates should have some background or at least interest in evolutionary genomics, bioinformatics and cell biology.

Richard Newcomb <Richard.Newcomb@plantandfood.co.nz>

CaliforniaStateU Northridge CoevolutionPopGenomics

Graduate student (MSci) opportunities in the Yoder Lab

The Yoder Lab at California State University Northridge seeks exceptional, motivated candidates for the M.S. program in Biology. The lab opens in fall 2017 to study the coevolution of interacting species, particularly how mutualists shape each others' genomic diversity, and how interactions between species can help or hinder adaptation to abiotic factors like climate.

Our research particularly focuses on the yucca-yucca moth brood pollination mutualism and the legume-rhizobium nitrogen fixation symbiosis, using population genetics and genomics, phylogenetics, ecological field-work and greenhouse experiments, and both mathematical and simulation-based modeling. Planned projects include population genomic study of adaptation to extreme climates and specialized pollinators by Joshua tree (*Yucca brevifolia* and *Y. jaegeriana*) and experiments to study climate adaptation in barrel medick (*Medicago truncatula*). Students will be encouraged to develop independent projects with these or other local systems.

CSUN and the Department of Biology offer graduate student support in the form of teaching assistantships and a variety of fellowships and aid programs. Research assistantships for up to one year of the two-year Master's program will also be available through startup funding, and students will work with the PI to identify and apply for external support such as the National Science Foundation Graduate Student Research Fellowship.

CSUN is in the San Fernando Valley in Los Angeles, surrounded by natural habitats ranging from coastal chaparral to the Mojave Desert and montane woodlands, and within a short commute of Santa Monica and Hollywood. CSUN was recently recognized by Nature as one of the top 25 Rising Institutions for Research in North America, and the Biology department has a reputation for turning out excellent Master's students who often

continue on to top-tier Ph.D. programs. The Yoder Lab is part of the Ecology & Evolution program, and our research offers connections to the department's other programs in Molecular, Cellular, and Physiological Biology, Marine Biology, Microbiology, and Genetics and Developmental Biology.

Ideal candidates will have previous research experience, familiarity with the R programming language, and a passion for science. Interested students should contact PI Jeremy Yoder at jbyoder@gmail.com. In your email, please describe your research interests, any previous research experience, and your career goals. Include a CV, if possible. Formal applications require GRE scores and transcripts, and are due February 15, though exceptions may be possible. The Yoder Lab values diversity, and members of groups under-represented in ecology and evolutionary biology are especially encouraged to apply.

For more information, consult the Yoder Lab website: <http://lab.jbyoder.org> Full text of this ad with supporting links is at: <http://lab.jbyoder.org/graduate-student-msci-opportunities-in-the-yoder-lab> –

Jeremy B. Yoder Postdoctoral Research Fellow Dept. of Forest and Conservation Sciences University of British Columbia

jbyoder@mail.ubc.ca jbyoder.org

jbyoder@gmail.com

ClemsonU

Vince Richards' lab in the Department of Biological Sciences at Clemson University is accepting applications for a USDA National Needs PhD fellowship. The fellowship provides three years of support (\$24,500/year) plus a \$6,000/year education allowance. Additional support for the remainder of the PhD is available. The general focus of study will be the application of genomics to problems in agriculture. Multiple research possibilities are available within this framework.

The anticipated start date is August 2017. Applicants should contact Vince Richards directly at vpricha@clemson.edu. Please provide a cover letter (describing research interests, experience, and career goals), CV, transcripts/GRE scores, and contact information for three references. Review of applications will begin immediately and continue until the position is filled. The position requires U.S. citizenship.

Clemson University is ranked 23rd among national public universities by U.S. News & World Report and is located on Lake Hartwell near the Blue Ridge mountains in beautiful Upstate South Carolina.

Vincent P Richards, Ph.D. Assistant Professor Department of Biological Sciences Clemson University Clemson, SC 29634 email: vpricha@clemson.edu Lab website: <http://www.vprichards-lab.com> Vincent Paul Richards <vpricha@clemson.edu>

DurhamU AncientDNA DeadlineExt

Deadline Extended: PhD studentship in Biosciences at Durham University, UK

Full funding open to all nationalities.

New deadline, January 11th by the end of the day

Project Title: Tracking the impact of Holocene environmental change in Patagonia on the distribution, dispersion and population dynamics of sea lions and fur seals using ancient DNA.

This project will involve ancient DNA and next generation sequencing to investigate the impact of Holocene

climate and environmental change on the population dynamics and connectivity of two pinniped species along the coast of Patagonia in Argentina. Although the distributions of these species overlap, they have different resource requirements and life histories. Hypotheses on the impact of environmental change on each species in the context of their life histories will be tested by the student using genetic analyses and coalescent modelling. Funding will be through the Durham Doctoral Scholarship program, and is open to applicants of all nationalities. A detailed flyer describing the project is available on request.

Application materials should include a c.v., academic records and at least two letters of reference sent to a.r.hoelzel@dur.ac.uk. Please contact Rus Hoelzel at the same email address with any questions about the project.

"HOELZEL, ALAN R." <a.r.hoelzel@durham.ac.uk>

Glasgow ViralGenomicsBioinformatics

FUNDED PhD OPPORTUNITY

Mapping the molecular specificity of virus-host interactions Prof David L Robertson, < <http://www.bioinf.manchester.ac.uk/robertson> >

A three and a half year PhD project is available in the CVR's Viral Genomics & Bioinformatics group, < <http://www.bioinformatics.cvr.ac.uk> > from September 2017. The project will be computer-based and will train the student in systems virology, evolutionary biology, bioinformatics/computational biology and network biology/modelling. Please direct enquiries to david.robertson@manchester.ac.uk, who will be moving to CVR in 2017. Note, the deadline for applications is 23rd January 2017.

Project description Viruses exploit the molecular system of an infected host in order to replicate. This requires an intricate set of molecular interactions between the virus and the host system, placing a high degree of specificity on the virus-host relationship. The key to better understanding this relationship will be to study the coevolutionary changes between viruses and their host, in particular the precise nature of the interactions involved, i.e., a viruses' ability to mimic host molecular interactions and events, in the context of the host's response to infection. Depending on the student's inter-

ests there will be some flexibility in terms of the focus of the project, e.g., a study of HIV/retroviruses versus bacteriophage infections. The aim will be to construct the virus-host interaction network at the species level and for case studies model the virus-host molecular interaction network. These molecular interactions can be represented as a dynamic network by considering both temporal and spatial aspects of infection of a cell. This will be represented as a directed network, and properties of the host proteins investigated, for example, their connectivity, control-status, and functional relationships. Questions to be addressed include: How many host species on average does a virus target? How do viruses so effectively use and control the host system? What changes contribute to host-switching? What constraints do the maintenance of host interactions place on viral evolution? Given the inherently hierarchical and multi-scale nature of function, how should infection be modelled? The project can be tailored to candidates with a background in virology, biology, bioinformatics, computer science, machine learning, statistics or mathematics.

To apply, please follow the steps detailed in 'How to apply for a research degree': < <http://www.gla.ac.uk/-research/opportunities/howtoapplyforaresearchdegree/> >. When applying, please search for "Mapping the molecular specificity of virus-host interactions" in the programme description box.

Interview Process Following selection for interview, you will be invited to come to Glasgow to visit the CVR in February 2017. The interviews will be held on Friday February 10th 2017 and all interviewees are registered for free and invited to attend the Glasgow Virology Workshop on Saturday February 11th. Reasonable travel expenses will be reimbursed and accommodation made available on the 9th and/or the 10th. Please be available on these dates.

We will consider any UK graduate (meeting the residency requirements) with a minimum 2:1 BSc, or equivalent, degree in a relevant discipline. A Master's degree and previous experience of computer-based research is advantageous. Candidates with a computer science or mathematics background are encouraged to apply.

We are currently inviting applications for the programme beginning in October 2017. Unfortunately, we cannot consider citizens from outside the EU for this programme. The deadline for applications is 23rd January 2017.

Funding Notes

There are strict eligibility criteria for MRC-funded predoctoral studentships. Students from the UK (UK pass-

port holders) are eligible. EU students (EU citizens) are eligible for this programme only if they have been ordinarily resident in the UK for the three years (continuously) prior to the start of the studentship (commencing the first week in October).

References

Dickerson JE, Pinney JW, and Robertson DL (2010) The biological context of HIV-1 host interactions reveals subtle insights into a system hijack. *BMC Systems Biology* 4:80.

MacPherson JJ, Dickerson JE, Pinney JW, and Robertson DL (2010) Patterns of HIV-1 protein interaction identify perturbed host-cellular subsystems. *PLoS Computational Biology* 6:e1000863.

Oyeyemi OJ, Davies O, Robertson DL, and Schwartz JM (2015) A logical model of HIV-1 interactions with the T-cell activation signalling pathway. *Bioinformatics*. 31:1075-83.

David Robertson <david.robertson@manchester.ac.uk>

GriffithU BioinformaticsGenomics 2

A PhD scholarship in Bioinformatics/Genomics is available at Griffith University, Nathan, Australia. We have a world class Genomics laboratory and have sequenced the genomes of penguins, humans and canines. We are looking for an enthusiastic student with immense interest in the bioinformatics analysis of next generation sequence data. The prospective student will be working on a project to analyse genome data (to be generated in this lab as well as those available in the databanks) to examine the patterns deleterious mutations in human populations.

An honors or master's degree in biological, physical or computational science is required. Persons with a non-biology degree should have some basic understanding of genetics, evolution and molecular biology.

Essential skills include: [We wouldn't expect a starting PhD student to have many of these skills, but an ability and desire to learn them is obviously essential]

Scripting: Perl/Python Unix command line (particularly to use parallel computing clusters) Programming: Java/C/C++ (OOPS concept) Database: maintenance and design; MySQL/PosgreSQL/SQLite or similar Familiarity with sequence databases and genome browsers (eg. NCBI/EMBL/DDBJ, UCSC) Familiarity with the

following software is desirable: Read mapping: BWA; Bowtie; GSMapper (454); SOAP De novo assembly: Velvet; SOAP de novo; Assembly summary: Samtools; GATK Population genetic software: PLINK; EIGEN-SOFT

English language requirements: A minimum overall band score of 6.5 on IELTS (Academic) with no sub-score of less than 6.0 or A minimum score of 575 of TOEFL (Paper) or A TOEFL iBT score of 79 (no score less than 19)

For further details please contact Sankar Subramanian (s.subramanian@griffith.edu.au) Regards Sankar

Sankar Subramanian Research Fellow Research Centre for Human Evolution Griffith University Nathan QLD 4111 Australia

Email: s.subramanian@griffith.edu.au Ph: 61-7-37357495 Fax: 61-7-37357459

Sankar Sankarasubramanian
<s.subramanian@griffith.edu.au>

Helsinki MathematicalEcolEvolution

PhD student position in mathematical ecology and evolution, Helsinki, Finland

The Biomathematics Group of the Department of Mathematics and Statistics, University of Helsinki, Finland, is looking for a highly motivated PhD student to join our research in mathematical ecology and evolution. We focus on population dynamics, including structured populations and metapopulations, and adaptive dynamics, with applications such as the evolution of dispersal, the evolution of pathogens, and more.

The candidate should have an MSc in mathematics (preferred) or graduate with this degree by June 2017, and have a background in mathematical modelling as well as interest in ecology/evolution. The detailed research program is negotiable within the profile of our group. The graduate studies will be supervised by Prof. Mats Gyllenberg, with possible co-supervision by Stefan Geritz or Eva Kisdi. Salary and social benefits according to the standard Finnish University Salary System. For more information, see <https://wiki.helsinki.fi/-display/BioMath/> (Biomathematics Group) and <http://mathstat.helsinki.fi/english/> (Department of Mathematics) or contact Eva Kisdi at eva.kisdi@helsinki.fi.

Applications including a CV, the list of publications (if

any), a letter of motivation, the extract from the register of undergraduate grades, and two reference addresses are to be sent in one pdf file to eva.kisdi@helsinki.fi with cc to mats.gyllenberg@helsinki.fi. The deadline for applications is 15 March 2017. Please write "Application for PhD student position in biomathematics" in the subject line.

Eva Kisdi Department of Mathematics and Statistics University of Helsinki, Finland

"Kisdi, Eva" <eva.kisdi@helsinki.fi>

ImperialC London 2 EvolutionInsectPollinators

Two PhD studentships advertised in the Gill lab at Imperial College London, UK, looking at insect pollinator evolutionary ecology. The current group's interests are looking at how insect pollinators (primarily social bees) respond to rapid land-use change by studying behavioural ecology and trait evolution.

1) Phenological responses of insect pollinators to rapid land-use change Supervisors: Dr Richard Gill & Dr Nick Isaac (NERC Centre for Ecology and Hydrology) Part of the NERC Centre for Doctoral Training in Quantitative and Modelling Skills in Ecology and Evolution

Application deadline: 19th January 2017 The past century has seen rapid rates of agricultural land use change, yet our understanding of how animal populations have responded to such newly-emerging agri-landscapes over decadal time frames is still limited. A further complication is that some species appear to have coped better with agri-LUC than others, resulting in so called 'winners and losers', and thus understanding the traits underpinning success or failure is key to their future protection. This project will look at an aspect of plant-pollinator phenology to investigate whether agri-landscapes have selected for change in insect pollinator life-history and functional response traits. For further details please see: <https://www.findaphd.com/-search/ProjectDetails.aspx?PJID=81136&LID=907> 2)

Social bee responses to landscape fragmentation Supervisors: Dr Richard Gill & Dr Samraat Pawar Part of the Science and Solutions for a Changing Planet (SSCP) Doctoral Training Partnership Application deadline: 16th January 2017 Social bees (e.g. honeybees & bumblebees) are central place foragers, and the increasing rate of floral habitat patchiness is likely to increase foraging distance requirements making it dif-

difficult to sustain the colony's energetic demands and so may have impacts on colony fitness. Furthermore, agricultural practices can cause both reduced nutritional diversity and pesticide exposure across the landscape. This project will focus on how these stressors affect bee behaviour (focusing on foraging performance) and colony development which will help to inform eco-evolutionary models predicting colony success under varying scenarios of environmental change. For further details please see: <https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=76796&LID=907> Eligibility of the studentships: Only available to UK and EU citizens who have been resident in the UK for 3 years prior to October 2017.

Application guidelines are found by following the links provided above. For any queries please email: r.gill@imperial.ac.uk

Kind Regards,

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

LundU EvolutionaryEcol

Urban avian ecology

Where: Lund University

PI: Ass Prof Caroline Isaksson (Caroline.Isaksson@biol.lu.se)

Deadline: 20th January 2017

Start date: March (as soon as possible)

Project description

As human populations grow, the habitats for many species are becoming increasingly urbanized. Thus, understanding how urbanization affects individuals, populations, and species is important to prevent loss of biodiversity and maintain functional ecosystems. The aim of the project is to investigate whether urban environmental stress, particularly with respect to air pollution, noise and artificial lighting at night, resulting in: (i) increased physiological stress response, which will be examined by measuring antioxidants, stress hormones

and gene expression; (ii) increased physiological damage which is examined by measuring the oxidative damage and telomere attrition, and/or (iii) changes in behaviors such as sleep and food intake. In particular, experimental studies with zebra finches will be implemented, but also field studies will be part of the project. The field work will be based in Southern Sweden and of urban and rural populations of tit species. The project is multidisciplinary with elements of evolutionary ecology, conservation, toxicology and biochemistry.

The PhD project will be part of the above project, however, the specific focus of the thesis will be developed by the candidate together with the supervisor when starting. The candidate is expected, regardless of the focus of the dissertation, to participate and run its own experiments and collect tissue samples both from captive and wild birds, and then analyze them in the lab. A student who is only interested in one or the other is not suitable for the project. Students are also expected to read a number of courses equivalent to 60 credits. These studies must be of both depth and width of the character.

Required qualifications

A masters degree in Biology focusing on either evolutionary ecology, molecular ecology and/or ecophysiology. For this position it is important to have experience with handling birds and to have laboratory experience: an advantage is to have training in molecular techniques. It is a requirement that spoken and written English is excellent. It is also a requirement to have a drivers license and a car at the starting date.

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

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

See more details: <http://www.lu.se/om-universitetet/-jobba-hos-oss/lediga-anstallningar?ref=D> Lediga anställningar | Lunds universitet www.lu.se Dr

Caroline Isaksson

Associate Professor Department of Biology Evolutionary Ecology Unit Lund University Sölvegatan 37 SE-223 62 Lund

Tele: +46 (0)46-2221780

Email: Caroline.Isaksson@biol.lu.se

<http://www.biology.lu.se/caroline-isaksson> Caroline Isaksson <caroline.isaksson@biol.lu.se>

MNHN Paris FunctionalMorphology

Two Open Phd Positions (MNHN, Paris, France)

1. Area of research: Functional morphology PhD Title: Long bone morphological and microanatomical adaptation to graviportality in Rhinoceroidea Supervisors: Dr. Alexandra Houssaye, Dr. Raphael Cornette & Dr. Guillaume Billet E-mails: houssaye@mnhn.fr, cornette@mnhn.fr, billet@mnhn.fr Research unit: UMR 7179 CNRS/MNHN - Mécanismes Adaptatifs : des Organismes aux Communautés Associated research units: UMR 7205 & UMR 7207 Host laboratory: Team FUNEVOL - Function & Evolution Subject: There is a strongly repetitive and convergent evolution of presumed graviportal specializations in amniote evolutionary history that highlights the major impact of biomechanical constraints on anatomical macroevolution. This project proposes to investigate the morphological and microanatomical changes in weight bearing long bones associated to the evolution of graviportality in rhinocerotoids.

Beyond the five extant species from the family Rhinocerotidae (that will be extensively analyzed), the diversity in Rhinoceroidea is much richer, with two additional families: Amynodontidae and Hyracodontidae. Very distinct morphologies are observed within this group and different ecologies with notably semi-aquatic and exclusively terrestrial forms.

Analyzing the changes observable between rather small and extremely large forms, but also between gracile and massive ones will be important to understand the skeletal changes associated with the repeated evolution of large body mass within this group. The aim will be to distinguish adaptations linked to graviportality and to a semi-aquatic lifestyle, respectively. The combination of these results with the ecological data available for extant taxa will enable to better characterize the link between

ecology, functional requirements and bone inner and outer structure. In addition to providing robust and integrative data about the inner and outer bone changes linked to graviportality, this project will also enable to perform paleoecological inferences on fossil forms.

This project will necessitate to perform 3D geometric morphometric (after acquisition by photogrammetry, surface scanning, or microtomography) analyses on limb long bones of a large sample of modern and fossil rhinocerotoids for a detailed comparison of bone shape. In addition, for the bones scanned using microtomography, the complete bone microstructure will be analyzed in 3D. The study requires thus an important time of 3D data analysis.

This PhD is part of an ERC project whose larger objective is to model the relationship between bone morphology, microanatomy and the functional requirements of body support and locomotion in graviportal taxa through amniote evolutionary history.

Financial information: The PhD will be financed as part of an ERC project.

The material necessary for this project is present in the collections of various museums. If many specimens are available in the collections of the MNHN, visits to several museums will be required in addition to loans. All the required technical support is available at the MNHN.

Start: 01/09/2017 / Duration: 3 years Candidate profile: Student with a Master in Biological Sciences and some experience in 3D data analysis; dynamic, able to work autonomously as well as in a team; good level in spoken and written English.

Please send a CV and a motivation letter by e-mail to houssaye@mnhn.fr. The copy of your Master Thesis would also be welcome. Deadline: April 1st, 2017

2. Area of research: Functional morphology PhD Title: Towards extreme gigantism - Long bone inner and outer adaptations in sauropodomorph dinosaurs Supervisors: Dr. Alexandra Houssaye, Dr. Raphael Cornette & Dr. Ronan Allain E-mails: houssaye@mnhn.fr, cornette@mnhn.fr, rallain@mnhn.fr Research unit: UMR 7179 CNRS/MNHN - Mécanismes Adaptatifs : des Organismes aux Communautés Host laboratory: Team FUNEVOL - Function & Evolution.

Subject: Giant forms evolved convergently in various amniote lineages. Among them, the largest land forms were sauropod dinosaurs. These forms naturally show adaptations for high body mass support and propulsion, which is naturally reflected in their bone design.

Sauropodomorph dinosaurs offer to analyze in parallel

increasing graviportal adaptations and the acquisition of a quadrupedal posture in their evolutionary history.

Increase in body size seems to have occurred quickly in sauropodomorphs, from small ancestral forms to ancestral sauropods weighting from 1 to 10 tons and to have been accompanied by changes in limb and bone proportions. Of particular interest is the supposed progressive shift in function of the forelimb from stronger grasping adaptations in the smallest forms to dominant and then exclusive locomotor function in the largest ones. The aim here will be to focus on the transition from small forms considered either obligate or facultative bipeds to giant

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MonashU FairyWrenEvolution

PhD scholarship to study effects of increasing temperature during early life in a tropical endangered fairy-wren in the Behavioural and Evolutionary Ecology of Birds Group @ Monash University, Melbourne, Australia, a PhD project is available to study how temperature affects nestling development using a combination of existing and newly-collected data. The research will focus on effects of nest temperatures on metabolism, growth, heat stress, immune maturation, adult performance and molecular aging and how these effects might be mitigated by cooperative breeding.

The project will focus on purple-crowned fairy-wrens, *Malurus coronatus* with field work taking place at AWC Mornington Wildlife Sanctuary in the Kimberley, a beautiful region in the monsoonal tropics of north-west Australia where the research group has been studying a fully colour-banded, known-age population since 2005.

Monash University is a member of Australia's Group of Eight coalition, and is internationally recognized for excellence in research and teaching. The School of Biological Sciences is home to a collegial and interdisciplinary research environment, with strengths in ecology, genetics and evolutionary biology. The Monash doctoral program includes additional training opportunities beyond the research program that enhance employability post degree. Monash is located in Melbourne, one of

the most liveable cities in the world and a cultural and recreational hub.

Requirements and further information The student must have self-motivation, enthusiasm, a background in ecology and evolutionary theory, a passion for studying wild animals in their natural environment, a strong work ethic, experience with (tropical) fieldwork and/or bird handling and/or relevant quantitative skills. The student will have considerable flexibility in developing the project.

Successful students will be offered a scholarship for living expenses (and fee-waiver in the case of international students) of approximately AU\$ \$26,000 AUD, tax-free for 3.5 years, for full time research.

Expenses for relocation, research, coursework, and conference attendance are covered. In order to be eligible, students must have four-year degree with relevant research experience, outstanding grades, and excellent English.

The application process takes place in two stages. Send your initial application to Anne Peters (anne.peters@monash.edu), consisting of: a letter of motivation; a CV; overview of your academic results, and translation if required, preferably indicating cohort rank or percentiles; English test results if available; and the names and contact details of 3 academic references. Deadline is 1 March 2017.

If you are selected, you will be sent an invitation to submit a formal application through the Monash University web portal.

See sites.google.com/site/petersresearchgroup/opportunities for further details. Contact Anne (anne.peters@monash.edu) if you would like further information on the project or the application process.

– Anne Peters Associate Professor | Future Fellow School of Biological Sciences 108, 19 Rainforest Walk (enter via 25 Rainforest walk) Monash University VIC 3800, Australia phone: +61 3 9905 6287

<https://sites.google.com/site/petersresearchgroup/>

<http://scholar.google.com/citations?user=-jpoOPNEAAAAJ>

Anne Peters
<anne.peters@monash.edu>

MPI Cologne Population Genetic Modeling

PhD in Population Genetics

The Hancock Lab (<http://www.mpipz.mpg.de/hancock>) is seeking a PhD student to work on an ERC-funded project to reconstruct adaptive histories of functional variation in Cape Verde Islands *Arabidopsis**. This project benefits from the unique set of samples we collected and sequenced from across the landscape in these islands as well as the wealth of information that comes from years of study in this model organism. The student will use spatially-explicit simulation-based population genetic modeling approaches to reconstruct neutral and adaptive histories within this island context.

Strong preference will be given to candidates who have training in population genetics as well as computational experience (i.e., familiarity with Linux/Unix command line, R, programming in C++, Java or Python).

To apply please send a letter of motivation, CV, academic transcripts and contact information for two references in a single file by February 25 to hancock@mpipz.mpg.de with the subject line 'PhD in Population Genetics'. English is the working language of the lab and the Institute, and applications should therefore be in English.

Location:

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

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

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

MPI Jena Evolution Insect Immunity

The Max Planck Institute for Chemical Ecology (Department of Entomology) in Jena has an opening for a PhD student (m/f).

Project Description The field of ecological immunology seeks to understand the evolutionary and ecological process which shaped and maintained variation in insect immunity. Recently, our group demonstrated that adaptation by the specialist *Heliothis subflexa* (*Heliothis*) to withanolides, an anti-herbivore compound of *Physalis* plants, directly and indirectly protect the larvae from bacterial pathogens [1]. Beyond simply countering plant-produced compounds, *H. subflexa* has succeeded in converting the inhibitory effects of withanolides into activation effects for its own advantage. In the context of a DFG funded project, the PhD student will work on the mechanisms by which *H. subflexa* overcame the inhibitory effects of withanolides. The project is based on three major objectives, (1) Identification and characterization of possible withanolide receptors or decoy proteins, (2) Analysis of withanolide metabolism, (3) Impact of withanolides on plant and larval gut microbiome. Furthermore, the PhD student will analyze the effects of other plant-produced anti-herbivore compounds on the immune system of specialist insects to identify general effects of plant chemistry on ecological immunology.

We are looking for a motivated student with a University degree (M.Sc. or equivalent) and a focus on molecular biology, biochemistry, immunology, zoology, evolution or equivalent discipline. We expect good verbal and written communication skills. Experience working with proteomic, transcriptomic and/or metabolomic data as well as knowledge of different research methodologies (e.g. PCR; DNA, RNA and protein extraction; Western Blot; Enzyme assays; Cell and/or bacterial cultures; Insect rearing) are a plus.

We offer excellent technical equipment and close supervision in an international environment. A structured PhD program is offered by our graduate school (IMPRS) which provides interdisciplinary training by seminars, lectures and scientific workshops. The payment and benefits are based on the TVöD guidelines and the appointment is for 3 years with possibility of extension. The position is available from now. The Max Planck Society is committed to increasing the number of indi-

viduals with disabilities in its workforce and therefore encourages applications from such qualified individuals. Furthermore, the Max Planck Society seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply.

Application Questions concerning the project or the position are welcome and should be addressed to Dr. Yannick Pauchet. To apply, please email a statement of motivation, CV and a letter of reference as a single PDF file to ypauchet@ice.mpg.de. Application deadline is February 28, 2017; however, applications will be accepted until the position is filled.

Reference [1] Barthel, A., Vogel, H., Pauchet, Y., Pauls, G., Kunert, G., Groot, A. T., Boland, W., Heckel, D. G., Heidel-Fischer, H. M. (2016). Immune modulation enables a specialist insect to benefit from antibacterial withanolides in its host plant. *Nature Communications*, 7: 12530

– Dr. Andrea Barthel Postdoc Max-Planck-Institute for Chemical Ecology Department of Entomology Hans-Knöll-Str. 8 D-07745 Jena Germany

Andrea Barthel <abarthel@ice.mpg.de>

MPIO Seewiesen EvolutionCognition

Announcement

PARROT COGNITION (TENERIFE)

MASTER PROJECTS / VOLUNTEER RESEARCH ASSISTANTS

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

The Max-Planck Comparative Cognition Research Group (CCRG) invites applications of Masters students and volunteer research assistants. The CCRG forms part of the collaboration between the Max-Planck Institute for Ornithology, Seewiesen, Germany, and the Loro Parque Fundación (LPF), Tenerife, Spain. We are currently running various comparative research projects on social and physical cognition in parrots. Interested candidates are encouraged to contact us to enquire about the ongoing projects. Successful applicants can expect to gain a solid insight in the field of Animal Cognition/Experimental Psychology and gain experience in working with psittacids in a dynamic,

international research environment. The research is carried out on captive parrots of the LPF, which holds the largest parrot collection and gene reserve in the world (ca. 350 subspecies) for conservation and research purposes.

Logistics:

Voluntary research assistant position /Master Project start and end dates are flexible but preference will be given to students who can start in February 2017. The position requires a minimum of 4 months, but ideally 6 months, continuous commitment at the research station in Tenerife, Spain. Free accommodation in a shared student apartment can be provided. Successful applicants will be responsible for their own transportation expenses to and from the research station (Puerto de la Cruz, Tenerife, Spain).

Important skills/qualifications:

Successful candidates will have:

completed a degree in Biology or any related field a strong interest in comparative cognition high motivation and commitment to the project reliability, efficiency and an ability to work independently confidence to interact with animals previous research experience good verbal and written English skills initiative to develop the project good team work attitude and social skills (shared accommodation between 3 students)

To apply:

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

QueensU AdaptationAtSpeciesRangeLimits

Graduate Research Opportunities in Adaptation Across Species' Ranges

We are recruiting two graduate students (MSc or PhD) to work on the ecology and genetics of adaptation and geographic range limits in flowering plants endemic to the wonderful Pacific coastal dunes of California and adjacent Oregon and Baja California. The students would be co-supervised by Chris Eckert (Queen's U) and Karen Samis (U Prince Edward Island) and based

in the Biology Department at Queen's University in Kingston, Ontario, Canada.

Our research programs provide opportunities for diverse graduate student projects, and PhD students, especially, are encouraged to develop their own research directions. Here are some examples:

- (1) Using experimental evolution to investigate constraints on adaptation at and beyond geographical range limits.
- (2) Contribution of hybridization to adaptation across geographic ranges.
- (3) Does geographic variation in metapopulation dynamics yield stable range limits?
- (4) Reproductive isolation during diversification of the mating system and life history across species' ranges.

All projects will involve considerable field work in California, Oregon and Mexico, field experiments and genomic analyses.

Here's some background reading:

Samis, K.E., A. López-Villalobos & C.G. Eckert. 2016. Strong genetic differentiation but not local adaptation toward the range limit of a coastal dune plant. *Evolution* doi: 10.1111/evo.13047

Hargreaves, A.L., K.E. Samis and C.G. Eckert. 2014. Are species' range limits simply niche limits writ large? A review of transplant experiments beyond the range. *American Naturalist* 183: 157-173.

Samis, K.E. and C.G. Eckert. 2009. Ecological correlates of fitness across the northern geographic range limit of a pacific coast dune plant. *Ecology* 90: 3051-3061.

Eckert, C.G., K.E. Samis & S.C. Loughheed. 2008. Genetic variation across species' geographic ranges: the central-marginal hypothesis and beyond. *Molecular Ecology* 17: 1170-1188.

Darling, E., K.E. Samis & C.G. Eckert. 2008. Increased seed dispersal potential towards geographic range limits in a Pacific coast dune plant. *New Phytologist* 178: 424-435.

Samis, K.E. & C.G. Eckert. 2007. Testing the abundant center model using range-wide demographic surveys of two coastal dune plants. *Ecology* 88: 1747-1758.

For more details and recent publications, please check out our web sites: http://post.queensu.ca/~eckertc/Eckert_Lab/ http://people.upei.ca/ksamis/Samis_Homepage/ The Biology Department at Queen's University (<https://biology.queensu.ca>) includes active research groups in diverse areas, including plant ecology & evolution, behavioural ecology, molecular population genetics & systematics, paleolimnology, and plant physiology & molecular biology. Our large community of graduate students provides a stimulating & friendly aca-

demic environment. Graduate students are guaranteed financial support of \$22,000/year from scholarships, research stipends & teaching assistantships (2 years for an MSc, 4 years for a PhD, <https://biology.queensu.ca/-academics/graduate/>).

The position is open to all students who are Canadian citizens. Acceptance of international students is contingent on successful application for a tuition waiver or independent funding to cover foreign student tuition fees.

If you are interested, please send a CV and contact information for at least 2 academic references plus a covering letter.

Informal inquiries are also welcome.

Dr. Christopher G. Eckert and Dr. Karen Samis
chris.eckert@queensu.ca ksamis@upei.ca

Christopher Eckert <chris.eckert@queensu.ca>

QueensU SeabirdPopGenomics

I am looking for a Canadian citizen or landed immigrant to fill a PhD position studying population genomics of arctic seabirds (abstract below). The student will be part of an NSERC Strategic project to aid conservation and management of several species. Applicants must have a background in evolutionary genetics. Practical experience with genomics and bioinformatics is an asset. Field work in remote arctic camps will be required. The successful applicant will join a dynamic group of faculty and students studying ecology and evolution at Queen's University. Please send a resume or curriculum vitae, informal transcript, and contact information for two academic references to Dr. Vicki Friesen (vlf@queensu.ca). Applications will be reviewed until the position is filled.

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 Email: vlf@queensu.ca Website: <http://post.queensu.ca/~birdpop/index.html> As numerically dominant apex predators, seabirds are key components of Canada's arctic marine ecosystem. Seabirds and their eggs also are important to the culture and diet of indigenous Arctic peoples. However, Arctic seabird populations are facing multiple simultaneous direct and indirect threats from climate change, shipping and industrial development. Unsurprisingly, many populations

are showing signs of stress such as reduced reproductive success or declining numbers. To avoid extinction, wildlife populations must adapt through (1) changes in behaviour or physiology, (2) dispersal, or (3) genetic changes. The capacity for seabirds to adapt through these three avenues is virtually unknown, but it is critical to maintenance of healthy populations. New genomic methods, especially when combined with on-going studies of behaviour and physiology, provide powerful opportunities to determine the long-term sensitivities of Arctic seabirds to climate change and industrial development. We will use genomic, behavioural and ecological data in a landscape context to estimate levels of phenotypic plasticity, dispersal, and genomic variation for seven seabird species that Canada has a global responsibility to protect. Results will help Environment and Climate Change Canada (ECCC) develop science-based policies for Arctic stewardship. The students will be responsible for analysis of one species, and will gain training in population and landscape genomics, bioinformatics, population modeling and arctic ecology.

Vicki Friesen <vlf@queensu.ca>

RHUL London
EvolutionInsectCognition

PhD Position: The fitness consequences of spatial cognition in the bumblebee *Bombus terrestris*

Closing date: Midnight, 31st January 2017

A fully-funded 3-year PhD studentship is available to join the Insect Cognition Lab at Royal Holloway University of London, under the supervision of Dr. Elli Leadbeater. The studentship covers tuition fees, a student stipend of 16 296 per year (in line with Research Council stipends) and research costs. The position is open to UK and Non-UK EU applicants, and must start on August 1st 2017 (although provision can be made for applicants who are due to finish a Master's degree in September 2017).

There is evidence from diverse animal groups that demand for high-level performance in spatial memory tasks selects for brain structural evolution, and foraging bees face spatial challenges on multiple levels. For example, long-term recall of visual landmarks is important in re-locating the nest or feeding sites, while on a shorter timescale, individuals must navigate through dense forage patches that may contain hundreds of flowers, with-

out revisiting inflorescences. Here, we will investigate the cognitive abilities that bumblebees employ to meet these demands. The PhD student will (a) seek to establish for the first time whether bees form working memories of individual flower locations (b) explore the capacity and temporal properties of such memories (c) evaluate the power of cognitive task scores to predict performance in a fitness-determining spatial assay.

The student will be based in the School of Biological Sciences at Royal Holloway University of London. Our department is a centre of excellence for social insect research, and the project will capitalize upon our EU-funded research apiaries. The PhD student will join a diverse and productive team of researchers in the Insect Cognition Lab. She or he will work independently in developing the protocols for the PhD project, but the position is part of a Leverhulme-Trust funded research project into the fitness consequences of cognitive abilities in bees, and the student will also contribute to data collection for the wider project and will work closely with the other team members. More information about the research that takes place in our group can be found at <http://ellileadbeater.wixsite.com/insectcognition>. Applicants should have a 1st Class or 2:1 Bachelor's degree in a relevant Biological or Psychological subject. A Masters degree is desirable, with a grade (or expected grade) of Merit or Distinction. Experience of working with insects is not essential, but the successful candidate will have experience of independent research with live animals (e.g. through an undergraduate or postgraduate research project) and must be able to provide strong evidence of aptitude and enthusiasm for research in Animal Behaviour, together with a broad knowledge of biological topics and a firm grasp of appropriate statistical methods.

Informal enquiries should be directed to Elli.Leadbeater@rhul.ac.uk. For details of how to apply, visit: <https://www.royalholloway.ac.uk/biologicalsciences/prospectivestudents/-postgraduateresearch/phdstudentships2017.aspx> Dr. Elli Leadbeater School of Biological Sciences Royal Holloway University of London elli.leadbeater@rhul.ac.uk

“Leadbeater, Elli” <Elli.Leadbeater@rhul.ac.uk>

SimonFraserU 2 EvolutionaryGenetics

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

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

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

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

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

Application information:

Funding is available for Canadian students, though preference may be given to students with sources of external support such as NSERC Postgraduate Scholarships. International students are also very welcome to apply, but may be considered subject to access to funding from their home country. Formal application information is available at http://www.sfu.ca/dean-gradstudies/future/-academicprograms/faculty_of_science/biology.html If you wish to apply, please send a Curriculum Vitae and a one-paragraph cover letter describing your background and interests, to: crespi@sfu.ca

Informal inquiries are also welcome

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

Possible start dates would include May 2017 or September 2017 or January 2018

MSc or PhD position in behavioral-genetic endocrinology at Simon Fraser University

A graduate student position is available for study of the genetic, epigenetic and behavioural bases of neurohormone production in healthy humans. This work will build on recent discoveries in the Crespi laboratory that have demonstrated novel links between oxytocin-associated genetic variation, psychology, and social behavior. The student will conduct experiments and engage in data collection on the genetics, epigenetics, and endocrinological bases of human sociality.

See <http://www.sfu.ca/biology/faculty/crespi/publicationsrr.html> (especially paper #s 176, 177, 178, 181) for examples of representative publications in this general area from the Crespi lab.

The successful candidate will have interests and/or background in evolutionary biology, genetics, endocrinology, and/or psychology.

Application information:

Funding is available for Canadian students, though preference may be given to students with sources of external support such as NSERC Postgraduate Scholarships. International students are also welcome to apply, but may be considered subject to access to funding from their home country. Formal application information is available at http://www.sfu.ca/dean-gradstudies/future/-academicprograms/faculty_of_science/biology.html If you wish to apply, please send a Curriculum Vitae and a one-paragraph cover letter, describing your background and interests, to crespi@sfu.ca

Informal inquiries are also welcome

Dr. Bernard Crespi, FRSC Professor, Department of Biological Sciences Burnaby, British Columbia, Canada V5A 1S6 crespi@sfu.ca

Possible start dates would include May 2017, September 2017 or January 2018

Bernard Crespi <crespi@sfu.ca>

Spain EvolutionSpeciation

We seek candidates for a predoctoral FPU contract, financed by the Spanish Ministry of Education, Culture and Sports (see <http://www.mecd.gob.es/-servicios-al-ciudadano-mecd/catalogo/general/educacion/998758/ficha/998758-2016.html#dg>) and for a predoctoral Aragon Government contract, financed by the Spanish Government of Aragon (see <http://www.boa.aragon.es/cgi-bin/EBOA/-BRSCGI?CMD=VEROBJ&MLKOB=943211364> 141), that will be associated to the following research grant projects financed to our research team: 1. Evolution of biological traits and speciation processes in the model grass genus *Brachypodium* through comparative and functional genomics (Spanish Ministry of Economy and Competitiveness, grant CGL2016-79790-P; 2017-2019), and 2. Perenniality, abiotic stress tolerance, and biomass allocation in *Brachypodium*, a model grass genus for bioenergy (US Joint Genome Institute, Community Science Program, grant 503006; 2017-2021).

The candidates could also apply to a predoctoral FPI contract, financed by the Spanish Ministry of Economy and Competitiveness (grant project CGL2016-79790-P), later in 2017.

Characteristics of the PhD thesis:

- Title: Evolution of perenniality, hybridization and speciation processes in the grass model genus *Brachypodium* using comparative and functional genomics and cytogenomics
- Length: 4 years PhD thesis (2017/18-2020/21).
- Centre: University of Zaragoza (High Polytechnic School of Huesca, Spain), Estacion Experimental de Aula Dei - CSIC, Zaragoza, Spain).
- Contract: 4 years contract, annually renewed, salary based on the predoctoral grant funding

Requirements of the candidates:

- European Community citizens or non-EC citizens with homologated degree
- Degree in Biology, Environmental Sciences, Agronomy or Forestry Engineering, Bioinformatics or similar degree obtained in January.2012 or later.
- Master of Sciences degree in a specialized research line related to the Bachelor degree or the subject of the PhD

thesis

Merits:

-Experience in laboratory (Molecular Biology, Genetics), computation (Bioinformatics), green-house work (hybridization), and/or field work (Botany, Ecology).

-English

Deadlines for applications:

February 3 2017: predoctoral FPU contract, Spanish Ministry of Educacion

February 6 2017: predoctoral contract, Spanish Government of Aragon

Interested candidates please contact Prof. Pilar Catalan (pcatalan @ unizar.es), Escuela Politecnica Superior de Huesca (Universidad de Zaragoza), Ctra. Cuarte km 1, 22071 Huesca (Spain) (<http://www.bifi.es/bioflora/>)

Pilar Catalan

Pilar Catalan <pilar.catalan09@gmail.com>

Sydney AssistedMigration

HIE: A Scientific Basis for Assisted Gene Migration Under Climate Change

The Hawkesbury Institute for the Environment (HIE)(opens in new window)Opens in a new window is one of three institutes within Western Sydney University. The plant adaptation group at HIE is widely recognised for their work testing the capacity to respond to climate through adaptive genetic variation and phenotypic plasticity.

We are now seeking a highly motivated PhD student to contribute to a NSW Environmental Trust project "A scientific basis for assisted gene migration under climate change". The project objectives are:

Characterise neutral and adaptive genetic variation to estimate demographic and evolutionary processes. Do warm/dry populations harbour adaptive variation for drought resilience? Determine the ecological and physiological capacity to respond to climate change. Do plants growing under rainfall regimes found in their native source population outperform plants from different climates ('local-is-best')? Do warm/dry populations have higher resilience to drought?

Understanding the capacity of trees to respond to climate change is essential for the maintenance of biodi-

versity, forest health and productivity. Climate change has increased the frequency and intensity of droughts, which has resulted in tree death and negatively affected essential ecosystem services. Adaptive land management is urgently needed in order to mitigate the risk of large-scale drought mortality in a rapidly changing climate. Assessing genetic adaptation and physiological tolerance to drought across species distributions is critically important if we are to develop management tools, such as assisted gene migration, for sustainable and productive forests in a drying climate.

The project will focus on dominant Eucalyptus species in eastern Australia and compare populations from coastal, tableland, and western bioregions with replication across latitudes. The student will undertake genotyping-by-sequencing (ddRAD) to assess genetic structure and identify adaptive variation for climate change. Temperature and water manipulations under controlled glasshouse conditions will be employed to test for genetic adaptation and determine physiological tolerance to drought and heatwaves.

The student will be based at HIE, working under the supervision of Dr Paul Rymer and Prof. David Tissue, and engage with the project partners Office of Environment and Heritage, Greening Australia, and Local Land Services.

What does the scholarship provide? Domestic students will receive a tax free stipend of \$27,000 per annum and a funded place in the doctoral degree. International students will receive a tax free stipend of \$27,000 per annum. Those with a strong track record may receive a fee waiver. Funding is available for project costs and conference travel.

Criteria We welcome applicants from a wide range of backgrounds, especially those with a strong grounding in ecology, genetics or plant biology who are keen to apply their quantitative skills to key questions in current biology. The successful applicant should:

1 - hold qualifications and experience equal to an Australian First Class Bachelor Honours degree or equivalent overseas qualifications
 2 - hold a full clean drivers licence
 3 - demonstrate strong academic performance in biology
 4 - have an interest in, or be willing to learn, population genetics and plant physiology
 5 - be enthusiastic and highly motivated to undertake further study at an advanced level

International applicants must also demonstrate a high level of proficiency in the English language. (opens in new window) Opens in a new window

How to apply Applicants should discuss their eligibility and interests with Dr Paul Rymer

p.rymer@westernsydney.edu.au or Prof. David Tissue d.tissue@westernsydney.edu.au

Please submit an application form https://www.westernsydney.edu.au/_data/assets/pdf_file/0005/733487/-Project_Scholarship_Application_Form_2017.pdf (PDF, 278.77 KB), CV, names and contact information of two referees, and a one-page document stating how your research interests align with the project's aims.

Contact the Graduate Research School at grs.scholarships@westernsydney.edu.au for further enquiries.

Applications close 31 March 2017

Paul Rymer <P.Rymer@westernsydney.edu.au>

UColoradoDenver PhysiologicalGenomics

PhD positions in physiological genomics of seasonal adaptation at the University of Colorado, Denver

The Ragland lab at the University of Colorado, Denver is seeking PhD students for Fall, 2017. We are broadly interested in physiological adaptations to variable climatic and biotic (e.g., resource) conditions. Several NSF-funded projects in the lab apply integrative approaches to understanding rapid life history diversification in *Rhagoletis* flies, text-book examples of ecological speciation with gene flow. In addition, a recently funded Dimensions of Biodiversity project will explore parallel diversification of parasitic wasp lineages that attack *Rhagoletis* flies, in collaboration with labs at the University of Notre Dame, University of Florida, and SUNY Binghamton. From a genetic perspective, we are interested in how genetic architecture constrains or facilitates rapid evolution of complex traits. From a physiological and developmental perspective, we are testing whether regulatory pathways influencing multiple life history transitions during development contribute to either constraint or modularity observed at the genetic level. Additional projects in the lab investigate mechanisms of developmental arrest during dormancy, the phylogeography and population genomics of Bark Beetles (Mountain Pine Beetle and European Spruce Bark Beetle) and developmental constraints on thermal physiology in *Drosophila melanogaster*.

Ideally, PhD candidates will have interests in physiology, developmental biology, evolutionary genomics,

or evolutionary ecology, and enthusiasm for learning command line environments and coding. Experience in basic laboratory techniques relevant to any of those fields and basic parametric statistics is desired. Competitive stipends and Research Assistantships are available for qualified applicants.

The University of Colorado, Denver, hosts a vibrant community of life science researchers on both the downtown Auraria campus and the Anschutz medical campus. The Department of Integrative Biology spans cell, molecular, ecological, and evolutionary research, with strengths in ecological physiology and developmental biology. Denver is a fantastic and progressive city with endless possibilities for outdoor activities, well-developed public transportation and cycling infrastructure, and excellent museums, theaters, restaurants, and breweries.

Please direct inquiries to Greg Ragland: gregory.ragland(AT)ucdenver.edu. I will be at the January 2017 SICB meeting in New Orleans and available to chat. Consider checking out the symposium 'Evolutionary Impacts of Seasonality', which showcases some excellent research which inspires many ongoing projects in my lab.

Websites:

<https://clas.ucdenver.edu/directory/faculty-staff/greg-ragland> <https://seasonaladaptation.org> "Ragland, Gregory" <GREGORY.RAGLAND@UCDENVER.EDU>

UGreifswald AnimalAdaptation

25-01-2017

Job announcement

University of Greifswald, Zoological Institute and Museum

PhD Position in Animal Ecology

Application deadline: 15.03.2017

A PhD position is available at the Zoological Institute and Museum, University of Greifswald. Starting date: May 1st 2017; duration: 3 years; salary scale: TV-L 13, 50%.

We invite applications from highly motivated candidates with passion for and experience in research related to animal responses to anthropogenic environmental change. 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 experimental designs in ecology and according statistical analyses, and (4) an excellent command of the English language.

To apply please send an email to Prof. Dr. Klaus Fischer (klaus.fischer@uni-greifswald.de) before March, 16th 2017 and refer the following reference number: 17/Wi02. Please attach a single PDF file to this email including a (1) cover letter, (2) scientific CV including copies of all degrees, (3) motivation letter including personal research interests, (4) contact details of two academic referees, and (5) the abstract of the latest thesis.

The University of Greifswald is an equal opportunity employer. Application expenses cannot be refunded by the state of Mecklenburg-Western Pomerania. The official version of this advertisement is published on the university's homepage.

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

Prof. Dr. Klaus Fischer Zoological Institute & Museum Greifswald University J.-S.-Bach-Str. 11/12 D-17489 Greifswald Phone: +49-3834-864266 Fax: +49-3834-864252

"kfischer@uni-greifswald.de" <kfischer@uni-greifswald.de>

UGroningen AvianBehaviour

PhD position on computational models of collective escape of bird flocks 1.0 fte (217006)

Organisation

Founded in 1614, the University of Groningen enjoys an international reputation as a dynamic and innovative center of higher education offering high-quality teaching and research. Flexible study programmes and academic career opportunities in a wide variety of disciplines encourage the 30,000 students and researchers alike to develop their own individual talents. As one of the best research universities in Europe, the University of Groningen has joined forces with other top universities and networks worldwide to become a truly global center of knowledge.

The Groningen Institute for Evolutionary Life Sciences (GELIFES) GELIFES, the largest institute of the Faculty of Mathematics and Natural Sciences (FMNS) fills a special niche in the life sciences by covering and in-

tegrating mechanistic, evolutionary and ecological approaches, aiming to understand adaptation on all levels of biological organisation. Researchers pursue fundamental questions while collaborating with partners from industry, medicine and other realms of society. Our research fields include behavioural biology, chronobiology, ecology, evolutionary biology, genetics and genomics, neurobiology, physiology and theoretical modelling, using a wide array of research tools. Research levels range from molecular and organismal to population and community, performed under laboratory, semi-natural and field conditions.

Job description

One of the advantages of group life, such as in birds, is increased protection against predation. Increased protection is, for instance, assured by the complex patterns of collective escape by bird flocks under attack. These patterns may confuse the predator. Collective behaviour of flocks is, however, difficult to investigate empirically. As a solution, the proposed project concerns the computational modelling of collective escapes. This is done with the help of empirical data collected by another PhD candidate using robot-falcons (RoboFalcons) for controlled attacks on flocks. The empirical study is aimed at driving flocks away in a specific direction for preventing collisions between flocks and airplanes. The PhD candidates will closely exchange data and results. The modelling project aims to gain understanding on what causes different patterns of collective escape under different conditions. For this, the PhD candidate will extend our computational model, StarDisplay, and may develop new models. The model will be informed by two empirical sources, namely, the experiments with RoboFalcons and the movies of huge starling flocks under attack by Peregrine falcons above Rome. The student will experiment with different escape strategies and attack strategies in the model to improve both understanding of the observations of patterns of collective escape and methods of driving flocks away.

Daily supervision will come from Prof. Charlotte Hemelrijk and Dr Hanno Hildenbrandt; Dr Colin Torney (Glasgow, UK) will co-supervise the project.

Qualifications

The successful candidate will have previous research experience in theoretical modelling, be in good command of the English language (oral and written) and possess excellent communication skills (indicated by the ability to write scientific papers and deliver presentations). Since studies on self-organisation are highly interdisciplinary, successful candidates are expected to demonstrate an active and supportive approach to interdisciplinary research and collaborate with other group

members. Suitable candidates can be either individuals with a background in the computational (life) sciences, with interest in evolutionary and biological questions, or evolutionary biologists with experience in computational modelling.

Candidates for the PhD position should have: - MSc in theoretical biology, a MSc in computational science with focus on biology or an MSc in computational physics with specialization in biology, MSc in Artificial Intelligence with a specialization in an area of computational or mathematical biology or a MSc in Biology, with a specialization in an area of computational or mathematical biology - experience with developing computer simulation code and a sufficient background in mathematics - a strong interest in collective, swarming behaviour, biomechanics of flight, attack and escape. Candidates with research experience in these areas are particularly encouraged to apply.

Conditions of employment

The University of Groningen offers a salary of euro 2,191 gross per month in the first year, up to a maximum of euro 2,801 gross per month in the final year (salary scale Dutch Universities), based on a fulltime position (1.0 fte) excluding a 8% holiday allowance and a 8.3% end of the year bonus. The position must result in a PhD thesis within the 4-year contract period. A PhD training programme is part of the

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U Groningen Evolutionary Biology

Erasmus Mundus 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, 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 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. Starting date: 15 August 2017

Application deadline: 1 February 2017

Please alert your students to this great opportunity!

More information and how to apply - please see www.evobio.eu Questions about the contents of the program:

Franjo Weissing (f.j.weissing@rug.nl)

Questions about the requirements and the application procedure:

Maartje Giesbers (m.c.w.g.giesbers@rug.nl)

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Postal address: Dr. Maartje Giesbers Administrative Coordinator MEME

Groningen Institute for Evolutionary Life Sciences University of Groningen P.O. Box 11103 9700 CC Groningen Visiting address: Nijenborgh 7, room 05-04

Phone +31 50 363 8462 Email m.c.w.g.giesbers@rug.nl

Working days: Monday, Tuesday, Thursday, Friday

Maartje Giesbers <m.c.w.g.giesbers@rug.nl>

UHannover MadagascarDemographics

Research assistant position (wissenschaftliche/r Mitarbeiter/in) The Institute of Zoology at the University of Veterinary Medicine Hannover (TiHo Hannover), Germany, invites applications for a research assistant position (65% TV-L 13 salary) in a project funded by the Deutsche Forschungsgemeinschaft (DFG). The position is available from the 1st of April 2017 for three years.

Marked climatic oscillations between glacial and interglacial periods had worldwide consequences for vegetation as well as animal population dynamics. This multidisciplinary project aims to integrate demographic inferences based on molecular datasets of mouse lemurs with validated high-resolution vegetation dynamics based on paleoecological reconstructions obtained from the same study sites reaching back to the Last Glacial Maximum (LGM). To reach these goals, study sites in northwestern and northern Madagascar will be visited for the joint collection of (paleo)ecological and population datasets and samples of mouse lemurs in direct vicinity to each other. The lemur samples will be analyzed by applying NGS technologies.

The successful candidate will join a multi-disciplinary field team and spend a period of 6 months in Madagascar for sample collection and the determination of lemur abundance in several study sites. We offer the opportunity for the acquisition of a doctoral degree in the framework of this study.

Applicants should hold a M.Sc degree in biology or equivalent qualification. A high motivation for a multifaceted project that includes substantial amount of field work under remote and basic living conditions as well as advanced bioinformatics techniques on large molecular datasets will be a prerequisite. Good language abilities in English, both orally and in writing, are required and some knowledge of French would be beneficial. Previous experience with tropical countries and with field techniques such as capture or handling of animals or distance sampling is a plus. Experience with molecular techniques such as sequencing and analysis of population genetic datasets would be highly beneficial. In addition, the applicant should have a high capability of self organization and the ability to work in a team as well as independently under difficult field working conditions.

Applications (in electronic form as single pdf file, subject line: mouse lemur demography) should consist of (I) a motivation letter, (II) a recent curriculum vitae including publications, (III) the abstract of the M.Sc thesis together with Master certificate, and (IV) contact information of two professional referees and should be sent until the 5th February 2017 by email to ute.radespiel@tiho-hannover.de.

For informal inquiries please contact Prof. Dr. Ute Radespiel ute.radespiel@tiho-hannover.de, Tel. +49-511-9538430

Prof. Dr. Ute Radespiel Institute of Zoology University of Veterinary Medicine Hannover Buenteweg 17 30559 Hannover Germany

Tel. 0511-9538430 Fax. 051-9538586 Email: ute.radespiel@tiho-hannover.de Web-page: <http://www.tiho-hannover.de/kliniken-institute/institute/-institut-fuer-zoologie/forschung/uag-radespiel/-uradesp/> "Radespiel, Ute" <ute.radespiel@tiho-hannover.de>

UHongKong ConservationGenetics

A fully funded PhD studentship is available for the study of population genetics and conservation biology of the endangered tree *Aquilaria sinensis* at the University of Hong Kong, in collaboration with Kadoorie Farm and Botanic Garden, Hong Kong.

Aquilaria sinensis, also known as incense tree or agarwood tree, is one of the most famous medicinal plants in Hong Kong and China. However, due to the rising demands for agarwood, this species is threatened by illegal felling throughout the region. To conserve and maintain healthy incense tree populations in Hong Kong, there is an urgent need to study the conservation genetics of this species. We now seek a high calibre student to (1) study the genetic diversity of *Aquilaria sinensis* in Hong Kong and understand how the genetic diversity is affected by illegal felling; (2) understand the genetic variation of *Aquilaria sinensis* at different age classes, and disentangle the gene flow patterns of this species. This work will contribute to the synthesis of a Species Action Plan and information gained from this project will be useful for conservation and restoration of this species in Hong Kong and throughout the region.

Prospective students with a background in conservation biology or population genetics are encouraged to apply.

A strong academic record, evidence of excellent writing and analytical skills, as well as enthusiasm for field and laboratory research will be a plus.

The PhD studentship includes a postgraduate scholarship, travel insurance and research support for four years. To apply, please send application materials, including a cover letter and copies of academic transcripts, resume and contact information for 3 references to saunders@hku.hk, gfisher@kfbg.org or hzhang@kfbg.org. Review of applications will begin immediately and continue until the position is filled.

Huarong Zhang, Ph.D.

Senior conservation geneticist

Flora conservation department

Kadoorie Farm and Botanic Garden

Hong Kong

hzhang@kfbg.org

UHull UK EvoParentalCare

We are advertising a cluster of projects on the evolution of parental care funded by University of Hull including two PhD studentships and a postdoctoral position supervised by Drs Isabella Capellini, Lesley Morrell and James Gilbert. For details about the postdoctoral position, soon to be open, please contact I.Capellini@hull.ac.uk.

To be considered for the shortlist, interested applicants are strongly advised to contact the relevant lead supervisor well in advance of application. Please enclose a CV and a brief explanation of why this position interests you, and any questions you have. Applicants should have at least a 2.1 undergraduate degree in Biology, Ecology, or related discipline, together with relevant research experience. A 1st class undergraduate degree or Masters level qualification are anticipated.

There are astonishing differences in whether, how, and for how long, animals care for their offspring. In most species, such as many marine fishes, parents abandon their fertilized eggs, which are mostly eaten by predators. By contrast, parents of other species, as in humans, provide protection and substantial amount of resources to their eggs or offspring.

PhD 1: Evolution of parents feeding offspring. Lead Supervisor: Dr James Gilbert, james.gilbert@hull.ac.uk

Parental feeding is rare among animals. The studentship

will focus on this crucial but little-understood behaviour. Insects are excellent for asking evolutionary questions about parental care: strategies are diverse, and often differ among related species. The student will first complete and publish a large reproductive trait database for insects, begun by Dr Gilbert, and second, in a broad comparative analysis across many species, address the following questions: (1) What ecological factors favour the evolution and/or maintenance of parental provisioning? Does provisioning evolve with harsh or stable environments; scarce, specialized resources; or predation? Is loss of offspring self-sufficiency a key precondition for the evolution of parental provisioning? (2) What are the evolutionary consequences of a food-provisioning strategy? Is optional (or partial) food provisioning behaviour inherently unstable? The project will deepen our understanding of an extremely important group, insects, and provides key comparisons not available in groups like mammals who uniformly feed offspring.

Further requirements: experience essential with at least one out of: database management, phylogenies, insect behaviour studies; two or more desirable. Experience with R desirable.

How to apply: Application is online at the following link: <https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=82439&LID=624> . PhD 2. Laterality and parental care in fish. Lead Supervisor: Dr Lesley Morrell, l.morrell@hull.ac.uk

Long thought to be unique to humans, lateralisation (or handedness) is now recognised as widespread in vertebrates. Animals show lateralisation in a wide range of organs and behaviours, and it is hypothesised that cerebral lateralisation can enhance cognitive abilities, particularly through the ability to attend to multiple tasks at one time (multitasking). For fish, this might be the ability to simultaneously forage and remain vigilant for predators, for example. In this project, we will investigate the potential link between lateralisation, parental care and other ecological factors in fish. More specifically, the project seeks to address the following questions: 1) Within and across species, are individuals that provide care more likely to be lateralised than individuals that do not? 2) How does laterality link to the ability to multitask in caring and non-caring situations? 3) How do environmental conditions shape laterality, and how does this link to the ability to multitask? Experimental work on the behaviour of fish in the University's aquarium facilities will be a key component of this project.

Further requirements: essential to the project are good skills and experience with experimental work, preferentially in behavioural ecology and/or with fish; experience

with R desirable.

How to apply: Application is online at the following link: <https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=82441&LID=624> . Positions will start on the 25th September 2017. Full-time UK/EU PhD Scholarships will include fees at the home/EU student rate and maintenance (pounds 14,121 in 2016/17) for three years, depending on satisfactory progress. Full-time International Fee PhD Studentships will include full fees at the International student rate for three years, dependent on satisfactory progress.

James.Gilbert@hull.ac.uk

ULeeds UK SeychellesWarblersFitness

A funded PhD studentship on "Individual variation in reproductive success in the cooperatively breeding Seychelles warbler" is available at the University of Leeds, UK, supervised by Dr Hannah Dugdale and co-supervised by Dr Simon Goodman. The PhD is in collaboration with Prof Terry Burke (University of Sheffield), Prof David S Richardson (University of East Anglia), Prof Jan Komdeur (University of Groningen) and Nature Seychelles (www.natureseychelles.org).

Accurate measures of fitness components, such as survival and reproduction, are fundamental to the study of evolutionary and conservation biology. However, fitness can be very difficult to measure in natural populations, e.g., individuals may disperse from the study area. Even in closed populations where survival can be monitored accurately, parentage can be hard to assign from behaviour alone, and requires the use of genetic markers. This requires genetic samples, which are usually obtained from offspring soon after hatching/birth. However, measuring fitness at this early life-history stage can be problematic as selection can act at different time points in life, affecting offspring at various ages. Fitness therefore needs to be measured at multiple life-history stages, and extend to grand-offspring, when investigating individual variation in reproductive success. Few studies have done this, as extensive, detailed long-term studies are required. The proposed study will use such data to investigate a range of key factors that impact on individual reproductive success in a cooperatively breeding system of Seychelles warblers. Understanding variation in reproductive success will provide important information to guide the long-term conservation efforts

of this once critically endangered species.

Why you should apply: The University of Leeds is in the world top 100 universities, globally recognised for its quality of teaching and research, and is in the leading group of UK universities, creating an excellent environment for a PhD. Dr Hannah Dugdale and Dr Simon Goodman will provide expertise in evolutionary biology. In particular, we will provide supervision in life-history evolution, social evolution and conservation biology, and we will encourage you to develop your own research ideas. You will gain specialist training in molecular ecology techniques, and you will gain fieldwork skills, conducting fieldwork for a minimum of three seasons (up to 3 months per season). You can develop your networking and team skills through collaborations with researchers on the long-term Seychelles warbler project (<http://seychelles-warbler-project.group.shef.ac.uk>). You will also benefit from a wide-range of training courses, such as: <http://www.emeskillstraining.leeds.ac.uk> and <http://www.fbs.leeds.ac.uk/postgraduate/professionaldev.php>. Funding: The studentship covers UK/EU tuition fees and a stipend at RCUK rates (~14,296 pa). Applicants from the UK/EU are eligible; international tuition fee payers are not eligible. Deadline: Monday, January 9, 2017. To apply: <http://www.nercdtp.leeds.ac.uk/how-to-apply/> < <http://www.fbs.leeds.ac.uk/postgraduate/researchdegree.php> >.

Further information: <http://www.nercdtp.leeds.ac.uk/projects/index.php?id=480> Hannah Dugdale <H.Dugdale@leeds.ac.uk>

ULeicester GreatApeGenomicDiversity

A fully-funded NERC studentship is available to European/UK Students, as part of the NERC DTP CENTA consortium (www.centa.org.uk), at the University of Leicester, UK

Subject: Sex-biased processes and the population structure and conservation of great ape species

Supervisors: Prof Mark A Jobling, Dr Celia A May, Dr Jon Wetton (Department of Genetics, University of Leicester, UK)

Informal enquiries to Prof Mark A Jobling, maj4@le.ac.uk, 0116 252 3427

For more details and how to apply, see: <http://www.centa.org.uk/themes/anthropogenic/17/> Applica-

tion Deadline: 23 January 2017

Overview

The population genetics and evolution of great apes (chimpanzees, bonobos, gorillas, orangutans) are of particular interest because this group is the most closely related to humans, yet critically endangered. Species and subspecies taxonomy has been labile over the last 20 years, and driven by molecular genetic data. Whole-genome data have given insights into gene flow between groups [1], with population isolates showing high genetic drift (particularly in mountain gorillas [2]), which has important implications for conservation genetics. Pathogens (e.g. Ebola) are decimating wild populations and imposing strong selection that will lead to adaptation. There is a clear need to better understand the structures of wild populations in their environments.

The genetic diversity of wild populations is strongly influenced by mating patterns and sex-biased dispersal, including the influence of sperm competition. Analysis of DNA variants in the male-specific region of the Y chromosome (MSY) and mitochondrial DNA (mtDNA) has contributed much to understanding these factors in many mammalian species. Until recently, typing of multiple short-tandem repeats (STRs) [3] has been the only way to assess MSY diversity in great apes. We have sequenced several megabases of MSY via next-generation sequencing (NGS), deriving a detailed MSY phylogeny (Fig. 1) containing thousands of single-nucleotide polymorphisms (SNPs) [4]. In our zoo-based sample this distinguishes well between (sub)species and reveals dramatic differences suggesting diverse sex-biased processes.

This project will expand the MSY tree by NGS analysis of additional great-ape individuals, to properly understand STR/SNP haplogroup relationships, and to develop methods to type MSY SNPs and STRs, as well as mtDNA, in non-invasive samples such as faeces and hair from wild populations. As well as allowing a large-scale approach to demography and sex-biased processes in samples from natural environments, such methods will be also be adapted for in-field analysis of bushmeat samples in order to combat a major threat to wild ape populations, thus aiding conservation.

The project will involve the initial establishment of 'conventional' methods for assessing diversity, including building fluorescent PCR multiplexes, analysis via capillary electrophoresis, set-up of software for automatic allele calling, PCR primer design, SNP typing, and Sanger sequencing.

PCR-based and sequence capture approaches will be established for next-generation (Illumina MiSeq) and third-generation sequencing platforms (MinION; Oxford

Nanopore Technologies). Methods will be adapted and validated for non-invasive samples from the wild, and MinION methods established for in-field analysis.

Phylogenetic analysis of DNA sequences and population-genetic statistical analysis will be undertaken to illuminate the population structures and evolution of great ape (sub)species, to understand the roles of sex-biased processes, and to aid in the establishment of conservation strategies.

Applicants must meet requirements for both academic qualifications and residential eligibility: <http://www.nerc.ac.uk/skills/postgrad/> To apply formally, please visit: <http://www2.le.ac.uk/research-degrees/funding/centa/how-to-apply-for-a-centa-project> References

1. Prado-Martinez J, Sudmant PH, Kidd JM, Li H, Kelley JL, Lorente-Galdos B, Veeramah KR, Woerner AE, O'Connor TD, Santpere G et al: Great ape genetic diversity and population history. *Nature* 2013, 499: 471-475.
2. Xue Y, Prado-Martinez J, Sudmant PH, Narasimhan V, Ayub Q, Szpak M, Frandsen P, Chen Y, Yngvadottir B, Cooper DN et al: Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. *Science* 2015, 348: 242-245.
3. Arandjelovic M, Head J, Rabanal LI, Schubert G, Mettke E, Boesch C, Robbins MM, Vigilant L: Non-invasive genetic monitoring of wild central chimpanzees. *PLoS One* 2011, 6: e14761.
4. Hallast P, Maisano Delser P, Batini C, Zadik D, Rocchi M, Schempp W, Tyler-Smith C, Jobling MA: Great-ape Y-chromosome and mitochondrial

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ULeicester HumanAncientDNA NAModernDNAanalyses

A three year-funded studentship, offered at the standard Research Council UK rate, is available to European/UK Students, at the Department of Genetics of the University of Leicester, UK

Subject: The slave-trade and beyond: the genetics of recent African migrations Supervisors: Dr Sandra Beleza, Prof Mark A Jobling (Department of Genetics, Univer-

sity of Leicester, UK) Application deadline: 7th February 2017

Informal enquiries to Dr Sandra Beleza, sdsb1@le.ac.uk, 0116 294 4548

For more details and how to apply, see: <http://www2.le.ac.uk/departments/genetics/postgraduate/phd-studentships> Overview: Human genetic variation commonly exhibits geographic structuring as a consequence of demographic history (such as population subdivision, migration, and admixture or replacement), as well as locus-specific forces such as selection, mutation and recombination. Thus, dissecting the patterns of this variation is important for the reconstruction of human evolutionary history, and can contribute to the understanding of the genetic basis of phenotypic adaptation and complex disease. Drawn by the knowledge of high levels of genetic diversity and low levels of linkage disequilibrium (which have important implications for the mapping of disease susceptibility loci), geneticists are increasingly turning their attention to Africa, the continent of origin of our species. The African Genome Variation Project has enhanced our understanding of the genetic variation in West, West-central and East Africa, and started to reveal the influence of pre-historical and historical large-scale migrations and expansions on the distribution of the genetic diversity across the continent.

Here, we propose to complement these studies with a detailed genomic study of our own collection of samples, and to provide a detailed characterization of the timing and extent of important recent migrations that occurred within Africa and from Africa to the Americas. Firstly, the student will combine public African datasets with our samples from Southwest and Southeast Africa to model the significant demographic shift in Sub-Saharan Africa that took place during the Bantu expansion. Secondly, they will combine this extended contemporary African dataset with ancient DNA (aDNA) analyses of human remains recovered from slave cemeteries located in the main receiving ports in Northeast and Southeast Brazil, and modern DNA analyses of descendants of enslaved Africans (Brazilians) collected in the same regions, to investigate the ethnic origins, demographic history and contemporary legacies of the trans-Atlantic slave trade. Given the historical evidence on different forced migratory routes from Africa to the Northeastern and Southeastern Brazilian ports, the shift in the relative importance of these routes through time, and the large number of slaves carried (ten times more than were carried to North America), the study of the African diaspora in Brazil provides a unique opportunity to understand the population dynamics of the trans-Atlantic slave trade. The student will apply both analytical and

simulation-based methods to test different evolutionary scenarios, and to infer the main population parameters (such as population sizes, divergence times, migration rates, and timing and magnitude of recent admixture events) that gave rise to the contemporary diversity of European and European-derived populations.

By using such a complete dataset and state-of-the-art techniques, the project will be able to shed light on the demographic history of Africa and of populations influenced by African migrations, and on the fundamental processes of human migration. Finally, pairing this genomic data with ecological, historical, linguistic and other socio-economical variables, as well as with morphological and biomedical trait values such as skin colour, body mass index and blood pressure, the student will be able to interpret a range of genetic and non-genetic dimensions of African variation, including disease susceptibility, morphologic variation, linguistic differentiation, and cultural and social practices.

Applicants should expect to hold a 1st or 2.1 BSc in a relevant field by the end of September 2017 when the studentship will commence. Those holding a 2.2 degree plus a Master's degree or >3 years relevant post-graduate experience may be eligible. Candidates with degrees from abroad may be eligible if their qualifications are deemed equivalent.

To apply formally, please visit: http://www2.le.ac.uk/research-degrees/phd/applyphd?uol_r=78572a95 Sandra Belez, PhD Lecturer in Genetics University of Leicester Adrian Building University Road Leicester, LE1 7RH UK

Phone: +44 (0)116 294 4548 email: sdsb1@leicester.ac.uk; sbeleza@gmail.com

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ULethbridge AvianEvolution

I am looking for outstanding students interested in pursuing a graduate degree in evolutionary biology. I have several potential projects on evolutionary ecology, population genetics, landscape genetics, and speciation of birds which are suitable for MSc or PhD projects.

Field work is an important aspect of the research and preference will be given to applicants who have banding/ringing experience. Experience with lab work (PCR, sequencing, genomics, genotyping) are also an asset. Preferred start dates are May 1 or Sept 1 2017.

Admissions criteria and deadlines for application can be found on the School of Graduate Studies website (<https://www.uleth.ca/graduate-studies/>) along with a list of internal funding opportunities:

<https://www.uleth.ca/graduate-studies/awards/sgs-tuition-scholarship> <https://www.uleth.ca/graduate-studies/awards/sgs-deans-scholarship> The University of Lethbridge has a strong research program in evolutionary biology and a diverse group of researchers. Graduate students are eligible for full funding packages through a combination of TA-ships and competitive internal scholarships (including tuition awards), and are encouraged to apply for external fellowships from a variety of Provincial and Federal sources.

Theresa Burg

Biological Sciences

University of Lethbridge

403 332 5299

<http://scholar.ulethbridge.ca/theresaburg/> “The only real mistake is the one from which we learn nothing”

“Burg, Theresa” <theresa.burg@uleth.ca>

ULondon EvolutionaryTheory

Graduate positions are available in evolutionary theory, mathematical modelling at the School of Biological Sciences of Royal Holloway, University of London. Some topics of interest are

- Modelling the spread of pathogens and symbionts in social insect colonies (Professor Vincent Jansen)
- The common good and alignment of evolutionary interest between endogenous retroviruses and their hosts (Professor Vincent Jansen)
- The fitness consequences of spatial cognition in the bumblebee *Bombus terrestris* (Dr Elli Leadbeater)

The deadline is 31/1/17, but contact the supervisors if an extension to the deadline is needed

For details see

<https://www.royalholloway.ac.uk/biologicalsciences/-prospectivestudents/postgraduateresearch/phdstudentships2017.aspx>

These are fully funded studentships, many available to applicants from the EU (some are restricted to UK residents)

Vincent Jansen

“Jansen, Vincent” <Vincent.Jansen@rhul.ac.uk>

UManchester PopulationGenomics

Funded PhD Opportunity

Title: Population genomics of *Aedes aegypti* mosquitoes, the vector of dengue, Chikungunya and Zika

Supervisors: Cathy Walton and Tucker Gilman at the University of Manchester, UK and Weiwei Zhai at the Genome Institute of Singapore

Location: As this studentship is part of the ASTAR programme with Singapore Institutes, the student would spend two years in the UK and 2 years in Singapore.

Application deadline: 22 January

To apply follow the link at: <https://www.findaphd.com/>-

[search/ProjectDetails.aspx?PJID=81544&LID=-1024](https://www.findaphd.com/search/ProjectDetails.aspx?PJID=81544&LID=-1024)

Informal enquiries can be made to catherine.walton@manchester.ac.uk and/or tucker.gilman@manchester.ac.uk

Project Description

Knowledge of dispersal in mosquitoes such as *Aedes aegypti*, the vector of dengue, Zika and chikungunya viruses, is critical to the implementation of several methods of disease control. For example, the effectiveness of insecticide spraying depends upon immigration rate of new mosquitoes into the treated area and spacing of the release of sterile males depends upon dispersal distance and ease of movement through the landscape. Population genetics methods potentially offer the most powerful approach to infer dispersal from estimates of gene flow. However, estimating gene flow on the ecologically relevant (i.e. recent) time frames for control of mosquito borne disease is non-trivial, as estimates are confounded by historical effects in most existing methods of analysis. Population genomics (i.e. population genetics on a genome wide scale) offers the potential for a new approach to tackle this problem due to the large amounts of data that can be generated. In this project, the student will generate and analyse genomic sequence data in a population genomics and landscape genomics framework to understand gene flow in and evolution of *Aedes aegypti* on a scale relevant for disease transmission control.

This studentship is suitable for students with either biological or mathematical backgrounds. During the studentship, the student will develop a deep understanding of population genetics theory. The project will involve a limited amount of fieldwork to collect mosquitoes and some molecular genetics work in the laboratory. However, the project will largely focus on the analysis of genetic data and, as necessary, the development of novel and modification of existing analytical approaches. The primary aim of the project is to characterise recent gene flow and any landscape barriers to mosquito dispersal. However, from the genomic data it will also be possible to infer demographic history and identify genes that may be under positive adaptive selection; such genes are likely to be particularly relevant to disease transmission and/or control. The methodological approaches developed will be relevant to a wide range of problems concerned with man-made environmental change (e.g. the spread of pest species and the conservation of species of conservation concern).

Funding Notes

The project is available to UK/EU candidates. Funding covers fees (UK/EU rate) and stipend for four years. Overseas candidates can apply providing they can pay

the difference in fees and are from an eligible country. Please check the website for information on eligibility. Candidates will be required to split their time between Manchester and Singapore, as outlined on our website. Applications should be submitted online and candidates should make direct contact with the Manchester supervisor to discuss their application directly.

References

1. Bennett KL, et al. (2016) Historical environmental change in Africa drives divergence and admixture of *Aedes aegypti* mosquitoes: a precursor to successful worldwide colonization? *Mol Ecol.* 25: 4337-54.
2. Kempainen P, et al. (2015) Linkage disequilibrium network analysis (LDna) gives a global view of chromosomal inversions, local adaptation and population structure. *Mol Ecol Res* 15:1031-1045.
3. Gilman RT, et al. (2012) Coevolution in multidimensional trait space favors escape from parasites and pathogens. *Nature* (2012) 483(7389):328-330.
4. Wang GD, et al. (2016) Out of southern East Asia: the natural history of domestic dogs across the world. *Cell Res.* 26:21-33.

Catherine Walton <Catherine.Walton@manchester.ac.uk>

UNamur Belgium Rotifer Evolution

2

A PhD position is available to study extreme stress responses in the notorious bdelloid rotifers, UNamur, Belgium

A PhD position is available immediately to start working on the oxidative stress responses of bdelloid rotifers following desiccation and radiation within the group of Prof. Karine Van Doninck (Laboratory of Evolutionary Genetics and Ecology) and Dr. Florence Chainiaux at the University of Namur (Belgium).

While several metazoan asexual lineages exist, the most notorious and successful clade is the bdelloid rotifers containing at least 460 morphospecies that seems to have evolved for tens of millions of years without sexual reproduction (including fertilization and meiosis with pairing of homologous chromosomes). Besides their asexual mode of reproduction, they are also well-known for their extreme desiccation and radiation resistance. Entering a desiccated state is however harmful in most animals and is expected to be accompanied by the generation of reactive oxygen species (ROS), known to induce damages at the DNA, protein and lipid level if not neu-

tralized by antioxidants. This PhD project will study and characterize in detail the oxidative stress generated during desiccation and radiation in the model bdelloid species *Adineta vaga* and investigate their antioxidant responses. Being funded by the European Space Agency, this Phd will also investigate the impact of simulated micro gravity on oxidative stress responses and be involved in space mission preparation.

This PhD position is for 1 year and can start beginning of February 2017, being funded by two projects, ESA (European Space Agency) and ARC (Actions de Recherche Concertées). An extension of another 3 years is possible but the candidate will be encouraged to apply for its own FRIA or FNRS Belgian PhD grant.

Prof. Karine Van Doninck recently acquired an ERC Consolidator Grant to study the mechanisms of genome evolution in the absence of meiosis in bdelloid rotifers; this ERC CoG will start in 2017. This PhD will join a very dynamic research lab including nowadays 5 post-docs, 2 PhD students and 3 technicians at UNamur. We employ interdisciplinary approaches (cellular and molecular biology, comparative genomics, bioinformatics and community level) to study evolutionary processes in the absence of sex and the mechanisms of extreme resistances. Our team obtained the first draft genome of the bdelloid rotifer *A. vaga* (Flot.etal.2013.Nature), we have optimized desiccation and radiation protocols (Hespeels.etal.2014.JEB) and recently we discovered horizontal gene transfer between *A. vaga* individuals sampled in the wild (Debortoli.etal.2016.Current Biology). Our laboratory works for this project in close collaboration with Dr. F. Chainiaux at UNamur, studying ageing and oxidative stress in human, with Prof. S. Lucas at LARN (UNamur) for the radiation experiments, with Prof. B. Hallet at UCL (Belgium) specialized in DNA repair studies and with Dr. S. Baatout of the SCK-CEN radiobiology unit (Mol, Belgium) for the microgravity experiments.

Contacts: For more information contact Prof. Karine Van Doninck, karine.vandoninck@unamur.be or Dr. Boris Hespeels, boris.hespeels@unamur.be from the University of Namur, Laboratory of Evolutionary Genetics and Ecology <http://www.lege-unamur.be> Application: Applicants should have a Msc degree in Biology or Molecular Life Sciences or Medical Biology with a specialization in molecular biology, evolutionary genetics, biochemistry or similar. The successful candidate should be proficient in English and should demonstrate his motivation to do a Phd and work in a multidisciplinary research team with a highly collaborative spirit.

The closing date for applications is 20th of January 2017.

Interested applicants should send a cover letter (briefly describing research experience, interests, and career goal), curriculum vitae (with list of publications if any), and the names of three references (including address, phone number and Email) to Karine VAN DONINCK (karine.vandoninck@unamur.be)

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Karine VAN DONINCK Full Professor Department of Biology

T. +32 (0)81 724 407 F. +32 (0)81 724 362 karine.vandoninck@unamur.be <http://perso.fundp.ac.be/~kvandoni/> Universite de Namur ASBL Rue de Bruxelles 61 - 5000 Namur Belgique

Let's respect the environment together. Only print this message if necessary!

Karine Van Doninck <karine.vandoninck@fundp.ac.be>

UNamur Belgium Rotifer Evolution

3

A PhD position is available to study extreme stress responses in the notorious bdelloid rotifers, UNamur, Belgium

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this Phd will also investigate the impact of simulated micro gravity on oxidative stress responses and be involved in space mission preparation.

This PhD position is for 1 year and can start in February 2017, being funded by two projects, ESA (European Space Agency) and ARC (Actions de Recherche Concertées). An extension of another 3 years is possible but the candidate will be encouraged to apply for its own FRIA or FNRS Belgian PhD grant.

Prof. Karine Van Doninck recently acquired an ERC Consolidator Grant to study the mechanisms of genome evolution in the absence of meiosis in bdelloid rotifers; this ERC CoG will start in 2017. This PhD will join a very dynamic research lab including nowadays 5 post-docs, 2 PhD students and 3 technicians at UNamur. We employ interdisciplinary approaches (cellular and molecular biology, comparative genomics, bioinformatics and community level) to study evolutionary processes in the absence of sex and the mechanisms of extreme resistances. Our team obtained the first draft genome of the bdelloid rotifer *A. vaga* (Flot.etal.2013.Nature), we have optimized desiccation and radiation protocols (Hespeels.etal.2014.JEB) and recently we discovered horizontal gene transfer between *A. vaga* individuals sampled in the wild (Debortoli.etal.2016.Current Biology). Our laboratory works for this project in close collaboration with Dr. F. Chainiaux at UNamur, studying ageing and oxidative stress in human, with Prof. S. Lucas at LARN (UNamur) for the radiation experiments, with Prof. B. Hallet at UCL (Belgium) specialized in DNA repair studies and with Dr. S. Baatout of the SCK-CEN radiobiology unit (Mol, Belgium) for the microgravity experiments.

Contacts: For more information contact Prof. Karine Van Doninck, karine.vandoninck@unamur.be or Dr. Boris Hespeels, boris.hespeels@unamur.be from the University of Namur, Laboratory of Evolutionary Genetics and Ecology <http://www.lege-unamur.be> Application: Applicants should have a Msc degree in Biology or Molecular Life Sciences or Medical Biology with a specialization in molecular biology, evolutionary genetics, biochemistry or similar. The successful candidate should be proficient in English and should demonstrate his motivation to do a Phd and work in a multidisciplinary research team with a highly collaborative spirit.

The closing date for applications is 31st of January 2017.

Interested applicants should send a cover letter (briefly describing research experience, interests, and career goal), curriculum vitae (with list of publications if any), and the names of three references (including address, phone number and Email) to Karine VAN DONINCK (karine.vandoninck@unamur.be)

Karine VAN DONINCK Full Professor Department of Biology

T. +32 (0)81 724 407 F. +32 (0)81 724 362
 karine.vandoninck@unamur.be <http://perso.fundp.ac.be/~kvandoni/> Université de Namur ASBL Rue de Bruxelles 61 - 5000 Namur Belgique

Let's respect the environment together. Only print this message if necessary!

Karine Van Doninck <karine.vandoninck@fundp.ac.be>

UOsnabruck IPK Gatersleben SteppePlantPhylogeography

The University of Osnabruck and the IPK Gatersleben invite applications for three PhD positions in Evolutionary Biology/Plant Systematics in a project inferring vegetation history of the Eurasian steppe belt. The project will involve fieldwork, NGS methods, and phylogeographic analyses for a set of about 20 plant taxa characteristic for the steppe vegetation. A more detailed description of the project and information regarding applications can be found through http://www.ipk-gatersleben.de/uploads/media/08_01_17_3PhDPositions_ETX_V1.pdf. Deadline for the application is February 28, 2017. Intended project start will be May or June 2017. Frank Blattner (blattner@ipk-gatersleben.de)

"Frank R. Blattner" <blattner@ipk-gatersleben.de>

UPlymouth AdaptationMechanisms ExtDeadline

****EXTENDED DEADLINE****

University of Plymouth, UK

Fully funded PhD studentship with Dr Mike Thom (Plymouth) and Dr Jon Bridle (Bristol) investigating the role of sexual selection in adaptation to variable environments.

The studentship will be available to start from 1st April

2017, and must start by 1st October 2017 at the latest.

Project Description Understanding how organisms adapt to changing environmental conditions is a central goal of evolutionary biology, and one which has important conservation application in helping to predict potential impacts of environmental challenges on species distributions and diversity. Two key theoretical questions are (1) how does temporal and/or spatial variability in the environment affect evolutionary response to change, and (2) how do various evolutionary mechanisms interact during adaptation? This project will use an experimental evolution approach with the model organism *Drosophila melanogaster* to explore evolutionary responses to a number of static and fluctuating environmental challenges, focusing on the interplay between sexual and natural selection during adaptation. The student will use a variety of behavioural, physiological and quantitative genetic techniques to investigate the phenotypic signatures and genetic architecture of population level responses to environmental variation.

The studentship is supported for 3 years and includes full UK/EU tuition fees plus a stipend of 14,296 per annum. The studentship will only fully fund those applicants who are eligible for Home/EU fees with relevant qualifications. Applicants normally required to cover overseas fees will have to cover the difference between the Home/EU and the overseas tuition fee rates (approximately 11,040 per annum).

Further info can be found at: <http://www.jobs.ac.uk/-job/AWA894/phd-studentship-evolutionary-mechanisms-of-adaptation-to-variable-environments/>

Apply here: <https://www.plymouth.ac.uk/study/-postgraduate>

Queries to me at michael.thom@plymouth.ac.uk

Michael Thom Lecturer in Evolutionary Biology Associate Head of School (Teaching and Learning) School of Biological Sciences Faculty of Science and Engineering University of Plymouth PL4 8AA +44(0) 1752 5 84473 Office: Portland Square A417

Michael Thom <michael.thom@plymouth.ac.uk>

UPortsmouth EvolutionFlowering

PhD opportunity at the University of Portsmouth, Project code: BIOL3150217 <https://www.findaphd.com/search/projectdetails.aspx?PJID=-73259> Please contact rocio.barrales@port.ac.uk for

details.

Title: Genetic causes and ecological consequences of flowering initiation in *Linum bienne*

Project description: Global warming has shifted the start of flowering in many plant species. Spring starts earlier in the UK and the North of Europe, where the flowering season has now extended. In Mediterranean countries, flowering also starts earlier, but its duration is shorter to avoid the summer period and the dry season. Although we have a relatively good understanding of the pathways that trigger flowering initiation, we are still far from understanding how plants perceive and respond to environmental and climatic variation to shift from vegetative growth to initiate flowering, and the level to which global warming affects it. Furthermore, an adaptive response to the stress imposed by global warming can only occur if plant populations harbour sufficient genetic variation in flowering initiation. In this project, we will investigate variation in flowering initiation and in other plant traits to assess how they affect seed production in *Linum bienne*. This will be done in populations across its geographic range between the South of Spain and the UK. The project will include greenhouse experiments and common garden experiments to estimate genetic and phenotypic variation, and heritability of flowering initiation and correlated traits and plant performance. This will allow detecting local adaptation associated to different environments and climates in Europe. It will also help identifying populations resilient to global warming and prompt to provide an adaptive response to climate change. Because *L. bienne* is the wild crop relative of cultivated flax, measures of traits with agronomic value will be included to assess the potential of *L. bienne* to improve cultivated flax.

Candidates must have a Master degree, and background in Plant Biology, Ecology and Evolution. The present project will suit candidates interested on Evolutionary Ecology, and with a profile in data analysis. The candidate should be familiar with R for data analysis of ecological and molecular data, and flexible to work in a team and independently. It is expected that (s)he will be active preparing grant proposal and manuscripts. The candidate will gain skills both in the field and the lab, plant breeding, crop research, and data analysis. The lab work and greenhouse experiments will be conducted in the facilities of The University of Portsmouth. The candidate will have access to the Graduate School Development Programme and Department Postgraduate Researcher Training, and will join the Biodiversity and Evolution research team at the School of Biological Science. Funding Notes: Home/EU applicants only. Please use the online application form and state the project code (BIOL3150217) and studentship title in

the personal statement section.

Funds will be provided for 3 or 4 years which will include: bursary (at current RCUK rates), University fees (UK/EU rate) plus pounds 1,500 pa project costs/consumables for the duration of the studentship.

Rocio Perez-Barrales Senior Lecturer School of Biological Sciences University of Portsmouth King Henry Building King Henry 1st Street Portsmouth PO1 2DY <http://www.port.ac.uk/> https://www.researchgate.net/profile/Rocio_Perez-Barrales/ Rocio Barrales <rocio.barrales@port.ac.uk>

UPoznan EvolutionSpecialization

Call for PhD student for the project: A bidirectional selection experiment to test the evolution of specialization and dispersal in the invasive wheat curl mite, *Aceria tosichella*

We seek a highly motivated student to carry out a PhD project in the Population Ecology Lab, Faculty of Biology, A. Mickiewicz University (AMU) in Poznań, Poland (<http://popocol.home.amu.edu.pl/-research/>). The project will be conducted in cooperation with the Centre for Ecology, Evolution and Environmental Changes, University of Lisbon, Portugal.

The goal of the project is to understand the evolutionary interplay between host specialization and dispersal. Specifically, we will investigate how evolution in constant or changing environments shapes the host range and dispersal ability of an invasive plant-feeding mite.

The PhD student is expected to carry out field work in agricultural landscapes in Poland (1st year), then to conduct selection experiments, assess dispersal efficiency, maintain mite stock colonies, measure population parameters, contribute to laboratory molecular analyses, participate in scientific discussions and write manuscripts.

We offer a position for 3 years and a friendly, supportive working environment. The scholarship allows for a reasonable standard of living in Poland.

Applicants should have: - a Master of Science degree in Biological Sciences (biology, ecology, zoology, biochemistry, etc.); - interest in ecology and evolutionary biology; - English language skills (fluent communication, both written and spoken); - organizational skills, self-reliance, willingness to learn, smooth and productive cooperation

within a team. Additionally, prior scientific activity (e.g. articles, conferences, fellowships) is desirable.

How to apply: Applications should include: motivation letter, CV including research experience and publication list, reference contacts to 2 researchers, and a scan of University diploma. Please send your application as soon as possible to: anna.skoracka@amu.edu.pl and include "PhD position" in the e-mail subject line, no later than 15 March 2017. Selected candidates will be invited for an interview (in person or via Skype). The successful applicant will then apply to the AMU Faculty of Biology as a PhD candidate following the standard procedure.

If you have any questions regarding this position please feel free to contact me: anna.skoracka@amu.edu.pl More information about the project and our research group can be found here: <http://popecol.home.amu.edu.pl/-research/evo-eco-erio/spec-disp/> – Anna Skoracka Adam Mickiewicz University in Poznań Faculty of Biology Population Ecology Lab Umultowska 89, 61-614 Poznań <http://popecol.home.amu.edu.pl/-lab-members/anna-skoracka/> Anna Skoracka <skoracka@amu.edu.pl>

UppsalaU Metagenomics

Hi,

See the link for a PhD position opportunity in my group at Uppsala University on metagenomics from ancient lake sediments

<http://www.uu.se/en/about-uu/join-us/details/?positionId=132979> Please, distribute to anyone you think is interested!

Regards

Laura

Laura Parducci Plant Ecology/ Dept of Ecology and Genetics Evolutionary Biology Centre Uppsala University Norbyvagen 18 D SE-752 36 Uppsala, Sweden EBC, House 7, floor 2

laura.parducci@ebc.uu.se +46-18-471 6414
www.ieg.uu.se/plant/research-groups/ [@laurapucci](http://www.laurap.it)

Laura Parducci <Laura.Parducci@ebc.uu.se>

UppsalaU Sweden Systematic Biology

PhD student in systematic biology, within mycology

A position as a PhD student working with the evolution of ectomycorrhizal fungi is available in Martin Ryberg's group at Uppsala University, Sweden. The full add, and link to application system, is available at: <http://-uu.se/en/about-uu/join-us/details/?positionId=130647> To be eligible for a PhD-student position the applicant must hold a master degree (or equivalent) in a relevant field. The ideal candidate is highly motivated with education/experience in mycology, bioinformatics, phylogenetics and/or molecular lab-work. Candidates must be fluent in English.

martin.ryberg@ebc.uu.se

UQuebecEnOutaouais VernalPoolBiodiversity

A graduate position is available from September 2017 at the Institut des Sciences de la Forêt Tempérée (ISFORT), Université du Québec en Outaouais. Since language policy of the University requires a good level of French for the position, details below are in French only:

Opportunité de bourse de doctorat PhD

Description du projet : La forêt tempérée feuillue de l'est du Canada, composée majoritairement par l'érable à sucre, revêt une importance socio-économique majeure. Ce biome forestier est caractérisé par la plus forte densité humaine au Canada, et génère d'importantes retombées économiques. Par ailleurs, cette forêt génère aussi un large éventail de services écosystémiques qui ont une valeur considérable pour la société (e.g. habitat pour la biodiversité, régulation du climat, cycle des nutriments, activités récréatives, qualité de l'air, régulation du climat, pollinisation, approvisionnement en eau). Cette forêt est soumise à de fortes perturbations en raison des activités anthropiques, dont l'industrialisation, l'urbanisation, la sylviculture et le déboisement à des fins

d'agriculture intensive. Concernant la sylviculture, deux principales approches de gestion forestière sont utilisées : les coupes à blanc (ou coupes totales, aménagement équienne) et les coupes de jardinage (ou coupes partielles, aménagement inéquienne). Malgré la pratique ancienne de ces deux approches, nous ne connaissons pas encore leur impact sur la biodiversité et les services écosystémiques. Afin d'étudier cet impact, ce projet évaluera l'effet de la gestion équienne et inéquienne sur la biodiversité des communautés d'amphibiens rencontrées dans les étangs vernaux de la forêt feuillue tempérée ainsi que sur la connectivité des populations. Ce projet se déroulera à Kenauk, une forêt privée de 230 km² sur laquelle différentes parcelles ont subi ces deux types d'aménagements. Dans un premier temps, ce projet permettra de valider l'utilisation du séquençage nouvelle génération pour obtenir une estimation précise et rapide de la biodiversité. Puis, la comparaison de la biodiversité de parcelles ayant subi des coupes totales ou partielles sera comparée à celle de parcelles n'ayant jamais été coupées afin d'estimer l'impact de différents aménagements forestiers sur la biodiversité. Enfin, l'impact de ces aménagements sur la connectivité fonctionnelle sera étudié par des méthodes de capture-marquage-recapture, télémétrie et de génétique du paysage. Le projet sera conduit en collaboration avec Kenauk Canada et Conservation de la Nature Canada, deux des propriétaires de la propriété forestières. Il apportera des connaissances inédites permettant d'améliorer l'aménagement forestier tout en préservant la biodiversité et les services écosystémiques. Le (la) candidat(e) évoluera dans l'environnement stimulant de l'Institut des Sciences de la Forêt tempérée (ISFORT; <http://isfort.uqo.ca/>).

Exigences : Le (la) candidat(e) doit avoir complété une maîtrise en sciences biologiques, ou sciences connexes. Il (elle) doit être disponible pour travailler sur le terrain en forêt durant l'été 2018 (ce terrain requière une bonne condition physique) et aimer travailler en équipe. Les expériences et compétences suivantes seraient un atout: -expérience de terrain en milieu forestier -compétences en biologie moléculaire (extraction d'ADN, PCR, qPCR, séquençage) -familiarité avec l'environnement UNIX et compétences en analyse de données (logiciel R) et programmation (Python) -connaissance des amphibiens (un atout)

Début du projet : Septembre 2017

Bourse : 20 000\$/an pour 3 ans

Supervision : Yann Surget-Groba (UQO-ISFORT) et Angélique Dupuch (UQO-ISFORT) Veuillez envoyer un relevé de notes de maîtrise, une lettre de motivation, un CV et le nom et les coordonnées de trois

références à Yann Surget-Groba et Angélique Dupuch aux adresses suivantes: yann.surget-groba@uqo.ca et angelique.dupuch@uqo.ca. L'examen des candidatures se poursuivra jusqu'à ce que le poste soit pourvu.

– Prof. Yann Surget-Groba Institut des Sciences de la Forêt Tempérée Université du Québec en Outaouais 58, rue Principale Ripon, Québec, J0V 1V0

Phone: +1 819 595 3900 ext. 2933 E-mail: yann.surget-groba@uqo.ca <http://www.surget-groba.ch>

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URochester MolluscShellEvoDevo

URochester.MolluscShellEvoDevo

PhD position in evolutionary development of gastropod shells

A graduate student position is available for study of the mechanisms of mollusc shell development. Molluscs are one of the most diverse and successful animal groups, in terms of body plans, species, and their ubiquity across ecosystems and niches. Their success is likely due in part to a key molluscan character– the shell, a strong and durable exoskeleton of calcium crystals.

Mollusc shells are a very powerful model system for morphological evolution. They are extremely diverse and disparate, and different morphologies can often be directly related to functional differences. They have an exquisitely detailed fossil record, which allows morphological change to be tracked through evolutionary time. Shells grow progressively, at the outer edge, so they record ontogenetic change like no other animal structure. Despite the diversity of mollusc shell morphology, the geometry of shell growth is relatively simple– even dramatic differences in shell form can be explained by differences in basic parameters of shell growth. This has made them a prominent system for modeling morphological change. Indeed, work on mollusc shells inspired the concept of morphospace– the theoretical representation of all the possible forms or structures of an organism. In addition, shell biomineralization has been extensively studied and is a model for materials science (Marin et al., 2012). Despite the many strengths of mollusc shells

for studies of morphological evolution, they have not been tractable for mechanistic studies of the evolution of development, because the developmental mechanisms that control shell growth are not known.

The successful candidate will extend recent discoveries in the Lambert lab at the University of Rochester. Studies will focus on the cellular behaviors in the mantle epithelium that control shell shape, and on the genes that regulate these processes. Methods will include cell proliferation assays, RNA-seq, in situ hybridization and gene knockdown studies. Further comparative and modeling projects are also anticipated.

To apply, please send a CV and a short statement describing your background and interests, to David Lambert at email address dlamber2@mail.rochester.edu.

- David Lambert Associate Professor Department of Biology University of Rochester <http://www.rochester.edu/College/BIO/labs/LambertLab/index.html> Office: 344 Hutchison Hall Lab: 338 Hutchison Hall 585 273-2482 (office) 585 275-7521 (lab) 585 275-2070 (fax) Shipping address: University of Rochester Department of Biology 213 Hutchison Hall River Campus Rochester, NY 14627-0211 Mailing address: University of Rochester Hutchison Hall RC Box # 270211 Rochester NY 14627-0211

“Lambert, David” <dlamber2@smtp-gw.rochester.edu>

UtrechtU EvolutionAntimicrobialResistance

Specifications - (explanation) Location Utrecht University, Faculty of Veterinary Medicine Function types Onderzoek, Ontwikkeling, Innovatie Scientific fields Gezondheid Hours 38.0 hours per week Salary euro 2191 - euro 2801 Education Universitair Job number 884786 Translations en nl About employer Universiteit Utrecht Short link www.academictransfer.com/38241 Job description Plasmid-mediated antimicrobial resistance (pAMR) occurs in both humans and animals and requires One-health solutions, which include a holistic approach integrating veterinary, medical and environmental disciplines. The susceptibility and contagiousness of pAMR depends on ecological and evolutionary processes in the microbiota of the host. A consortium of Utrecht University (UU) and Wageningen University (WU) will study the ecological and evolutionary dynamics of pAMR in gut microbiota of chickens using mathematical modelling and experiments in the project, entitled “Microbiome Invasion and Transmis-

sion of plasmid-mediated Antimicrobial Resistance”, a.k.a. “MITAR”, supported by a grant of ZonMW.

We are seeking a motivated PhD candidate, who wants to contribute to our fundamental understanding of the ecology and evolution of pAMR with an eye for application of the results to obtain better interventions and risk analyses. Tasks of the candidate include development and analyses of mathematical models, development of theory and analysis methodology, as well as validation of these methods with experimental data sets. Furthermore, the candidate will design, conduct and analyse in vivo experiments using chicken.

The candidate will work at UU in close collaboration with a post-doc in evolutionary microbiology at WU.

The project will be supervised by Prof Arjan Stegeman (UU), Prof Arjan de Visser (WU), Dr Egil Fischer (UU) and Dr Mark Zwart (WU).

Requirements A suitable candidate for this project has analytical skills with an original and innovative mind. The candidate is required to work independently and in collaboration with the Post-doc at Wageningen UR, other PhD-students at UU, technicians and her/his supervisors.

A suitable candidate holds an MSc degree recognized by the board of promotions in one of the life sciences with a strong quantitative component, such as theoretical biology, systems biology, physics, chemistry or epidemiology. The candidate should be able to use at least one programming language, preferably R or Wolfram Mathematica, and have proven experience with the use and development of computational models for the study of (biological)dynamical processes. Experience and affinity with working with experimental animals is preferred.

Dissemination of the results will consist in writing a PhD-thesis and peer-reviewed articles in scientific journals, as well as presentations at international conferences and stake-holder meetings. Therefore, a suitable candidate has a high level of English in writing and speech according to CEFR proficiency level C.

Conditions of employment We offer a 1,0 fte position an initial period of one year, with the possibility of extension for in total three FTE years. Salary starts at euro 2,191 and increases to euro 2,801 (scale P of the Collective Labour Agreement of the Dutch Universities) gross per month for a full-time employment in the fourth year of the appointment (according to NWO standards). Salaries are supplemented with a holiday bonus of 8 % and a year-end bonus of 8.3 % per year. In additions, there are outstanding secondary benefits such as a minimum of 29 days holiday per year (for a fulltime appointment), study facilities, and a pension plan. For

further information: working at Utrecht University.

Employer A better future for everyone. This ambition motivates our scientists in executing their leading research and inspiring teaching. At Utrecht University the various disciplines collaborate intensively towards major societal themes. Our focus is on Dynamics of Youth, Institutions, Life Sciences and Sustainability.

The Faculty of Veterinary Medicine of Utrecht University (FVM-UU) is the only Veterinary School in the Netherlands and belongs to the international top in education, research and veterinary medical patient care. FVM-UU is one of the few European veterinary schools accredited by the American and Canadian Veterinary Medical Associations and the European Association of Establishments for Veterinary Education. The faculty employs approximately 900 veterinarians, scientists and support staff and counts 1,500 students.

The Department of Farm Animal Health focuses on the three core tasks of education, research and patient care. However patient care at the Department of Farm Animal Health facilitates education and research. In our research and education, we pay attention to the individual animal,

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UWindsor SalomEvolutionaryGenetics

The Heath Research Group has three advertisements < <http://www1.uwindsor.ca/glier/heath-research-group/42/employment-opportunities-with-the-hrg> > for funded graduate positions. Could you please send these on (e-mail, FB, tweet) to whomever you think might be interested? There are some really interesting projects centred around:

- Evolutionary genetics of early life history variation in salmon
- Gene expression and physiology of reintroduced Atlantic salmon
- Competition with and predation of reintroduced Atlantic salmon

Cheers,

Sara

—
Sara Jamieson Research Coordinator (part-time), Heath Research Group Great Lakes Institute for Environmental Research (GLIER) University of Windsor 2990 Riverside Dr West Windsor ON N9C 1A2

Office hours: Monday and Thursday mornings.
Phone: 519-253-3000 x 4933 Fax: 519-971-3616 e-mail: saraj@uwindsor.ca

Website: Heath Research Group < <http://www1.uwindsor.ca/glier/heath-research-group/> >

Mattias.Johansson@uwindsor.ca

UZurich MatingSystemEvolution

A PhD position funded by the University Research Priority Program (URPP) “Evolution in action” is available from January 2017 at the Department of Systematic and Evolutionary Botany/Plant and Microbial Biology, University of Zurich, for a period of four years. The position is to study the molecular bases of mating system evolution using *Brassica rapa* as a model, co-supervised by Prof. Florian Schiestl and Prof. Ueli Grossniklaus. The project will utilize a unique population of *Brassica* plants, that evolved increased autonomous selfing during nine generations of experimental evolution with hoverfly pollination (Gervasi and Schiestl in press). Within the project, the molecular bases of this rapid adaptive evolution will be investigated using various molecular and bioinformatics tools.

You should have a Master degree in any field of (molecular) biology and a thorough interest in evolutionary biology. A good knowledge of molecular and bioinformatics techniques is desirable. The successful candidate will work in an exciting research environment, offered by the two departments and the URPP, comprising research groups from several different biological disciplines. Our departments are located in the botanical gardens and house modern molecular and ecological labs, including greenhouses and climate chambers for plant cultivation. The University of Zurich has a very broad coverage of organismal and molecular biology, and several research groups work on evolutionary topics (www.lifescience-zurich.ch). The city also offers excellent quality of life

through cultural programs and infrastructure, as well as an attractive surrounding.

If you are interested in the job, please send by e-mail a letter describing your motivation, C.V., copy of degrees, publications (manuscripts), and e-mail addresses of two academic referees, by 20th of February 2017. If you have any further questions, don't hesitate to contact me (florian.schiestl@systbot.uzh.ch).

Gervasi, D. and F. P. Schiestl. in press. Real time divergent evolution in plants driven by pollinators. *Nature Communications*.

Florian Schiestl <florian.schiestl@systbot.uzh.ch>

Vienna PopulationGenetics

Reminder (plus two new topics!): The 2017 call for PhD students at the Vienna Graduate School of Population Genetics is closing, soon:

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

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

Available Topics:

- Evolution of gene expression
- Understanding thermal adaptation
- The impact of new transposable element insertions on adaptation to a new environment
- Wolbachia infection dynamics in evolving *Drosophila* populations
- The adaptive value of diversity produced by recurrent whole genome doubling
- Epigenetic variation in *Arabidopsis*
- Genetic footprints of adaptive introgression
- New methods for modelling and analysis of data from experimental evolution

- Maximum likelihood inference of population genetic parameters using genome-wide data from nearly neutral sites

- Macroevolutionary dynamics of selfish DNA unravelled by third generation sequencing

- Dynamics of a selfish DNA invasion

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by January 08, 2017 will be considered. Two letters of recommendation need to be sent directly by the referees.

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at (Twitter @PopGenViennaPhD)

Julia Hosp <Julia.Hosp@vetmeduni.ac.at>

Western Washington U Evolutionary Biol

The Biology Department at Western Washington University has openings for graduate students starting Fall 2017. Faculty members in the department offer a wide range of expertise, from molecular biology to ecology. Graduate students are eligible for teaching assistantships, which fund the majority of tuition and provide a stipend of \$12,116 per year. WWU is located in Bellingham, WA, a coastal city north of Seattle at the base of Mt. Baker in the northwestern part of the state.

More information can be found at: <https://cse.wwu.edu/biology/biology-graduate-program> or by contacting Dr. Ben Miner, Graduate Program Advisor, at benjamin.miner@wwu.edu

Potential advisors

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

Aspergillus is a key colonizer of such plastics but its ability to break down polymers is unclear, as is the extent of toxin formation during plastic colonization. <https://cse.wvu.edu/biology-faculty/brodham> Lina Dalberg: The Dahlberg Lab uses the model organism *C. elegans* to probe the neurobiological, cellular, and behavioral role for proteins involved in a ubiquitin-dependent processes called Endoplasmic Reticulum Associated Degradation (ERAD). This project will use a variety of techniques, including fluorescence microscopy, behavioral assays, and biochemical characterization to investigate how ERAD targets neural receptors for degradation. A second, NSF-funded project focuses on improving metacognitive skills in undergraduate Biology students; students interested in this project must have experience (via coursework or research) in education and pedagogy research. <https://cse.wvu.edu/biology-faculty/dahlbec> 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. <https://cse.wvu.edu/biology-faculty/hooper> 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.

<https://cse.wvu.edu/biology-faculty/kodnerr> Suzanne Lee: The long-term research goals of the Lee Lab are to better understand the molecular mechanisms that underlie gene regulatory pathways that target RNA. The biological importance of gene regulation at the post-transcriptional level is underscored by the fact that many human diseases result when RNA metabolism goes awry. Currently, the Lee lab is investigating pathways that target aberrant RNA transcripts for degradation through engagement of RNAi machinery or the nonsense-mediated decay pathway. We use an early branching eukaryote, the ciliate *Tetrahymena thermophila*, as a model eukaryotic system in our research, as it offers the unique opportunity to uncover both broadly applicable mechanisms and interesting points of organism-specific diversification. Students pursuing research in our lab have the opportunity to learn a broad array of experimental tools used in biochemistry and molecular and cell biology. Project opportunities exist for 1-2 Masters' students with prior experience in cloning, PCR, protein purification, and/or microscopy. <https://cse.wvu.edu/biology-faculty/lees65> 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

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Bergen Norway GroupLeader MarineEvolution	61	MuseumOfNewZealand TePapa InvertebrateCurator	70
BrownU ResAssist EvoDevo	62	NHM London SeniorCurator	70
CaliforniaStateU SanMarcos PopGenetProgrammer	62	NHM UDenmark PopulationGenomics	71
CCharleston EvolutionaryMicrobiologist	63	NOAA NMFS Seattle MolGeneticist	72
ChicagoBotanicGarden UndergradSummer	64	ReedC Oregon 2yr GeneticsGenomics	73
CityUNewYork EnvironmentalEvolutionaryEcol ...	64	Smithsonian ConservationGenomics	73
CityUNewYork TeachingBiostatistics	64	StockholmU PlantSystematics	74
DukeU Summer Undergrad	65	TexasAMU ConservationGenetics	74
Estonia PhD-PDF-GroupLeader HumanPopGenomics	2	UCalifornia LosAngeles BiomathTeacher	75
.....	65	UChicago LabManager ResearchScientist	76
Gothenburg BiodiversityProjCoordinator	66	UHalle LivestockPopulationGenomics	76
ImperialC London EvolutionAntifungalDrugResistance	66	UMinnesota FieldTech PollinatorNutrition	77
Inra France 4 EvolutionaryGenetics	67	UMontana Tech PopGenomics	78
INRA UParisSud CropGeneticDiversity	67	USalzburg EvolutionaryBiol	78
MethodsEcolEvolution EditorVacancy	68	USaskatchewan GroundSquirrelHeadTech	80
MichiganStateU 2 GeneticsAdapation	68	UWarsaw FieldAssist BirdPopulations	80
MissouriBotanicalGarden SummerUndergrad	69	Virginia DirectorResearchCenter Bioinformatics ...	81
MuseumNatSci NorthCarolina PartTimeMolluskTech	69	Worcester Massachusetts ResAssoc DrosophilaMolEvol	82

Bergen Norway GroupLeader MarineEvolution

Group Leader Positions available at the Sars Centre for Marine Molecular Biology, Bergen, NORWAY (Researcher I, code 1110) 6 year contracts)

<http://www.sars.no/jobs/2017-868.group%20leaders.chourrout.php>

The Sars Centre is seeking outstanding candidates addressing fundamental questions in organismal biology using marine species. Although all current groups work on animals, projects on other marine organisms will also be considered. A contract of six years will be offered to successful candidates, with competitive resources for the research (postdocs, PhD students, technicians, lab space and project-specific facilities) as well as a competitive salary. The contract may be prolonged after six years, depending on performance and available funding at the time of review. Group leaders at the Sars Centre are encouraged to obtain additional funding through grant applications to national and international funding agencies.

Qualifications and personal qualities:

- The applicant must hold a PhD considered equivalent to the Norwegian PhD degree - Ability to train and lead junior scientists and technical staff towards a common goal defined in the group leader proposal - Ability to de-

velop collaborations with other research groups located in and out of the institution

We can offer:

- A good and professionally challenging working environment, in modern research facilities - Starting salary at pay grade 79, code 1110 (currently NOK 766.200) upon appointment - Enrolment in the Norwegian Public Service Pension Fund - A position in an inclusive workplace (IA enterprise) - Good welfare benefits

Your application in English must include:

- A description of past and present research (3 pages) - A proposal for the research at the Sars Centre (3 pages) - A detailed CV and contact information for 3 references

Application Deadline: 24 March 2017. All shortlisted candidates must be available for a seminar and interview by the Sars Centre Scientific Advisory Committee held in Bergen on 26-27 April 2017.

The application and appendices may be uploaded at JobbNorge. Please note that applications will be assessed only with the information available in JobbNorge when the deadline expires. It is the applicant's responsibility to ensure that all relevant attachments are submitted by the deadline.

Applications by e-mail only will not be considered.

For further information about the position please contact the Sars Centre Director (Daniel.Chourrout@uib.no tel +47 5558 4360) and/or visit our website (www.sars.no).

General information:

The state labour force shall reflect the diversity of Norwegian society to the greatest extent possible. Age and gender balance among employees is therefore a goal. It is also a goal to recruit people with immigrant backgrounds. People with immigrant backgrounds and people with disabilities are encouraged to apply for the position.

We encourage women to apply. If multiple applicants have approximately equivalent qualifications, the rules pertaining to moderate gender quotas shall apply.

The University of Bergen applies the principle of public access to information when recruiting staff for academic positions.

Information about applicants may be made public even if the applicant has asked not to be named on the list of persons who have applied. The applicant must be notified if the request to be omitted is not met.

The successful applicant must comply with the guidelines that apply to the position at all times.

“andreas.hejnol@uib.no” <andreas.hejnol@uib.no>

BrownU ResAssist EvoDevo

Brown University Research Assistant position for Developmental Biology

Location: Brown University, Molecular Biology Cell Biology Biochemistry Department (Providence, RI)

We are looking to hire an excellent full-time research assistant who is encouraged to conduct her/his independent research under PI's supervision. The area of research includes developmental biology, molecular biology, evolutionary developmental biology, live imaging, proteomics, RNA-IP-seq, and CRISPR genome editing technology. Basic skillset and knowledge in molecular biology (e.g. cloning, PCR) and a good accomplishment in her/his undergraduate work are prerequisite. Other necessary trainings (e.g. microinjection, confocal imaging, proteomics) will be provided by the PI. The successful individuals will be given own projects to conduct and finish (hopefully with lead author publications) within one-two years of appointment. This is an excellent job opportunity for individuals who seek to proceed to graduate school or medical school with a good research accomplishment.

Any interested individuals should contact me via e-mail: mamiko_yajima@brown.edu. Please enclose your CV,

title of your undergraduate thesis, and name of your thesis advisor. Reviews will begin immediately and continue until position is filled. Desired start date is March 1, 2017.

Mamiko Yajima <mamiko_yajima@brown.edu>

CaliforniaStateU SanMarcos PopGenetProgrammer

Job Description:

The Sethuraman lab of population genetics at California State University San Marcos is looking to hire a scientific research programmer. Primary responsibility will be to assist in development of a model-based population genomics pipeline, and development of a graphical front-end to be hosted in the Galaxy Project platform. This position is funded by an NSF grant to Dr. Arun Sethuraman (CSU San Marcos - www.arunsethuraman.weebly.com) and Dr. Jody Hey (Temple University - <https://bio.cst.temple.edu/~hey/>) and will have ample opportunities for collaborative development of statistical and evolutionary genetic applications across both labs. The position will be based out of CSUSM (San Marcos, California). This work requires experience in C/C++, Perl/Python/Shell across Unix and Windows platforms. Experience with development of applications for the Galaxy Project is desired. Experience with software programming best practices, including test automation (e.x. travis-ci, jenkins.io) and task management (e.x. Jira, waffle.io) will be an added plus.

The position is funded for three years, with possibilities for continued funding. The programmer/postdoc will report directly to both PI's and also have the opportunity to train and mentor graduate and undergraduate students (2-3 per year) in scientific programming and software development.

Please contact Arun (asethuraman@csusm.edu) with any questions regarding the position.

Qualifications:

A Master's degree in computer science or bioinformatics with extensive experience in scientific programming is required. Candidates with a PhD in computational biology or bioinformatics, or some allied field will also be considered.

University Auxiliary and Research Services Corporation

(UARSC) was founded in 1990 as a 501(c) 3 public, non-profit corporation to support the mission of Cal State San Marcos, the 20th campus in the California State University system. CSUSM is a recipient of the Chronicle's 2014 Great College to work for. UARSC offers an excellent benefits package which includes medical, dental, vision, retirement plan, life and long term disability insurance, paid holidays, and generous vacation and paid time off leave benefits. For more information about UARSC, visit our website at www.csusm.edu/uarsc. "JEANNE CLERY ACT AND CAMPUS FIRE SAFETY RIGHT-TO-KNOW LAW" NOTIFICATION - See Police Department's website located at: <http://www.csusm.edu/police/Clery.pdf> Application Procedure:

Please apply by clicking "Apply" on this page, and be sure to submit a cover letter and resume along with your online employment application. UARSC is an Equal Opportunity Employer and does not discriminate against persons on the basis of race, color, creed, religion, ancestry, sex, gender, gender identity, gender expression, genetic information, pregnancy, sexual orientation, age, medical condition, military service, veteran's status, marital status, national origin, physical or mental disability, or any other status protected by federal, state or local laws.

For questions or if you experience any difficulties with the online application process, please contact UARSC Human Resources at (760) 750-4700.

-

Thank you!

Arun

Arun Sethuraman, PhD

Assistant Professor Department of Biological Sciences
California State University San Marcos

<http://arunsethuraman.weebly.com/> Arun Sethuraman
<asethuraman@csusm.edu>

CCharleston EvolutionaryMicrobiologist

Microbiologist (second position)

The Department of Biology at the College of Charleston invites applications for a tenure-track position in Microbiology at the Assistant Professor level to begin August 2017. This position is the second of two ongoing searches in the Biology Department; the other is targeting a Microbial Geneticist. Candidates must have a Ph.D. in Biology or a related field and a strong commitment to teaching and maintaining an active research program involving undergraduates. We are especially interested in a colleague who will develop collaborations with existing faculty (<http://biology.cofc.edu/about-the-department/faculty-staff-listing/index.php>). Primary teaching responsibilities include undergraduate courses in Microbiology lecture and laboratory, introductory biology and perhaps specialty courses in an area of expertise. The College of Charleston, located in Charleston, SC, is a public liberal arts and sciences institution of 12,000 students, with MS programs in Marine Biology and Environmental Studies, and a commitment to excellence in teaching and research. Information about the department is available at <http://biology.cofc.edu/>. Applicants should submit electronic (pdf) copies of their curriculum vitae, statements of teaching and research interests, up to three relevant publications, and three letters of recommendation to <http://jobs.cofc.edu/postings/5765>. Questions regarding this position can be directed to Dr. Courtney Murren, search committee chair, at murrenc@cofc.edu. This is a nine-month appointment; salary is competitive and commensurate with experience and qualifications. Review of applications will begin Feb 19, 2016 and will continue until the position is filled. The College of Charleston is an Affirmative Action, Equal Opportunity Employer and does not discriminate against any individual or group on the basis of gender, sexual orientation, gender identity or expression, age, race, color, religion, national origin, veteran status, genetic information, or disability.

< <http://jobs.cofc.edu/postings/5765> >

Assistant Professor of Biology (microbiology) < <http://jobs.cofc.edu/postings/5765> > jobs.cofc.edu

Biology Faculty and Staff - College of Charleston < <http://biology.cofc.edu/about-the-department/faculty->

[staff-listing/index.php](http://biology.cofc.edu/staff-listing/index.php) > biology.cofc.edu Faculty and Staff Listing ... ROSTER FACULTY; Bidwell, Deborah: Senior Instructor 843.953.7107: bidwelld@cofc.edu

Department of Biology - College of Charleston < <http://biology.cofc.edu/> > biology.cofc.edu The role of the Department of Biology is to provide students with an understanding of the science of living systems within the context of a liberal arts education.

“Murren, Courtney J” <MurrenC@cofc.edu>

ChicagoBotanicGarden UndergradSummer

Summer Research Experiences for Undergrads (REU)

The Chicago Botanic Garden welcomes undergraduates* interested in plant biology and conservation to apply to our REU program, funded by the National Science Foundation. This 10 week internship program, offered from June - August 2017, provides undergraduate participants an opportunity to explore a diverse array of scientific fields related to plant biology and conservation spanning genetic to ecosystem levels of inquiry. Interns work with a mentor to conduct an independent research project, participate in training and professional development programs, and present their results to a broad audience. Travel, room and board, and research costs are covered by the program. Participants also receive a \$5,000 stipend. *Application deadline is February 1, 2017.* For more information, please visit our website at: <http://www.cbgreu.org/> . **You must be a current undergraduate student (enrolled spring and fall 2017) and a citizen or permanent resident of the United States or its territories to qualify for this internship.*

“christopherwoolridge2017@u.northwestern.edu”

CityUNewYork EnvironmentalEvolutionaryEcol

The person we are replacing is a systematist. Even though it doesn't explicitly state it, we are looking for someone with an evolutionary biology bent to their work.

FACULTY VACANCY ANNOUNCEMENT The Department of Natural Sciences at Baruch College, City University of New York, invites applications for a full-time, tenure-track position at the rank of Assistant Professor of Biology/Environmental Studies/Evolutionary Ecology starting September 1, 2017. The candidate is expected to establish an externally funded research program that will complement the collaborative, interdisciplinary environment at Baruch College. Teaching responsibilities will include introductory courses and advanced courses for Biology majors and Environmental Studies minor. Baruch College offers modern laboratory equipment/facilities and its location in midtown Manhattan provides access to a diverse range of research institutions and collaborators. Competitive applicants should have a strong publication record and the desire to work collaboratively in an interdisciplinary environment.

QUALIFICATIONS Ph.D. degree in Biology, Environmental Science, or a related field is required by September 1, 2017 when the appointment begins. We welcome applicants working in any area of environmental biology from molecular through ecosystem levels, however, experience in global change biology, coastal ecology, or urban ecology is desirable. All applicants should show promise of teaching excellence and a commitment to mentoring undergraduate researchers. Competitive applicants will have relevant teaching experience and peer-reviewed publications in their field.

Please apply at: https://home.cunyfirst.cuny.edu/-psp/cnyepprd/GUEST/HRMS/c/HRS_HRAM.HRS_CE.GBL?Page=HRS_CE_JOB_DTL&Action=A&JobOpeningId046&SiteId=1&PostingSeq=1

Rebecca Spokony <rebecca.spokony@gmail.com>

CityUNewYork TeachingBiostatistics

The Department of Biology at York College, CUNY seeks an individual to teach an undergraduate course in Biostatistics for the upcoming Spring 2016 semester (January 30, 2017–May 26, 2017). Candidates should hold a degree in biostatistics or a related field (e.g. biology with extensive data analysis experience). Preference will be given to candidates with a proven record of teaching excellence who are familiar with R programming.

Day and evening availability may be required. QUALIFICATIONS For Adjunct Lecturer: - Master's degree in

area(s) of expertise required For Adjunct Assistant Professor: - Ph.D. degree in area(s) of experience or equivalent required COMPENSATION Adjunct Lecturer: \$64.84/hr Adjunct Assistant Professor: \$73.53/hr Commensurate with qualifications and experience. HOW TO APPLY Please send a letter of application (indicating area of expertise and availability for day and/or evening) to Dr. Margaret MacNeil (mmacneil@york.cuny.edu) along with a CV and the names and contact information for three professional references.

Equal Employment Opportunity York College is committed to enhancing our diverse academic community by actively encouraging people with disabilities, minorities, veterans, and women to apply. We take pride in our pluralistic community and continue to seek excellence through diversity and inclusion. EO/AA Employer

Laura Beaton <lbeaton@york.cuny.edu>

DukeU Summer Undergrad

The Patek Lab in the Biology Department at Duke University is recruiting one high school and one undergraduate student researcher through the US Army Educational Outreach Program (AEOP) during the summer of 2017. The students will participate in projects examining fast, impulsive movements of animals in the natural environment. The focal systems for the project are catapult jumping in frog hopper insects and underwater foraging attacks in dragonfly larvae. Responsibilities of the student researchers may include collecting study organisms from local habitats, obtaining high-speed videos of animals, analyzing high-speed videos using computer software, performing statistical analyses and scientific writing. The details of responsibilities and tasks will be determined based on mutual interests of the students and the mentors. There are also possibilities for the students to develop individual projects under our mentorship.

We are looking for motivated, reliable students who are excited about having first-hand research experience at the intersection of biology and physics. Skills to perform the above-mentioned tasks are not required. We especially value students who are curious, hard-working and have an open mind about the possibilities of basic, scientific research. For more information about The Patek Lab, please visit our website: www.thepateklab.org DEADLINE: February 28, 2017, 11:59 pm. All applicants must submit two letters of recommendation,

transcripts and must have maintained a cumulative GPA of at least 3.2 in their coursework. Applicants must also include a brief essay that explains their interest in this research and how it relates to their future goals.

Go to the below links and:

Click "Apply" at the bottom of the page

* Fill out the forms

* When you get to "Please select your 1st preference of URAP location.", Select "BDUN53 Duke University"

For high school students, please apply through the HSAP program:

<http://www.cvent.com/events/2017-high-school-research-apprenticeship-program-hsap-/event-summary-a0d910ce30ff4c848b66358e0e028871.aspx>

For undergraduate students, please apply through the URAP program:

<http://www.cvent.com/events/2017-undergraduate-research-apprenticeship-program-urap-/event-summary-ccf8d39466294c8391d60121495cfcdf.aspx>

Chi-Yun Kuo Postdoctoral Associate Patek Lab, Duke University Personal website <https://pateklab.biology.duke.edu> 919-613-0994

Chi-Yun Kuo <chi.yun.kuo@duke.edu>

Estonia PhD-PDF-GroupLeader HumanPopGenomics 2

Hello,

Please find below three open positions at the Estonian Biocentre in Tartu in the fields of modern and ancient human population genomics. Deadline for all applications is 31st January 2017 (i.e. in ~2 weeks).

See

http://www.ebc.ee/index.php?option=com_content&view=article&id=12&Itemid=&lang=en for details and application procedure.

Please spread the information to anybody you think might be interested.

I'm sorry for spam as some of you might get this e-mail from multiple sources.

The Estonian Biocentre Evolutionary Biology group is

interested in human genetic diversity and reconstructing human evolutionary history through migrations, population splits and admixture as well as adaptation. We generate modern and ancient DNA genomic sequences and genotype data from around the world and share all the published data (www.ebc.ee/free_data) to the scientific community.

1) Pre-Doc: a four years position with one year probationary period. The candidate will chose one of three research areas in the realm of modern human population genomics (see website for full details) and will apply for a PhD at the University of Tartu, starting in fall 2017. Salary: negotiable up to 15 600 EUR/year depending on experience level. Net salary after all taxes (incl. coverage of medical insurance and pension) is up to 15 600 EUR/year.

2) Post-Doc: a three years Post-Doc position on modern human population genomics. Candidates are encouraged to submit a short research proposal along with their CV, or to choose one of the proposed research themes (see website for full details). Salary: negotiable up to 24 000 EUR/year depending on experience level. Net salary after all taxes (incl. coverage of medical insurance and pension) is up to 20 000 EUR/year.

3) Group Leader: a 3-years Senior Research Fellow position as head of the Ancient DNA group and lab. The candidate will be responsible for establishing a research group of ancient population genomics and hiring and supervising postdocs and graduate students as well as managing the newly built aDNA lab. Salary: up to 42 000 EUR per year (Net salary after all taxes incl. coverage of medical insurance and pension is up to 35000 EUR/year.).

Potential candidates are encouraged make informal contact with Luca Pagani (lp.lucapagani@gmail.com), Senior Researcher in human population genomics or with Mait Metspalu (mait@ebc.ee), Director of the Estonian Biocentre. Best, Luca

Luca Pagani <lp.lucapagani@gmail.com>

Gothenburg BiodiversityProjCoordinator

We are looking for a Scientific Project Coordinator for the newly established Gothenburg Global Biodiversity Centre (GGBC) and our own research group (<http://antonelli-lab.net>). Both are located in Gothenburg,

Sweden.

GGBC has two main goals: to further develop biodiversity research, and to bridge the gap between scientists, the public and industry through various outreach activities. The Centre represents a long-term collaboration among the following institutions at the University of Gothenburg: the Department of Marine Sciences, the Department of Biological and Environmental Science, the Department of Geosciences, Herbarium GB, the Centre for Sea and Society, and the Linnaeus Centre for Marine Evolutionary Biology. Moreover, it comprises the following organisations: Department of Energy & Environment, Chalmers University of Technology, Havets Hus, Maritime Museum and Aquarium, Nordens Ark, The Gothenburg Museum of Natural History, and Universeum Science Centre.

Please spread the word to potentially suitable candidates. For more information please visit:

<http://www.gu.se/omuniversitetet/aktuellt/-ledigaanstallningar/?id=19144&Dnr=814992&Type=E>

Application deadline: January 26, 2017

Alexandre Antonelli, PhD Professor in Systematics and Biodiversity <http://antonelli-lab.net> Alexandre Antonelli <alexandre.antonelli@bioenv.gu.se>

ImperialC London EvolutionAntifungalDrugResistance

Technician working on the evolution of antifungal drug resistance

Imperial College London - Department of Infectious Disease Epidemiology

The Fisher lab is seeking an experimentalist to join a research group investigating the evolutionary dynamics of multi-azole resistance in pathogenic *Aspergillus* fungi. The Technician will join a large multidisciplinary research group working on a range of pathogenic fungi that threaten human, wildlife and ecosystem health. The project's primary objective is to use fungal population genomics in order to uncover the mode and tempo by which an aggressive human pathogen, *Aspergillus fumigatus*, evolves resistance to antifungal drugs in the environment. The research is funded by NERC and the post will require extensive work in fieldwork settings, mainly the UK, and therefore a UK driving licence is required.

The post is full time for a fixed term of two years and the salary is 26,650 to 29,410 per annum

For informal enquiries please contact Professor Matthew Fisher (matthew.fisher@imperial.ac.uk)

<http://www.jobs.ac.uk/job/AWM108/technician-in-antifungal-drug-resistance/> Job closes on the 27th of January

“matthew.fisher@imperial.ac.uk”
<matthew.fisher@imperial.ac.uk>

Inra France 4 Evolutionary Genetics

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 32 Research Scientists (PhD or equivalent) through open competitions and offering permanent positions.

Positions are open in a wide range of scientific disciplines such as human nutrition, intestinal microbiota, plant genetics, animal genetics, quantitative genetics, population dynamics and genomics, neurobiology of behaviour, animal nutrition, plant ecophysiology, functional and behavioural ecology, modelling of plant cell walls, process engineering and biotechnology, systems biology and synthetic biology, animal health, life science and environmental mathematics and informatics, economics, sociology and organizational sciences.

INRA offers including 4 positions in genetics:

- Adaptive genomics of agricultural insects - Evolution of viruses in interaction with resistant and tolerant plants
- Genetic analysis of health and feed efficiency in cattle
- Mathematical modelling of robustness genetics

Applications are available until to March 1st, 2017.

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 ATTENTION, merci de noter le changement de mon adresse e-mail .

Vera FERNANDES

Gestionnaire Communication RH

Vera.Fernandes@inra.fr

INRA - DRH

Cellule Communication interne RH Tél. : +33 (0)1.42.75.95.27 147 rue de l'Université 75 338 Paris Cedex 07 France

www.inra.fr
<vera.fernandes@inra.fr>

Vera Fernandes

INRA UParisSud Crop Genetic Diversity

The post-doc will investigate the impact of farmers' network organizations on the evolution of crop genetic diversity. He/she will analyze genetic diversity data coming from on-farm and participatory plant breeding programs in bread wheat. Based on estimated parameters and a participatory process, and using a crop metapopulation simulation programme already developed in the team, the candidate will perform forward crop metapopulation simulations to explore different scenarios of collective management of crop genetic diversity. The objective is to understand evolutionary consequences of farmer' social organization and farming practices on crop genetic diversity.

The project will be jointly supervised by Isabelle GOLDRINGER (INRA, Gif-sur-Yvette) and Mathieu THOMAS (CIRAD, Montpellier) and developed in collaboration with Frederic Hospital (INRA, Jouy-en-Josas).

We offer a 2 years Postdoctoral Fellowship starting at 1836 euro (net) per month depending on the experience. The position will be located at GQE - Le Moulon (INRA, CNRS, Univ. Paris-Sud, AgroParisTech) near Paris (~30km), France. The position is funded by the H2020 DIVERSIFOOD research program (2015-2019).

Expected outputs :

- research papers in evolutionary genetics and manage-

ment of genetic resources in situ / on farm

- feedbacks to stakeholders involved in crop diversity management (farmers, citizens, farmers' and citizens' organizations, policy makers)

Expected starting date: March, 2017

Qualifications: * PhD degree obtained in population / quantitative genetics or evolutionary biology * Experience or interest in developing expertise in population genetic modeling * Skills in statistics (R or Python programming) * Interest in farmers/researchers interface and management of crop diversity

To apply:

Applicants should submit by email a short statement of interest, a CV and the name of three referees.

Isabelle GOLDRINGER

isabelle.goldringer@inra.fr

Diversity Evolution and Adaptation of Populations

INRA, GQE - Le Moulon, Gif-sur-Yvette, France

Mathieu THOMAS

mathieu.thomas@cirad.fr

Diversity Dynamic, Societies, Environments

CIRAD, AGAP, Montpellier – Mathieu THOMAS

+33 (0)4 67 61 49 67 +33 (0)6 74 16 02 66 Chercheur dans l'équipe Dynamiques de la Diversité, Sociétés et Environnements

CIRAD UMR AGAP TA A-108/03 Avenue Agropolis 34398 Montpellier Cedex 5 France

Mathieu Thomas <mathieu.thomas@cirad.fr>

MethodsEcolEvolution EditorVacancy

Dear all,

The British Ecological Society is seeking a Senior Editor for the journal *Methods in Ecology and Evolution*.

This is an excellent opportunity for an individual wishing to become involved with the work of one of the premier international journals in ecology at a time when exciting changes are occurring in the publishing environment.

Full details are at: <http://www.britishecologicalsociety.org/about/vacancies/>

senior-editor/

Closing date: 7 February 2017

Please see the link for contact details with regards to the post.

Kind regards, Andrea.

Andrea Baier Senior Managing Editor *Journal of Ecology* @JEEcolgy *Methods in Ecology and Evolution* @MethodsEcolEvol EDITOR VACANCY: apply by 7 Feb!

British Ecological Society | Charles Darwin House | 12 Roger Street London WC1N 2JU, UK | Tel: +44 (0)207 685 2517

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Andrea Baier <andrea@britishecologicalsociety.org>

MichiganStateU 2 GeneticsAdaption

The Lowry Lab at Michigan State University is currently seeking to hire two research technicians to study the genetics of adaptation.

The first technician will be hired through Michigan State University and will participate in projects focused on identifying the genetic mechanisms of evolutionary adaptations. The goals of the research are to understand how adaptations contribute to the formation of new species and how those adaptations can be exploited to improve bioenergy and food crops. The lab uses three flagship systems for research: Monkeyflower (**Mimulus guttatus**), Switchgrass (**Panicum virgatum**), and Common Bean (**Phaseolus vulgaris**). The successful applicant will assist with research on all three systems. Applicants should send their resume/CV and contact information for at least two references to David Lowry at dlowry@msu.edu. All applicants must also formally apply for the job through the following link: <https://jobs.msu.edu/applicants/jsp/shared/>

[frameset/Frameset.jsp?time=3D1484159189609](#) . This position will initially last for one year, with the possibility of annual renewal contingent on the availability of funding and satisfactory performance.

The second technician will be hired through the University of Texas, but be stationed at the Kellogg Biological Station in Hickory Corners, MI. This research will be focused on a large collaborative project studying adaptation in the bioenergy feedstock switchgrass. The research will utilize new genetic mapping populations to identify genomic regions responsible for adaptation between northern upland and southern lowland ecotypes of switchgrass. These mapping populations have been planted at an unprecedented geographical scale, spanning ten common garden field sites distributed over 17 degrees of latitude, making them ideal for studies of regional adaptations. The technician will be primarily responsible for maintaining and gathering data from the switchgrass common garden located at MSU's Kellogg Biological Station (KBS). The technician will also work in the laboratory of David Lowry on MSU's main campus, especially during winter months. The research will often involve all-day physical activity outdoors. The technician will be expected to organize data collection efforts and coordinate these efforts with the larger team across the central United States. For more information please on this position, please contact David Lowry directly at dlowry@msu.edu.

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

MissouriBotanicalGarden SummerUndergrad

Summer 2017 REU in Botany and Conservation Biology

The Missouri Botanical Garden in St. Louis, MO will be offering an NSF-funded Research Experiences for Undergraduates summer program in 2017. Ten students will be chosen to participate in a ten-week program involving full-time work on an independent research project, with the guidance of a staff mentor, in addition to educational seminars, discussion sessions and field trips. Available research projects deal with subjects including taxonomy, population genetics and speciation, conservation biology, restoration ecology, biodiversity

modeling, and crop development. Students will receive a weekly stipend as well as housing, food, transportation, and funding for research supplies. Eligible students are U.S. citizens or permanent residents who will be returning to school in the fall semester after the REU program. Students from schools with limited research infrastructure and from underrepresented groups are particularly encouraged to apply. Review of applications will begin on March 20, 2017. Further information on the program, available mentors and projects, and how to apply can be obtained from the website: www.mobot.org/reu . Wendy Applequist <wendy.applequist@mobot.org>

MuseumNatSci NorthCarolina PartTimeMolluskTech

The North Carolina Museum of Natural Sciences (NCSM) is looking to hire a 4 month, part-time project technician in the Mollusk Unit of the Research and Collections Section. This position will be funded via an US Fish and Wildlife grant. The person in this position will work closely with the Collections Manager of Mollusks in the processing of recently-acquired collections. Processing will include all aspects of curation, such as stabilizing, labeling, databasing, etc.

Essential Functions: Stabilizing specimens in ethanol and archival trays(dry specimens) - Cataloging specimens using an Microsoft Access database - Georeferencing locality information - Updating taxonomic information - Labeling and shelving specimens

Qualifications Preferred: Bachelor's Degree in biology or related field - Curatorial experience in natural history collections - Databasing experience, preferably with Microsoft Access - Efficient attention to detail - Ability to work both independently and as part of a team - Must be able to lift up to 50 lbs and work with various chemicals.

There is a possibility that this grant will be extended past the four months.

Location: NCSM Research Lab, located at 1671 Gold Star Drive, Raleigh, North Carolina, 27606. Approximate starting date Mid-February 2017. Please submit a cover letter and resume to Jamie Smith (Jamie.Smith@naturalsciences.org) by January 31, 2017.

Jamie M. Smith Collections Manager, Invertebrates North Carolina State Museum of Natural Sciences Phone: (919)707-8869 Fax: (919)715-2294

North Carolina Museum of Natural Sciences
MCS 1626, Research Laboratory, Raleigh, NC 27699-1626

Shipping Address for FedEx, UPS not US Postal Service

North Carolina Museum of Natural Sciences

Research Lab

1671 Gold Star Drive

Research Laboratory

North Carolina Museum of Natural Sciences

Raleigh, NC 27607

E-mail correspondence to and from this address may be subject to the North Carolina Public Records Law and may be disclosed to third parties.

“Smith, Jamie” <jamie.smith@naturalsciences.org>

MuseumOfNewZealand TePapa InvertebrateCurator

Curator - Invertebrates

Museum of New Zealand Te Papa Tongarewa (Te Papa),
Wellington, New Zealand

For nearly two decades, Te Papa has nurtured the legacies of New Zealand/Aotearoa its people and its environment. We are built on a foundation of innovation and co-creation and as a result we are looking for a new generation Curator, Invertebrates. You will be the newest member of a hard working team that produces science in a museum setting, working with national collections and other forms of cultural heritage.

This role requires:

* a PhD or equivalent experience and skills in Invertebrate sciences research in relation to New Zealand, * Undertaking research projects that contribute to the key research themes within the invertebrate policy, * Developing, implementing and monitoring collection development plans in the context of Te Papa’s national obligations and expectations for the Invertebrates portfolio, ensuring that collection objects are managed to accepted standards (both internal and external) in storage, conservation and documentation, * Experience of working with scientific objects and collections, * A knowledge of regulations and international standards for collection care, maintenance and acquisition, * Experience and

comfort in communicating in a range of forms and media to diverse audiences, * Familiarity with digital platforms and social media, * The ability to work in multidisciplinary teams on a range of museological outputs across exhibitions, digital channels, research publications, and public programmes, * A network of experts, communities and stakeholders you can bring to complement the team’s existing contacts.

If you are ready to take part in one of the most important, challenging and inspiring evolutions in both New Zealand and the museum sector worldwide, then we would love to hear from you.

For more information see: https://jobs.tepapa.govt.nz/-jobtools/jncustomsearch.viewFullSingle?in_organid=-17768&in_jnCounter=222719485 For enquiries, please contact Dr Dean Peterson, Head of Science: Dean.Peterson@tepapa.govt.nz.

Applications close on Thursday, 9 February 2017

Applicants must have the legal right to work in New Zealand.

Lara Shepherd <Lara.Shepherd@tepapa.govt.nz>

NHM London SeniorCurator

Senior Curator in Charge, Historical Collections and British and European Seed Plants

The Natural History Museum - Department of Life Sciences

The Natural History Museum is one of the world’s leading museums, internationally recognised for its dual role as a centre of excellence in scientific research and as a leader in the presentation of natural history through exhibitions, public programmes, publications and the web.

Embedded within the Algae, Fungi and Plants Division of the Department of Life Sciences, the Senior Curator in Charge (SCiC) Historical Collections and British and European Seed Plants will lead and manage the Historical Collections and the British and European seed plant herbaria, ensuring best practice in collections care and strategic development of the collections. An expert in a relevant field, the SCiC will provide a high level of scholarship across these collections specifically in collections-based science (e.g. taxonomy, systematics, organismal biology). Working towards maximising the significance of the collections for their various purposes,

emphasis will be on achieving the strategic goals and values of the NHM. This post will report to the Principal Curator in Charge of the Algae, Fungi and Plants Collections.

For further details please see the Natural History Museum's jobs page: <https://-nhm.irecruittotal.com/CONFIG/NHM/StaticPages/-CAC/SearchVacancy.aspx?EmploymentTypeID=-0&Intranet=0> "M.Carine@nhm.ac.uk" <M.Carine@nhm.ac.uk>

NHM UDenmark PopulationGenomics

Associate Professor of Population Genomics

*The Natural History Museum of Denmark Faculty of Science**University of Copenhagen*

The Natural History Museum of Denmark invites applications for a 3-year Associate Professor position in the Science of population genomics, starting 1 July 2017 or as soon as possible thereafter.

Subject Area

The candidate is expected to lead original scientific research addressing fundamental questions in population genomics, with a particular focus on investigating human evolutionary history using ancient genomics. The ideal candidate will have extensive expertise in the computational analysis of large-scale population genomic datasets, ideally with prior experience in the inference of demographic and selective processes using both modern and ancient human genomes. A strong record of peer-reviewed publications in human genetics and other relevant fields is expected.

Applicants are required to have university level teaching experience, documented teaching competencies and must be able to explain and reflect upon own teaching practice and portfolio. Formal pedagogical training or supervision equivalent to the University of Copenhagen teacher training programme for assistant professors is required.

Specific qualifications

Extensive expertise in the computational analysis of large-scale human population genomic datasets with particular emphasis on low coverage genomic datasets incl. inference of patterns of admixture (d-statistics, f3 statistics)

Proficiency in programming and statistical analysis (in particular R)

Experience in analyses of demographic history and inference of natural selection in human genomic data.

Duties include the applicant's own research, development of the field, assessment tasks, grant applications, and research management such as supervision and training of research fellows and other staff. The successful applicant must also teach, supervise, prepare and participate in examinations, and fulfil other tasks requested by the Department.

Assessment of applicants will primarily consider their level of documented, original scientific production at an international level, including contributions to developments in their field, as well as their documented teaching qualifications. Managerial and out-reach qualifications of applicants including ability to attract external funding will also be considered.

Centre for GeoGenetics is a Centre of Excellence financed by the National Research Foundation. We are located at the Geological Museum, and there are currently more than 100 researchers working at the Centre. More information about the Centre for GeoGenetics at <http://-geogenetics.ku.dk/> Further information on the Department is linked at <http://www.science.ku.dk/english/-about-the-faculty/organisation/>. Inquiries about the position can be made to center director Eske Willerslev at ewillerslev@snm.ku.dk.

The position is open from 1 July 2017 or as soon as possible thereafter.

The University wishes our staff to reflect the diversity of society and thus welcomes applications from all qualified candidates regardless of personal background.

*Terms of employment *The position is covered by the Memorandum on Job Structure for Academic Staff.

Terms of appointment and payment accord to the agreement between the Ministry of Finance and The Danish Confederation of Professional Associations on Academics in the State.

Commencing salary is currently up to DKK *449,720* including annual supplement (+ pension up to DKK *76,902*).

Negotiation for salary supplement is possible.

The application including all attachments must be in English and submitted electronically by clicking APPLY NOW below.

*Please include *

- Curriculum vitae including information about external

funding - Diplomas (Master and PhD degree or equivalent) - Research plan - description of current and future research plans - Description and documentation of teaching experience and qualifications according to university guidelines (http://uddannelseskvalitet.ku.dk/quality-assurance-of-study-programmes/university-guidelines/-pedagogic-basis-and-guidelines/teaching_portfolio/)
 - Complete publication list - Separate reprints of 5 particularly relevant papers

The deadline for applications is 12 February 2017, 23:59 GMT +1*. *

After the expiry of the deadline for applications, the authorized recruitment manager selects applicants for assessment on the advice of the Interview Committee.

You can read about the recruitment process at <http://employment.ku.dk/faculty/recruitment-process/> .

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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>

NOAA NMFS Seattle MolGeneticist

This is most definitely directed toward evolutionary biologists, with an emphasis on marine fisheries biology. Here is the text:

Marine Molecular Geneticist III

Lynker Technologies, LLC has an immediate opening for a qualified marine molecular geneticist to fill a position on a contract with the NOAA Fisheries service.

This role involves supporting Lynker's National Marine Fisheries Service (NMFS) operations at the Northwest Fisheries Science Center (NWFS) within the Conservation Biology Division (CB), Genetics and Evolution Program.

In this role, I will work with senior CB Genetics and Evolution Program staff members as the main scientist responsible for curating and adding to the Marine Forensic Voucher collection. I will also assist in development and implementation of species identification assays of rockfish species of interest. My responsibilities include coordinating with the University of Washington Fish Collection's staff to identify, subsample, and enter the samples into the Collections archive; performing DNA

analysis and sequencing for each sample at 3 or more appropriate loci required for accurate species identification (e.g., ID of record); and curating the GEP's local database, submitting cleansed and verified data to public databases (Barcode of Life and Genbank). For the Rockfish work, I am also responsible for bioinformatics analyses of rockfish data and collaborates with NOAA in preparing next-generation sequencing libraries for several species of Sebastes.

Your work will contribute directly to NOAA's and the world's understanding of rockfish DNA, which provide critical inputs to the management and conservation of these important commercial fishing species.

To be considered, you must meet the following minimum qualifications: * A Master's degree from an accredited college or university in a related field of study with emphasis in molecular biology, populations genetics, evolutionary biology, or forensic science or a clearly related field and a minimum of five (5) years demonstrated field capability and experience related directly to the individual task order. * Four (4) years of progressively higher graduate education leading to a Ph.D. from an accredited college or university with a major in a field of study with emphasis on molecular population genetics, evolutionary biology, forensic science or a clearly related field may be substituted for three (3) years of required experience. * Extensive experience with genetic species ID of Pacific Northwest marine fish species required. * Multiple years experience with entering data into the Barcode of Life Database is essential. * Knowledge of voucher collections and their use in forensics is essential. * Experience with next-generation sequencing platforms and data required. * Experience with all or the following tools: + Sanger DNA sequencing, high-throughput microsatellite genotyping ABI3100 + qPCR and TaqMan SNP genotyping ABI7900HT, Fluidigm EP1 + RAD-library preparation, Mi-Seq high-throughput sequencing, molecular cloning + PCR and RFLP gel electrophoresis + DNA extraction: various tissue types + Liquid-handling robotics: Qiagen BioRobot 8000, QiaCube, and Matrix Hydra + Genetic analysis tools: CodonCode, Colony, STACKS, FSTAT + Statistical packages: SYSTAT, and R 2.15 + Data management tools: Microsoft ACCESS, Filemaker, LIMS.

Please send your resume, list of references, and explanation of how you meet the requirements above to recruiting@lynkertech.com. Let me know if you need anything further from me for the posting. Thanks! Liz

- Elizabeth J. Tarquin Director, Marine Sciences Division Lynker Technologies LLC (808) 747-3065 ltarquin@lynkertech.com www.lynkertech.com Lynker - a

HubZone- and ISO-certified company

Liz Tarquin <ltarquin@lynkertech.com>

ReedC Oregon 2yr GeneticsGenomics

Visiting Position in Genetics/Genomics at Reed College

The Biology Department at Reed College invites applications for a two-year visiting faculty member in Genetics and/or Genomics. We seek candidates with demonstrated excellence in biological research related to genetics or genomics, for example but not limited to molecular biology, bioinformatics, population or evolutionary genetics, epigenetics, or synthetic biology. Qualifications include a PhD and postdoctoral experience.

Reed is a distinguished liberal arts college with ~1400 students that offers a demanding academic program to bright and dedicated undergraduates (<http://academics.reed.edu/>). In addition to advising senior theses for Biology and Biochemistry and Molecular Biology majors, teaching duties will include an upper level lecture/laboratory course in genetics (for examples of current offerings, see the Reed course catalog: https://www.reed.edu/registrar/registration_info.html) and an advanced course in the candidate's area of expertise. Formal teaching experience at the college level will be viewed favorably but is not required. Reed biology faculty maintain active, rigorous research programs involving undergraduate students. The successful candidate will be provided lab space and resources to facilitate continued research, thus applicants demonstrating an ability to involve undergraduates in their research program are preferred.

The Reed community believes that cultural diversity is essential to the excellence of our academic program. Applicants are invited to address how their teaching, scholarship, mentoring, community service, or other activities could support Reed's commitment to diversity and inclusion in their application materials (see <http://www.reed.edu/diversity/>).

Application materials include a cover letter, curriculum vitae, a research statement (two page maximum length), and 3 representative publications. In addition, applicants should provide contact information for three references. All materials should be submitted through Interfolio at <http://apply.interfolio.com/40102> by February 17, 2017 for full consideration. An equal

opportunity employer, Reed College encourages applications from members of underrepresented groups. Specific inquiries should be directed to Dr. Sarah Schaack (schaack@reed.edu), the chair of the search committee.

Sarah Schaack, PhD Associate Professor Reed College schaackmobile@gmail.com <https://sites.google.com/site/schaackwork/> Sarah Schaack <schaackmobile@gmail.com>

Smithsonian ConservationGenomics

Secretary's Scholars Job Opportunity

Molecular Pathogen Scientist

Center for Conservation Genomics

Smithsonian Conservation Biology Institute

National Zoological Park

SALARY RANGE: Starting at \$77,490, commensurate with experience

OPEN PERIOD: 15 January - 15 February 2017

DUTY LOCATION: Washington, DC

The Center for Conservation Genomics (CCG), Smithsonian Conservation Biology Institute (SCBI), National Zoological Park, invites applications for the position of Molecular Pathogen Scientist. The successful candidate will be an exceptional scientist with a strong track record of published research involving the molecular analysis of animal pathogens, especially those of concern for animal health and conservation.

The selected candidate will be expected to build an outstanding research and clinical analysis program in molecular pathogen science. The candidate should have experience in developing and applying "next generation" DNA lab analysis methods and bioinformatics, as applied to pathogen diagnostics, characterization and/or function. Knowledge of the biology of one or more groups of animal parasites or pathogens is also expected. The ability to communicate effectively with a wide variety of audiences, including the public, is essential. The successful candidate will be expected to participate in activities, such as exhibits programs and educational outreach, to be involved with professional associations and other organizations within the scientific community, and to compete successfully for extramural funding.

Full-time, 5-year temporary appointment with full Smithsonian benefits to be filled at the IS-12 level, equiv-

alent to Federal GS-12. Proof of authorization to work in US required. The zoo's authorized salary for this position at this time is \$77,490 per annum. Qualified candidates who are referred to the hiring official will be asked to submit educational transcripts and proof of U.S. accreditation for foreign study.

KEY REQUIREMENTS:

* Pre-employment Background Investigation must be successfully completed.

* Must be able to travel and work independently as well as within a team environment.

Candidates may qualify for this position by demonstrating the experience outlined above, by completion of three full years of progressively higher level graduate education leading to a Ph.D. or equivalent doctoral degree related to the position, or by a combination of experience and education.

The Smithsonian Institution offers a competitive salary and a comprehensive package of benefits. This is not a Federal Position, but has similar requirements and benefits. For a complete description of benefits, please visit www.sih.si.edu. Interested candidates should submit to fleischerr@si.edu (1) their curriculum vitae, (2) a cover letter, and (3) research statements detailing their research interests and general experience for the position by 15 February 2017. Please include the position title in the subject line of your e-mail. CVs should include a description of your paid and non-paid work experience that is related to this job; starting and ending dates of job (month and year); and average number of hours worked per week. They should also include educational history (including degrees awarded), listings of publications, scientific and public presentations, grants received, and honors and awards.

To learn more about the CCG, SCBI and NZP please visit <https://nationalzoo.si.edu/center-for-conservation-genomics>. For more information, contact Robert Fleischer (fleischerr@si.edu).

The Smithsonian Institution is an equal opportunity, affirmative action employer. Candidates of all backgrounds are encouraged to apply.

“Fleischer, Robert” <FleischerR@si.edu>

StockholmU PlantSystematics

Stockholm University seeks to appoint an Associate Professor in Plant Systematics. Closing date: 10 February 2017

The position encompasses research and teaching within the broad subject area of plant systematics, including land plants, algae or fungi.

For a full job description and for how to apply see: <http://www.su.se/english/about/vacancies/vacancies-new-list?rmpage=3Djob&rmjob=2395&rmlang=UK>

Contact: Further information about the position can be obtained from the Head of the Department, Professor Ove Eriksson, telephone: +46 8 16 12 04, ove.eriksson@su.se.

For questions regarding the application process, please contact administrator Mikael Stenberg, telephone: +46 8 16 20 86, mikael.stenberg@su.se.

(In Swedish: <http://www.su.se/om-oss/ledig-anst%C3%A4llningar/lediga-jobb-ny-lista?rmpage=-job&rmjob=2393&rmlang=SE>)

“Catarina.Rydin@su.se” <Catarina.Rydin@su.se>

TexasAMU ConservationGenetics

Title: Conservation Genetics Lab Technician

Agency: Texas A&M University, Institute of Renewable Natural Resources

Location: Dallas, TX

Job Description: Mussel Research Group at Texas A&M University Institute of Renewable Natural Resources is looking to hire a highly motivated Lab Technician. The individual will assist research in conservation genetics of freshwater mussels in Texas. Primary job duties include archiving tissue samples, DNA extraction, polymerase chain reaction (PCR), DNA sequencing, and fragment analyses; however, the individual should expect occasional field sampling of mussels. Fieldwork includes visual and tactile search for mussels (wading and snorkeling), mussel identification, and data entry. Typical

work schedule: 5 days per week, 8 hrs per day. Occasionally, longer workdays may be required to complete field sampling.

Applicants must be self-motivated, enthusiastic, and enjoy working with others. Applicants should anticipate residing in Dallas, Texas.

Salary: \$900 every 2 weeks

Qualifications: Bachelor's degree in Biology or related field; experience extracting DNA and PCR; excellent communication skills and competency to work independently. Preference will be given to applicants with strong background in phylogenetics/population genetics, work experience in a molecular genetics laboratory, and/or familiarity with population genetics and phylogenetic analysis software.

Tentative Start Date: February 28, 2017. This position is initially for 4 months; however, it may be extended depending on performance and there is the possibility to switch to a graduate degree at Texas A&M University.

As a single email attachment, submit cover letter, resume, and contact information for 3 references to Kentaro Inoue (kentaro.inoue@ag.tamu.edu). Review of applications will start February 10, 2017 and continue until a suitable candidate is found.

Website: <http://irnr.tamu.edu/> |
<http://tamuirnrmussels.weebly.com/>

Kentaro Inoue <Kentaro.Inoue@ag.tamu.edu>

UCalifornia LosAngeles BiomathTeacher

I would like to post the following ad on EvolDir for an instructor of math for life Science students at UCLA. We have an innovative new course that is taught out of life sciences that emphasizes modeling and dynamic systems, and other mathematical approaches that are used by evolutionary and ecological biologist. I am really trying to reach potential applicants that combine excellent math skills with solid biological background.

University of California, Los Angeles

INTRODUCTORY INSTRUCTOR : MATH FOR LIFE SCIENCE STUDENTS

The Life Sciences Core Curriculum seeks an Academic Administrator III. The position is full time and the Salary range is between \$64,920-\$90,168. The position

will provide curriculum development and instruction for LS 20, LS30A, and LS30B in the Life Sciences Core Curriculum on quarterly basis including summer sessions.

Overview of the Position: Provide curriculum development and instruction for two-quarter, introductory math series (LS30A and LS30B) called Mathematics for Life Scientists, and for a one-quarter course (LS20) called Quantitative Concepts for Life Sciences. Responsibilities for each course include preparing and giving student-centered, inclusive lectures, overseeing the computational laboratory components and connecting modeling applications to concepts covered in lectures, offering office hours, giving students regular feedback as well as preparing and submitting student grades, and supervising/mentoring the graduate student teaching assistants (TAs). This position also entails administering the undergraduate Learning Assistants (LA) program associated with each course, with responsibilities that include coordinating the recruitment and hiring of undergraduate LAs, co-facilitating the LA pedagogy training course (LS192), and mentoring the undergraduate LAs in LS20, LS30A, and LS30B. This position involves interactions with the Program for Excellence in Education and Research in the Sciences (PEERS), with responsibilities that include helping to recruit effective graduate student collaborative learning workshop facilitators and co-developing worksheets used by PEERS students in the workshops.

Instruction and Curriculum Development

The Academic Administrator will provide curriculum development in the LS Core and when necessary instruction as directed by the Chair of the Life Sciences Core Curriculum, a cross-divisional instructional program. Duties include the following: - Develop course materials for LS20, LS30A, and LS30B to support the ongoing improvement and implementation of these interdisciplinary courses. New course materials could include pre-class quizzes, note-taking guides, in-class activities, discussion and computational laboratory section activities, and homework assignments. Development of these materials will be guided by the biology education literature, faculty feedback, and evidence-based best practices for promoting learning, diversity, and inclusivity in large enrollment mathematics courses. - Prepare and deliver student-centered, inclusive lectures in LS20, LS30A, and LS30B that incorporate evidence-based teaching practices; oversee the computational laboratory components of each course, make clear to students the connections to the modeling applications of concepts covered in lectures; supervise through weekly meetings the graduate student teaching assistants (TAs) for each course, and ensure that they incorporate effective teaching practices in laboratories and discussion sections; offer a minimum

of 2 office hours per course per week; provide students regular and timely feedback on all assignments, ensuring TAs do the same; and submit student grades in accordance with university policy. - Facilitate the transition to student-centered teaching in these interdisciplinary courses. Provide additional support for other LS20, LS30A, and LS30B instructors, such as: technical support with clickers, CCLE, and video lectures. Assist instructors and TAs in creating custom activities for class meetings and discussion sections (e.g., clicker questions, worksheets, computational problem sets, exam questions). Promote discussion of pedagogy and teaching philosophy to support student success, diversity, and inclusion. - Work effectively with LS Core staff to coordinate scheduling. - Solicit feedback from faculty, instructors, graduate student TAs, undergraduate LAs, and enrolled undergraduate students on the effectiveness of the LS20, LS30A, and LS30B courses. - Administer the undergraduate Learning Assistants (LA) program associated with LS20, LS30A, and LS30B in coordination with UCLA's LA Program Director for the Sciences in the Center for Education Innovation and Learning in the Sciences (CEILS); Responsibilities include recruiting and hiring qualified undergraduate LAs, co-facilitating the LA pedagogy training course (LS192), and mentoring the undergraduate LAs in LS20, LS30A, and LS30B through weekly meetings focused on course content.

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UChicago LabManager ResearchScientist

Lab Manager/Research Scientist - University of Chicago
- Thornton Lab

The Thornton Lab at the University of Chicago is seeking a lab manager/research scientist. We work at the interface of evolution, molecular biology, and biochemistry, combining phylogenetic and experimental approaches to reconstruct the historical mechanisms and dynamics of protein evolution. We are a medium-sized group of very collegial postdocs and students from a range of scientific disciplines, working together to answer central questions about the evolution of biological molecules.

The lab manager/research scientist plays an important role in the lab, conducting independent research, coordinating many aspects of the lab's operations, and training/helping others in the lab to develop, optimize, and perform experiments and analyses. Substantial laboratory experience in molecular biology and biochemistry is essential, as is the ability to work constructively as part of a collegial scientific group. Experience in evolutionary biology, phylogenetics, and/or computational biology is a plus but is not necessary. Good writing skills are highly valued. The ideal candidate will demonstrate scientific creativity, rigor, true curiosity about evolution, and a sense of humor.

The job announcement and instructions for applying can be found here: <https://jobopportunities.uchicago.edu/applicants/jsp/shared/position/JobDetails.css.jsp?postingId=667056> Please do not be put off by the title (Laboratory Manager - Research Technician), which the University assigns to positions like this. The job requires experience, independence, and leadership; the person who holds it is treated accordingly.

The University of Chicago is a fantastic place to do science, particularly at the interface of evolution and other disciplines. Chicago is a great city rich in high and low culture; it is also a hipster heaven and, in the summer, a fun beach town.

Please don't hesitate to contact me if you have any questions.

Joe Thornton joet1@uchicago.edu

Joseph W Thornton <joet1@uchicago.edu>

UHalle LivestockPopulationGenomics

The Martin Luther University Halle-Wittenberg (MLU), Central Natural Science Collections, under the funding directive "Networking - Developing - Researching: An alliance for university collections" of the German Federal Ministry for Education and Research, in the project "The Domestic Pig: Selective Breeding and Prevailing Taste - Morphology and Genetics in 100 Generations - Sus 100", is looking for a

1. Scientific Researcher in livestock sciences and domestication research and
2. Scientific Researcher (PhD student) in the field of population genomics.

1. position: Scientific Researcher in livestock sciences and domestication research

This is a full-time position, limited to three years. The salary will be commensurate with the qualifications of the successful candidate within the salary scale 13 TV-L.

Requirements: - Master degree in biology, agricultural sciences, veterinary sciences or related disciplines; PhD preferred - Experiences in livestock sciences and domestication research preferred - Expert knowledge in evolutionary biology, molecular genetics and biometry mandatory - Being a good team player with excellent communication and interpersonal as well as organizational skills for managing a huge international research collaboration; own initiative and willingness for longer stays at other institutions in Germany and abroad - Excellent track record of peer-reviewed papers requested

Responsibilities: - Leading coordination and implementation of the project - Revision of the historical collection and archive material - Geo-morphometric research and statistical analyses of historic as well as recent osteological material - Main authorship of synthesis papers on aspects of evolutionary biology, domestication history and pig breeding - Coordination and content-related compilation of the genetic- statistical evaluation and integration of the sociohumanistic studies - Co-supervision of a PhD and organization of workshops on the subject

Martin Luther University Halle-Wittenberg is an equal opportunity employer. Disabled candidates with equal qualifications will be given preference. Women are strongly encouraged to submit an application.

Please submit your full application (in electronic form as single pdf file) with registration number: 3-11858/16-D in the subject line until January, 31, 2017 to Dr Frank Steinheimer, E-mail: frank.steinheimer@zns.uni-halle.de

Applications should consist of (I) a motivation letter, (II) a recent curriculum vitae, (III) a list of publications, (IV) academic degrees and certificates, and (V) contact information of two individuals who could provide an evaluation of the candidate upon request.

The announcement takes place pending on fund availability and any possible budget restriction. Application expenses cannot be reimbursed by the Martin Luther University.

2. position: Scientific Researcher (PhD student) in the field of population genomics.

This is a part-time position (65%), limited to three years. The salary will be commensurate with the qualifications of the successful candidate within the salary scale 13 TV-L.

Requirements: - Master degree in biology, agricultural

sciences, veterinary sciences or related disciplines - Experiences in livestock sciences and domestication research preferred - Expert knowledge of and scientific lab practice in molecular genetics and their analysis; work practice in ancient DNA research preferred - Well-founded work practice in computer-steered biostatistics of genome data - Being a good team player with excellent communication and interpersonal skills; own initiative and willingness to perform most work at the Museum für Naturkunde (MfN) Berlin Responsibilities: - Leading coordination, implementation and analysis (including publication) of all molecular genetic studies in the project; linking with respective data of modern breeds from the Leibniz Institute for Farm Animal Biology in Dummerstorf - Publication of results in international scientific journals - Supervision of preparation of modern pig skeletons at the MfN - Joining institutional teaching requirements, supervising a technical student assistant and preparation of workshops - Own academic qualification (PhD) desirable

Martin Luther University Halle-Wittenberg is an equal opportunity employer. Disabled candidates with equal qualifications will be given preference. Women are strongly encouraged to submit an application.

Please submit your full application (in electronic form as single pdf file) with registration number: 3-11857/16-D in the subject line until January, 31, 2017 to Dr Frank Steinheimer, E-mail: frank.steinheimer@zns.uni-halle.de

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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>

UMinnesota FieldTech PollinatorNutrition

Field Technician: Nutrition of Roadside Plants for Pollinators

We are seeking a field technician for a state-funded project on the nutrition of roadside plants for bumblebees and monarchs. The technician would be responsible for surveying roadside sites, harvesting and processing plant material and pollinator specimens, organizing data, and coordinating research assistants. Funding is guaranteed for at least two months. Pending state legislature

approval (May 2017), the position would be funded for an entire year. The position would start July 1, 2017. Salary: \$42,000, approximately 40 hrs/week.

The applicant must have a bachelor's of science in a related field (e.g., biology, entomology, plant sciences), relevant research experience, a valid driver's license, ability to use GPS to locate established points, and ability to communicate well both orally and in writing. An ideal candidate would have experience conducting and coordinating field research, expertise in plant and pollinator identification, and familiarity with methods for pollen and nectar collection. Field work will require long hours working along roadsides under variable weather conditions.

The technician will join a team of researchers at the University of Minnesota, including Emilie Snell-Rood (primary supervisor), Marla Spivak, Dan Cariveau, Karen Oberhauser, Elizabeth Borer and Clay Carter. To apply, please submit a CV, a 1-2 page personal statement (e.g., relevant experience and how this position would support your long-term career goals), and contact information for 2-3 references. Applicants should apply through <http://humanresources.umn.edu/jobs> Job ID# 315299. Review of applications will begin March 15th, with a decision by April 1st. For questions, please contact Emilie Snell-Rood, emilies@umn.edu. More background on the research itself can be found at: <http://www.lccmr.leg.mn/proposals/2017/original/152-f.pdf> <<http://twitter.com/SnellRoodLab> >

"emilies@umn.edu" <emilies@umn.edu>

UMontana Tech PopGenomics

GENETICS LAB TECHNICIAN for ENVIRONMENTAL DNA and POPULATION GENOMICS

Project: Aquatic invasive species: understanding drivers of spread

Principal Investigators: Steve Amish and Gordon Luikart, Flathead Lake Biological Station and Montana Conservation Genomics Laboratory, Division of Biological Sciences, The University of Montana. gordon.luikart@umontana.edu (406-982-3301 x249), stephen.amish@mso.umt.edu (406-243-6749)

Start Date & Duration: February or March 2016; 1 year with likely multi-year extension

Project Description/Summary: Aquatic Invasive Species

(AIS) such as zebra and quagga mussels, Euarasian watermilfoil, Asian carp and many others are spreading across North America and causing massive economic and ecological problems. Sensitive eDNA tests are available for early detection, monitoring, and preventing the spread of these AIS. This position will involve research and monitoring using new eDNA technologies to help understand the drivers (or ecological correlates) of spread of AIS. We are especially concerned about stopping the spread of zebra mussels which were discovered in Montana last summer (2016) (Fig. 1). The applicant may also work on additional exciting population genomics projects including trout and stonefly adaption to extreme environments (captive, climate change), and conduct sampling in beautiful areas such as Glacier National Park, Yellowstone National Park, Flathead Lake, and streams across Montana. Skills required: The applicant should have substantial experience conducting qPCR. The applicant should have demonstrated ability to write and publish papers, and organize and manage lab supplies. Proven ability to communicate with others from diverse groups (managers, researchers, the public).

Applications: Send a brief letter (< 1 page) describing your motivation and background, your CV, and the names and contact information for three references to both G. Luikart and S. Amish. Review of applications will start February 1st and remain open until a suitable candidate is hired.

Salary: Negotiable, but likely approximately \$26,000 to \$33,000 the first year depending on experience and CV. We would consider hiring a postdoc with higher salary if the applicant has demonstrated high productivity, experience, and is passionate about understanding drivers or correlates of AIS invasions (including fish-killing pathogens).

Key references: see our web pages, videos: <<https://flbs.umt.edu/giving/default.aspx?id=1>>; & contact us.

Figure 1 (a) zebra & quagga mussels, (b) encrusted research equipment, and (c) a crayfish encrusted with zebra mussels. Native bull trout threatened by AIS and climate warming.

"Luikart, Gordon" <gordon.luikart@mso.umt.edu>

USalzburg EvolutionaryBiol

Applications are invited for the position of

Full Professor of “Evolutionary Biology of Animals” in the Dept. Ecology & Evolution at the Paris-Lodron University Salzburg, Austria. The desired starting date is 01 Oct. 2017.

We seek an innovative scientist with an outstanding track record in research and experience in academic teaching to fill the professorship of “Evolutionary Biology of Animals” at the Dept. Ecology & Evolution (<http://www.uni-salzburg.at/ecoevo>). The successful candidate must have demonstrated a well-established expertise in evolutionary biology and is expected to combine experimental laboratory and field approaches. The candidate’s research should cover aspects of meta-zoan evolution with a focus on genotypic and/or phenotypic adaptation of species or species groups (individuals/populations/communities) to long-term or short-term environmental changes. Internationally recognized expertise in research areas such as population genetics/genomics, evolutionary ecology, adaptive trait evolution, speciation, and/or coevolution and the application of state-of-the-art methods (e.g., next generation sequencing, transcriptomics) are expected. The university’s geographic location offers excellent opportunities for researchers particularly interested in alpine environments.

The appointee will be teaching the entire range of animal evolutionary biology and diversity for the university’s Bachelor “Biology” curriculum, the recently implemented Master “Biology/Ecology & Evolution” curriculum, the Teachers’ Education Program, and the Doctoral Studies program, including the university’s newly established Doctorate Schools. Teaching and evaluating students in both German and English will be required.

The new professorship will complement the existing research priorities of the Dept. Ecology & Evolution and further strengthen its scientific profile. Cooperation with researchers from the other biological departments and further related and/or complementary disciplines within the University of Salzburg as well as with local and national non-university research institutions is encouraged. The successful candidate is expected to initiate, acquire and implement novel externally funded national and international research programs, e.g. Austrian Science Fund (FWF), FWF research groups, European or other international joint projects, etc., to establish a research group, to show active participation in the academic self-administration and a willingness and the relevant qualification to take on a leadership position.

Salzburg offers not only an attractive research environment, but also excellent quality of life in a medium-sized city with a rich cultural life, close proximity to moun-

tains and lakes and easy access to the major urban centres of Vienna and Munich.

*Minimum general requirements for the appointment are:

1. A completed PhD compatible with the advertised position; 2. the qualification to teach at the university level (*venia docendi* or equivalent qualification); 3. excellent scientific abilities; 4. excellent pedagogical and didactical skills; 5. managerial skills necessary to lead an academic organization; 6. evidence of integration within the international research community (e.g. peer review of manuscripts and proposals, international experience and cooperations); 7. proficiency in written and spoken German.

The position is permanent and full time following by-law UG 2002 and the Employee Act of Austria. The payment will be according to collective agreement for university employees of the group A1, with a minimum salary of euro 4.842,70 before tax (14 annual payments).

The University of Salzburg is committed to increasing the share of women in research and teaching positions and therefore explicitly encourages female candidates to apply. In the event of equal qualifications, preference will be given to women.

Disabled candidates or people with chronic illnesses with the required qualifications are explicitly invited to submit their applications.

Travel and accommodation expenses arising from this application and any potential visit cannot be reimbursed.

Applications, including the standard documents (curriculum vitae, list of publications, teaching record, teaching evaluation, research projects and other relevant activities), as well as a description of the future research and teaching concepts should be addressed to the Rector of the Paris Lodron University of Salzburg, Univ.-Prof. Dr. Heinrich Schmidinger and sent by email to bewerbung@sbg.ac.at. Informal enquiries can be directed to ulrike.berninger@sbg.ac.at.

Applications must be received by 27 Jan. 2017.

Dr. Anja Hörger University of Salzburg Department of Ecology and Evolution Hellbrunnerstr. 34 5020 Salzburg Austria

email: anja.hoerger@sbg.ac.at Tel: +43 662 8044-5501

anja.hoerger@sbg.ac.at

USaskatchewan GroundSquirrelHeadTech

We are looking for a head field technician to assist with, and coordinate, fieldwork on the ecology of two wild populations of Columbian ground squirrels. The head technician will supervise 4 student interns and coordinate with graduate students involved with the project for the period of Apr 10 to Aug 31, 2017. Fieldwork will involve monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals, data entry and data verification. The two populations are separated by an approximately 1.5 hr. drive and will each be monitored by two separate teams of interns. As such, it is expected that the head technician will display strong organizational abilities, responsibility and oversight.

This is an excellent opportunity for someone with previous field experience, looking to advance their career in wildlife biology or move towards graduate school. All fieldwork is carried out in the spectacular Rocky Mountains of southwestern Alberta, Canada, home to some of the most majestic wildlife in North America. The head technician will have the opportunity to view many of these iconic species as well as interact with other researchers in the area working on a diversity of species and research projects.

Skills required: The successful candidate will have previous fieldwork experience in a similar work environment. Good organizational, multi-tasking and supervisory abilities are essential. Possession of these skills, as evidenced through previous experience supervising field crews, is desirable. Specific field skills required are: ability to trap, handle and observe wild mammals. The successful applicant will also have experience in data entry, checking and management of databases. A displayed interest in ecology, wildlife, field biology, and animal behaviour is also required. An undergraduate degree in one of these, or a related, field is required. The applicant must be able to work well with members of their own team, as well as other users of the area (i.e., other researchers, tourists).

Salary will be \$1800-2100/month, based on level of experience. Food and accommodation are provided. The successful candidate will be required to provide for their own travel to Saskatoon, Saskatchewan. Travel between the field station and Saskatoon is provided.

If you wish to apply for this position, please send a CV with a cover letter and contact details of three references (with e-mail address), by email to Jeff Lane (contact info below) before February 15, 2017. Please indicate in your application that you are applying for the head technician position (we are also posting for student interns). All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. Only those selected for interview will be contacted.

Contact:

Dr. Jeff Lane

Department of Biology

University of Saskatchewan

usaskcgsproject@gmail.com

www.lanelab.ca

“jeffrey.lane@usask.ca”

<jeffrey.lane@usask.ca>

UWarsaw FieldAssist BirdPopulations

Field assistant position for

great and blue tit population monitoring

We seek 2 field assistants in urban ecology to work in the Wild Urban Evolution & Ecology Lab (<http://leem.cent.uw.edu.pl>) at the Center of New Technologies (CeNT), University of Warsaw (Poland) for a period of 3 months from April to June 2017 or mid-April to mid-July. The position is part of a 2-year Polonez grant from the Polish Science Foundation (NCN) that aims to investigate the effects of trace metal exposure on great and blue tit physiology (i.e. oxidative stress, telomere length) and fitness (i.e. reproduction and survival) in a gradient of urbanisation.

Background - Current anthropogenic activities are responsible for considerable modifications of the natural environment. Those include light, noise and chemical pollution, which may have considerable impact at the individual level and in terms of populations' dynamics and functioning. Given the rapid increase in urbanisation worldwide, it is becoming increasingly important to better understand the underlying mechanisms and the potential impacts of anthropogenic pollution on natural populations. Chemical pollution such as trace metals are of particularly timely concern given their implication

in several human diseases and their noxious effect on wildlife (e.g. oxidative stress).

Job description - The field assistants will participate in fieldwork, in collecting phenotypic data (i.e. morphometric measurements) and other biological information. The field assistants may also oversee sample preservation and transportation to the lab. The team will be split into couples to monitor all sites located in gradient of urbanisation; most sites can be reached by public transports.

Job requirements - We seek motivated candidates with a strong interest in field work of wild bird populations. A previous experience in field work, in population monitoring or in bird handling would be appreciated. Preferentially, the candidate should have a theoretical background in ecology, in physiology or in population biology. Operational Polish language is essential, but because English is the working language in the group, the candidate should be able to understand and speak English. Driving licence and ringing licence are a plus.

Employment - Part or full-time position. The field assistant may work on any day of the week including weekend and the working hours are flexible.

Salary - depends on the assistant qualifications and time involvement in the project.

How to apply - Your application should include in PDF format: a cover letter and C.V. (including your research experience, formation and contact information). Please send your application to marion.chatelain@cent.uw.edu.pl as early as possible and no later than the 31th of January 2017 with the term "Field assistant position" as e-mail subject line. Selected candidates will be invited for live interview.

Field assistant position for arthropod sampling and identification

We seek 2 field assistants in urban ecology to work in the Wild Urban Evolution & Ecology Lab (<http://leem.cent.uw.edu.pl>) at the Center of New Technologies (CeNT), University of Warsaw (Poland) for a period of 3 months from mid-April to mid-July 2017. The position is part of a 2-year Polonez grant from the Polish Science Foundation (NCN) that aims to investigate the effects of trace metal exposure on great and blue tit physiology (i.e. oxidative stress, telomere length) and fitness (i.e. reproduction and survival) in a gradient of urbanisation.

Background - Current anthropogenic activities are responsible for considerable modifications of the natural environment. Those include light, noise and chemical pollution, which may have considerable impact at the individual level and in terms of populations' dynamics

and functioning. Given the rapid increase in urbanisation worldwide, it is becoming increasingly important to better understand the underlying mechanisms of anthropogenic activities on natural populations. The differences of food availability between urban and rural sites during the breeding season and more particularly during chicks' rearing would explain part of the effects of urbanisation on wild populations. Therefore, it is essential to measure food availability (i.e. arthropod richness, abundance and diversity in the case of great and blue tits) to then draw a detailed outline of urbanisation effects on urban wild populations.

Job description - The field assistants will take care of arthropod sampling (in the field), counting and identification (in the lab) to estimate food availability in great and blue tits. Depending on their interest and availability, they may also participate in collecting phenotypic data (i.e. morphometric measurements) and other biological information in great and blue tits. Both assistants will work together,

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Virginia Director Research Center Bioinformatics

Director, Center for the Study of Biological Complexity
Richmond, Virginia Rank: Associate to Full Professor

VCU Life Sciences seeks a Director of the Center for the Study of Biological Complexity (CSBC). VCU Life Sciences is a University matrix organization that promotes Life Sciences Research and Education. CSBC has been in existence for 15 years and offers undergraduate and graduate degrees in bioinformatics. Administrative offices are on the Monroe Park campus. Degree programs are Bachelor of Science in Bioinformatics, Master of Science in Bioinformatics with a traditional thesis and a non-degree option (Professional Master's program). Doctoral students have a specialized track in the Integrative Life Sciences doctoral program, which also operates under VCU Life Sciences. The new director would be expected to bring their own research program, but also recruit a diversified set of junior tenure faculty, increasing the research portfolio with extramural funding and expanding enrollment in the existing degree programs.

Virginia Commonwealth University is a major, urban public research university with national and international rankings in sponsored research. VCU is designated as a research university with very high research activity by the Carnegie Classification of Institutions of Higher Education and is recognized as a community institution by the Carnegie Foundation. VCU takes great pride in its commitment to creating a campus community that embraces diverse perspectives, cultures, experiences and people. Located in downtown Richmond, VCU enrolls more than 31,000 students in 226 degree and certificate programs in the arts, sciences and humanities. Sixty of the programs are unique in Virginia, many of them crossing the disciplines of VCU's 13 schools and one college. Medical College of Virginia Hospitals and the health sciences schools including the Schools of Medicine, Dentistry, Nursing, Pharmacy and Allied Health Professions comprise VCU Medical Center, one of the nation's leading academic medical centers. Today, VCU serves an integral role in the economic health of the city of Richmond and the region by educating the current and future workforce, advancing research, and enhancing patient care. VCU, its health system and other related entities have assets of approximately \$3.0 billion, which includes \$840 million in endowment funds.

Responsibilities

- Represent the Center to Life Sciences, the University, and the community (local, regional, and national).
- Provide scholarly leadership by maintaining independent research program and graduate student mentorship.
- Supervise 10 full-term and tenured/tenure research and teaching faculty. Assign specific teaching and service responsibilities to faculty.
- Supervise full-classified staff members who run the Center for High Performance Computing (CHiPC).
- Assume primary responsibility for recruitment, retention, tenure and promotion, and compliance with university guidelines regarding faculty appointments.
- Negotiate and supervise the departmental budget.
- Grow enrollment in BNFO degree programs (B.S., M.S.) with over 120 graduate and undergraduate majors and a curricula comprised of 30+ courses.
- Build on existing cross-initiatives to strengthen linkages across campus.

Required Qualifications

- Doctoral degree in related discipline from an accredited university
- Ten years of experience in discipline

- Tenured faculty member at a research active institution.

- Demonstrated experience working in and fostering a diverse faculty, staff, and student environment or commitment to do so as a faculty member at VCU

Preferred Qualifications

- Demonstrated commitment to undergraduate and graduate education

- Current federal research funding

- Demonstration of ability to recruit tenure track faculty and support research

- Demonstrated experience with budget management

- Excellent leadership, communication and interpersonal skills

Application Process

If interested, please apply online at <https://www.vcujobs.com/postings/58027> to submit cover letter, application, CV, and a list of three references. For additional information, please contact Paul Fawcett, Ph.D. at paul.fawcett@vcuhealth.org.

Projected start date is July 1, 2017. This position offers a competitive salary, start-up, and relocation package.

Virginia Commonwealth University is an equal opportunity, affirmative action university providing access to education and employment without regard to race, color, religion, national origin, age, sex, political affiliation, veteran status, genetic information, sexual orientation, gender identity, gender expression, or disability.

Rodney J. Dyer, PhD Department of Biology Center for Environmental Studies Virginia Commonwealth University

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Worcester Massachusetts Res Assoc Drosophila MolEvol

The Findlay Lab in the Department of Biology at the College of the Holy Cross seeks a full-time Research

Associate for an NSF-funded project on the impact of newly evolved genes on male reproduction in *Drosophila*. A primary responsibility of this position is to manage the laboratory on a day-to-day basis and assist in the training of undergraduate research students. However, the research associate will also have an independent research project relating to the function and evolution of a newly evolved gene(s).

The associate will be responsible for:

- training undergraduate research students in *Drosophila* husbandry and genetics and in basic molecular biology and cytology
- constructing transgenic fly lines through molecular cloning and fly crossing
- maintaining all lab fly stocks
- monitoring, aliquoting and ordering lab reagents
- developing experimental procedures and written protocols that are accessible to student researchers
- complying with lab safety regulations and interacting with the college's lab safety officer
- modeling and implementing appropriate data management practices
- assisting, on occasion, in the preparation of materials for teaching laboratories or outreach demonstrations
- preparation of media and reagents and maintenance of a well-organized, orderly lab
- contributing to the preparation of research publications and presentations

Required qualifications: At least two years of full-time, wet-lab experience. Hands-on experience with the husbandry and genetics of *Drosophila* fruit flies, as well as with common molecular biology protocols such as PCR, cloning, and nucleic acid isolation. Strong skills in data analysis and oral and written communication. Ability to teach undergraduates in a lab setting.

Preferred qualifications include an advanced degree (Master's or PhD) in genetics, cellular/molecular biology, or a related field; experience with immunofluorescence and confocal microscopy; experience with CRISPR/Cas9-mediated genome editing; experience with molecular evolution techniques and genome

databases; and, experience mentoring undergraduate students.

Additional Information:

This is an Exempt level position. The College is an Equal Employment Opportunity Employer and complies with all Federal and Massachusetts laws concerning Equal Opportunity and Affirmative Action in the workplace. Holy Cross is a member of the Higher Education Consortium of Central Massachusetts (HECCMA) and the Boston Consortium.

To review our Employee Benefit Options, please go to: <http://www.holycross.edu/human-resources/benefits> Application Instructions:

To apply for this position, please submit: a cover letter that describes your interest in the position and qualifications; a CV; and, the names and contact information of two references who can provide letters of recommendation upon completion of the search. In your cover letter, please include a brief reflection on how you might contribute to the College's commitment to diversity and inclusion (see <http://holycross.edu/diversity>). Furthermore, we encourage candidates to review the College's mission at <http://holycross.edu/mission>, and include any reflections on contributions you might make in that area.

To learn more about the Findlay Lab, see: <https://sites.google.com/a/holycross.edu/findlaylab/> Questions about the Findlay Lab can be directed to the PI, Geoff Findlay (gfindlay@holycross.edu). Questions about the application process should be directed to Deb Paquette in the HR department (dpaquett@holycross.edu). To apply, visit: <https://holycross.interviewexchange.com/jobofferdetails.jsp?JOBID=3D80382> – Geoff Findlay, PhD Assistant Professor Department of Biology College of the Holy Cross (508) 793-2655 gfindlay@holycross.edu <https://sites.google.com/a/holycross.edu/findlaylab/> “gfindlay@holycross.edu” <gfindlay@holycross.edu>

ASN Regional Meeting Awards	84	PeerCommunity in Evolutionary Biology	91
Call for Papers Male Competition Speciation Current Zoology	84	PLE Pennsylvania Schwartz Career Fellowship	91
Call SMBE Award Nominations	85	PLE Pennsylvania Summer Res	92
ESEB Outreach Fund Deadline Mar 15	86	QUBES Faculty Mentoring	92
Field Museum Chicago NSF REU Biodiversity Evolution	86	Reed Warbler Blood Samples	93
Freshwater Diatoms rbcLa gene	87	South Africa VolRes Assist Cooperative Behaviour	93
Gamboa Panama Intern Butterfly Speciation	87	South Africa VolRes Assist Social Mole Rats	94
Georgetown U REU	87	Systematics Research Fund	94
Greifswald U Climate Adaptation Exchange Grants	88	UCalifornia Riverside Trinidad Research Internships	95
Harvard U VolRes Assist Anolis Adaptation	88	UKansas EEB REU program	95
IIASA Austria Summer Fellowships Evol Modeling	89	UMichigan Biol Station Summer Res	96
Instagram Course	90	UOxford VolRes Assist Seabirds	96
Low Recombination	90	US govt scientists	97
NSF Syst Biodiversity Rotating Prog Officer	90	UTexas Austin Summer Undergraduate Res Plant Genetics	97

ASN Regional Meeting Awards

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

The American Society of Naturalists solicits proposals from organizers of regional meetings in the fields of ecology, evolution and behavior. The purpose of these small awards is to promote increased participation in regional meetings that fall along the research interests supported by the ASN and to use this support as a way of recruiting new membership to ASN. The awards typically provide subsidized registration for ASN members at these regional meetings. Please note that these awards are not intended to support workshops. Previous awardees have included meetings such as SEEPEG, SEEC, EVO-WIBO, and OE3C. Organizers of regional meetings should submit a brief proposal describing the research focus of the meeting for which funds are requested as well as details of the meeting such as anticipated number of participants, meeting venue and dates.

Instructions: Proposals should include two components. One should clearly describe the (1) overlap of the regional meeting with ASN research interests, (2) extent that the support would reach out to new audiences to grow ASN's membership, and (3) potential size of the impact on ASN membership. The second component should include a brief budget justifying the amount requested and detailing how the funds will be used. To standardize the applications, there is a strict one-page

limit (US Letter size paper, 1" margins, standard [e.g., Times] 12-point font, and no more than six lines per inch) for each component (i.e., 1 page for proposal, 1 page for budget description and use of funds). We anticipate funding 4-6 awards, typically valued at \$2000-\$3000.

Please send proposals to the ASN Regional Society Liaison Committee Chair Rebecca Kimball (rkimball@ufl.edu) by Feb. 15.

"Kimball, Rebecca T" <rkimball@ufl.edu>

Call for Papers Male Competition Speciation Current Zoology

We are excited to solicit papers on male competition and speciation for a special column in an upcoming issue of Current Zoology. Please feel free to contact any of the guest editors with inquiries.

SPECIAL COLUMN: Male Competition and Speciation (<https://academic.oup.com/cz/pages/malecompetition>)

GUEST EDITORS: Alycia Lackey (alycia.reynolds@gmail.com), Michael Martin (mdmartin7@gmail.com), and Robin Tinghitella (Robin.Tinghitella@du.edu)

DESCRIPTION: Despite our long-standing pursuit to understand the evolution and maintenance of new species, we still lack a clear understanding of mechanisms of speciation. Speciation remains an important

focus due to its role in the evolution and maintenance of biodiversity; this is particularly critical given current and predicted global change and loss of biodiversity. Sexual selection is a powerful source of rapid evolutionary change, and there is a long-standing hypothesis that it can cause reproductive isolation (i.e., when male mating signals and female preferences for those signals diversify). However, this understanding of speciation by sexual selection is largely limited to sexual selection via female mate choice. Male competition for mates, Darwin's second mechanism of sexual selection, can also favor rapid and dramatic phenotypic and genotypic changes, yet it has been all but overlooked in speciation research.

This special column will address when and how male competition can generate or maintain population or species differences. The aims of this special column are to: 1) expand our current speciation framework to include the contribution of male competition to speciation by sexual selection 2) examine the importance of male competition at different stages of divergence (e.g., within populations, between diverging populations, between distinct species) 3) explore the diversity of mechanisms by which male competition drives divergence 4) motivate future work by identifying unanswered questions

TIMELINE: Deadline for title submission: April 1, 2017 (email to guest editor) Deadline for manuscript submission: June 10, 2017 Manuscript handling (paper reviewing + revision): August 30, 2017 Publication: 6th issue, 2017

A title should be sent to the guest editors and manuscripts should be submitted before the deadline. Manuscripts received after the deadline will be considered as submissions for regular issues.

Submitted papers should not have been published previously, nor will be under consideration for publication elsewhere. Submitted manuscripts are accepted with the understanding that they are subject to peer review and editorial revision. Publication is free of page charges.

An example special column: Here is a recent special column on sexual selection and speciation. Scroll down to "Editorial" and the "Articles" that follow. <https://academic.oup.com/cz/issue/58/3> Alycia R. Lackey Postdoctoral Researcher Whiteman Lab 2112 Biology Building Murray State University Murray, KY 42071 office: 270-809-3224 alyciarlackey.weebly.com

alycia.reynolds@gmail.com

Call SMBE Award Nominations

In 2015, SMBE instituted four new awards for: Early-Career, Mid-Career, and Lifetime Research Achievements, and Service to the SMBE Community. We are now calling for nominations for these awards and ask you to consider nominating your colleagues.

The nominations will be due on 15 February, 2017.

Briefly, the Junior Award for Independent Research is intended for nominees in tenure-track positions at the Assistant Professor level or equivalent; the Mid-Career Award is for the research contributions of faculty nearing promotion to Full Professor or in the early stages as a Full Professor; the Lifetime Contribution Award is for exceptional contributions to the published literature in the field of molecular biology and evolution; and the Community Service Award recognizes outstanding efforts on behalf of the Society and the broader scientific community. Awardees will receive a cash prize and a trip to the 2017 SMBE Annual Meeting.

Here are links to the pages describing these awards:
Allan Wilson Junior Award for Independent Research <http://www.smbe.org/smbe/AWARDS/-AllanWilsonJuniorAwardforIndependentResearch.aspx>
Margaret Dayhoff Mid-Career Award <http://www.smbe.org/smbe/AWARDS/-MargaretDayhoffMidCareerAward.aspx>
Community Service Award <http://www.smbe.org/-smbe/AWARDS/CommunityServiceAward.aspx>
Motoo Kimura Lifetime Contribution Award <http://www.smbe.org/smbe/AWARDS/-MotooKimuraLifetimeContributionAward.aspx>

Nominations require a nomination letter, which should clearly indicate the award under consideration and also serve as a recommendation letter; a separate one-page summary of the nominee's qualifications for the award; a CV of the nominee; and an additional letter of recommendation. Self-nomination is not allowed. The nominator need not be an SMBE member, but the nominee must be a member of SMBE to be considered for the award.

The materials should be compiled into a single PDF file, and should be emailed to clapine@allenpress.com.

Best Regards,

Joe Felsenstein,

SMBE Awards Committee Chair

Laura Landweber President, Society for Molecular Biology & Evolution

lff2124@cumc.columbia.edu

ESEB Outreach Fund Deadline Mar 15

****ESEB Outreach Fund****

The European Society for Evolutionary Biology (ESEB) welcomes applications to the ESEB Outreach Initiative Fund for projects that promote evolution-related activities. The goal of this initiative is to improve public knowledge about evolution globally.

Applications for funding will be accepted for educational initiatives that promote evolution, translation of evolutionary material (books, films, and websites) intended for a general audience, public outreach seminars, public exhibitions, etc. Please note that scientific meetings are not supported by these funds. While most projects will be financed for a sum between 1000-1500 Euro, exceptions can be made if a strong argument is provided for additional funds.

Please use the application form, which can be found at <http://eseb.org/prizes-funding/outreach-fund/>. Applications will be accepted twice yearly (deadlines March 15, September 15) and should be submitted by email to Ute Friedrich (office@eseb.org; Subject: Outreach).

– Dr. Ute Friedrich ESEB Office Manager Email: office@eseb.org European Society for Evolutionary Biology - www.eseb.org office@eseb.org

FieldMuseum Chicago NSF REU Biodiversity Evolution

NSF Research Experience for Undergraduates (REU) in the Evolution of Biodiversity across the Tree of Life We are looking for 8 undergraduate students to participate in hands-on research in biodiversity science and receive training in cutting-edge techniques and analysis in evolutionary biology for 10 weeks during the summer of 2017.

Applications close February 10, 2017.

Students will learn research techniques that include DNA sequencing and computational analysis of genetic and genomic data, morphological measurements and phylogenetic analysis, and microbiology and next-generation microbial sequencing. Scientific projects to be conducted by the students in 2017 include:

Forest Canopy Response to the Paleocene-Eocene Thermal Maximum (PETM) Greenhouse Event Evolution of Mitochondrial DNA in Ferns Diversity in Mediterranean habitats - insights from lichenized fungi Habitat-driven Morphological Syndromes in New Zealand Water Beetles Systematics and Taxonomy of Cichlids in the Genus Thorichthys Does diet influence the evolution of body size in ants? Morphometric analysis of the elaborate soldier head in turtle ants A Small World: Uncovering Hidden Diversity in Early Land Plants

In addition students will receive career mentoring in a diversity of STEM fields, gain experiences in public outreach and science communication, receive training in ethics/responsible conduct of research, and participate in a diversity workshop to help overcome bias in science.

<https://www.fieldmuseum.org/REU> <https://www.fieldmuseum.org/2017-reu-program-offerings>

Students will be provided a stipend, dormitory housing, and assistance with travel costs.

Participants must be U.S. citizens or permanent residents, and an undergraduate during the entire period. We especially encourage students from groups traditionally underrepresented in science to apply.

To apply, please send complete the online application: <https://www.fieldmuseum.org/2017-reu-program-offerings> Applications close February 10, 2017.

Please direct any questions to Emily Hallock (ehallock@fieldmuseum.org).

Please share widely.

Thank you, Corrie Moreau

Corrie Saux Moreau, Ph.D. | MacArthur Associate Curator - Insects | Integrative Research Center | Department of Science and Education | Field Museum of Natural History | 1400 South Lake Shore Drive | Chicago, IL 60605 USA | Office: (312) 665-7743 | Fax: (312) 665-7754 | Email: cmoreau@fieldmuseum.org | Moreau Lab website: <http://www.moreaulab.org/> | FMNH website: <http://fieldmuseum.org/users/corrie-moreau> | Field Museum Women in Science: <http://fieldmuseum.org/womeninscience> cmoreau@fieldmuseum.org

Freshwater Diatoms rbcLa gene

Dear list members,

I am a PhD student in New Zealand studying freshwater ecology. I am interested in surveying diatom species richness using the rbcLa gene region. I was wondering if anyone had any suggestions for which primers to use for amplification of this region. I have found a number of primers published in the literature, but it does not seem like there is a “standard”.

Any help is much appreciated, and I am happy to compile the responses and repost in the answers section.

Many thanks in advance,

Whakawhetai koe,

Justin Pomeranz

justin.pomeranz@pg.canterbury.ac.nz

Justin Pomeranz <justin.pomeranz@pg.canterbury.ac.nz>

Gamboa Panama Intern Butterfly Speciation

Internship on butterfly speciation project in the tropics

We are seeking a research intern to work at the Smithsonian Tropical Research Institute (STRI) in Panama from April 2017 for a period of at least one year. The internship will focus on behaviour and diversification in Heliconius butterflies (for more information please see <http://www.heliconius.org>).

The intern will work as part of a team involving collaboration between the University of Cambridge, Ludwig-Maximilians-Universität in Munich and STRI.

The intern will join a vibrant community of scientists studying the origins and maintenance of tropical diversity (see <http://www.stri.si.edu>).

The project is based in Gamboa and the intern will be assisting a project investigating the genetic basis of reproductive and ecological isolation between two sympatric Heliconius species. The project involves breeding butterflies, managing crossing experiments and conduct-

ing behavioural assays. Applicants must be able to work independently and be committed to working full time in Panama for the duration of the project. A knowledge of Spanish and the ability to drive would be useful but are not essential.

A stipend of US\$900/month will be provided to cover accommodation and living costs in Panama.

An application form can be downloaded from <http://heliconius.zoo.cam.ac.uk/blog/2017/01/research-intern-posit-ion-panama/>. Please send applications, or questions, to Richard Merrill (r.merrill@zoo.cam.ac.uk). Please use the subject header: “PANAMA RESEARCH ASSISTANT” before 14th February 2017.

Richard Merrill <r.merrill@zoo.cam.ac.uk>

GeorgetownU REU

Dear Colleagues,

Please share this call for applications with interested students. Some of the potential mentors work on a range of topics in evolutionary biology, including behavior, evolutionary ecology, evolutionary genetics, mathematical modeling of biological systems, and extremophiles and exobiology.

Environmental Science and Policy in the Nation’s Capital

An NSF Research Experience for Undergraduates (REU) Program at Georgetown University

Summer 2017

Georgetown University’s REU Site program in Environmental Science and Policy in the Nation’s Capital is seeking talented and engaged undergraduate students. This ten-week program will bring a cohort of ten students to Washington, D.C. to conduct hands-on research in environmental science at Georgetown University and to take part in a mini-curriculum that builds research skills and also explores the intersections of science and public policy. Participating research mentors have expertise in fields including behavior, ecology, conservation biology, evolutionary ecology, evolutionary genetics, mathematical modeling of biological systems, hydrology, statistics for environmental and biological studies, and earth science. See mentor research descriptions on the program web site. Interested students are encouraged to contact potential mentors directly.

The 2017 program will run from May 31 - August 5.

Students will be housed on the Georgetown campus and will receive a \$5250 stipend plus an allowance for food. To be eligible, applicants must be U. S. citizens or permanent residents, full-time students as of August, 2017, and available to participate full-time during the program. We are striving for a diverse group, so students from groups typically underrepresented in STEM fields are strongly encouraged to apply.

Review of applications will begin on February 17, 2017 and will be accepted on a continuing until all positions are filled.

For more information on the program and to apply, visit: <http://reunvscigeorgetown.weebly.com/>

For inquiries, contact the program manager Dr. Manus Patten (mmp64@georgetown.edu), the principal investigator Dr. Matthew B. Hamilton (matthew.hamilton@georgetown.edu), or co-principal investigator Dr. Martha Weiss (weissm@georgetown.edu).

Sincerely, Matt

Matthew B. Hamilton, PhD

Associate Professor

Georgetown University

Department of Biology, Regents Hall 506

37th and O Streets NW

Washington, DC 20057

202-687-5924 office 202-687-5662 fax

202-784-7105, 202-784-7181 lab

<http://hamiltonlabpage.weebly.com/> <http://reunvscigeorgetown.weebly.com/> Matthew B Hamilton <hamiltm1@georgetown.edu>

GreifswaldU ClimateAdaption ExchangeGrants

Call: RESPONSE Exchange Grants

The DFG funded Research Training Group RESPONSE (Biological Responses to Novel and Changing Environments; <https://tinyurl.com/GRK2010-RESPONSE>) invites applications for Exchange Grants. In order to foster collaborations between RESPONSE members and other scientists, researchers are invited to spend a period of 2-12 weeks at one of the RESPONSE labs in Greifswald, Germany. Exchange Grants should involve the execution of a collaborative research project relevant

to RESPONSE, i.e. on issues related to environmental change. We particularly aim to integrate research across multiple levels of investigation, including ecology, evolution, genetics, physiology, behaviour, theory or modelling. The deadline for grant applications is March 1st 2017.

Eligibility

Grantees must be hosted by a participating researcher of RESPONSE (<https://tinyurl.com/GRK2010-RESPONSE>) and undertake high quality scientific research at the University of Greifswald. Funding by RESPONSE must be acknowledged in publications resulting from the grantee's work in relation to the Exchange Grant. Persons affiliated with Greifswald University are not eligible.

Application Procedure

Applications for RESONSE Exchange Grants should include the following information:

- scientific CV including a publication list,
- letter of acceptance from the prospective RESPONSE host,
- project title and short description of the proposed project (max. 1200 words),
- proposed starting date and duration,
- estimated travel costs.

Applications should be submitted as one PDF file to the spokesperson of the research training network (email to klaus.fischer@uni-greifswald.de). Funding decisions will be made by the RESPONSE Executive Board based on scientific quality and relevance to the aims of RESONSE.

Allowance

Exchange Grants are reimbursed on the basis of an allowance of 400 EUR per week (for 2-12 weeks) plus actual travel expenses up to a maximum of 500 EUR. The grants do not cover health insurance, taxes, or retirement scheme contributions.

Michael Schöner <schoenerm@uni-greifswald.de>

HarvardU VolResAssist AnolisAdaptation

The Losos Lab at Harvard University (<http://lososlab.oeb.harvard.edu>) is looking for a field assistant (undergraduate or graduate level) to join a team of re-

searchers studying thermal adaptation and speciation in brown anole lizards in The Bahamas. The period of this assistantship will be from 3 May - 30 June, 2017. The project will involve both lab and field work. Prior field experience is preferred, but not necessary. All travel and living expenses will be paid for, but no salary will be provided. For more information (and to apply) please contact Mike Logan at mike.logan1983@gmail.com.

Michael Logan <mike.logan1983@gmail.com>

IIASA Austria SummerFellowships EvoModeling

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 to August 2017 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 IIASA's 24 member countries - Australia, Austria, Brazil, China, Egypt, Finland, Germany, India, Indonesia, Iran, Japan, Korea, Malaysia, Mexico, the Netherlands, Norway, Pakistan, Russia, South Africa, Sweden, Ukraine, the United Kingdom, USA, and Vietnam - are eligible for fellowships that provide full coverage of travel, accommodation, and living expenses.

Model-based summer research projects are invited in the following indicative areas:

Evolution of cooperation Governance of common goods Systemic risk and network dynamics Eco-evolutionary dynamics Evolutionary community ecology Food-web evolution Vegetation dynamics Adaptive speciation Disease ecology and evolution Evolutionary conservation biology Fisheries management Fisheries-induced evolution Adaptive dynamics theory and models Spatial models in ecology and evolution

Applicants are encouraged to prepare a research proposal that corresponds to their scientific interests and to EEP's research agenda. Accepted applicants will begin work before the summer, by planning their re-

search 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 highly welcome to send informal inquiries regarding their specific research interests and plans to EEP's program director Ulf Dieckmann (dieckmann@iiasa.ac.at).

Online applications will be accepted until Wednesday, January 11, 2017 (24:00 CET).

Since 1977, IIASA's annual Young Scientists Summer Program (YSSP), has attracted 1800+ students from 86 countries. The YSSP 2017 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:

+ Information about IIASA's Evolution and Ecology Program <http://www.iiasa.ac.at/eep> + Details about the summer program, and online application <http://www.iiasa.ac.at/web/home/education/-yssp/Apply/ConditionsEligibility/Conditions-and-Eligibility.en.html> + Examples of successful YSSP projects <http://www.iiasa.ac.at/web/home/-research/researchPrograms/EvolutionandEcology/-AbouttheProgram/YSSP-in-EEP.en.html> + General information about IIASA http://www.iiasa.ac.at/-web/home/about/whatisiiasa/what_is_iiasa.html Ulf Dieckmann Program Director Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

Email dieckmann@iiasa.ac.at Phone +43 2236 807 386 Phone secretary +43 2236 807 231 Fax +43 2236 807 466 or +43 2236 71313 Web www.iiasa.ac.at/Research/EEP Online reprints www.iiasa.ac.at/~dieckman Google Scholar scholar.google.com/citations?user=rAcGGSgAAAAJ

DIECKMANN Ulf <dieckmann@iiasa.ac.at>

Instagram Course

Subject line: New class - Boost your science with Instagram

Dear colleagues, Instagram can be a powerful social media tool for scientists. When used effectively, Instagram can advance research careers and further outreach goals. Unfortunately, very few researchers receive any training on how to use Instagram for professional purposes.

That's where SciFund Challenge, an outreach-focused nonprofit, comes in with our new class: Using Instagram to Boost Your Science. Over three weeks, you'll learn how to use Instagram to further your science. Additionally, since Instagram is focused on photos, we'll also teach you how to create better images. Even better, by the end of the class, you'll have created a personal Instagram plan to further your research or outreach goals.

This class is being taught in partnership with the Louisiana State University's College of Science and Communication across the Curriculum program. The class will be running for three weeks, from January 27-February 17, 2017. The class is intended for academics that are new to Instagram and it is open to academics at any level, in any discipline. The class will be online, so all countries are welcome.

The deadline to apply is January 26th, but our classes usually fill up early. Act soon if you are interested! Here's the link for more information: <http://bit.ly/2hLnMQo>
Questions? Comments? Please send them my way. Jai Ranganathan jai@scifund.org

jai.ranganathan@gmail.com
jai.ranganathan@gmail.com

Low Recombination

Request: information on species with low levels of recombination

Dear all,

We are currently conducting a review of species with low levels of genome-wide recombination. Apart from

species in which one sex does not recombine and with the exception of some specific chromosomes with zero recombination (e.g., dot chromosomes in *Drosophila*), most species appear to undergo at least one crossover per chromosome pair and meiosis. We would be very grateful for any hints on species, in which this is not the case, that is, species with chromosomes that are less than 50cM of total genetic length (if such species exist) or, equivalently, that undergo less than one crossover per meiosis. An alternative would be species, in which crossovers occur exclusively at the ends of the chromosomes, and hence with low levels of recombination within chromosomes.

With best wishes and many thanks for any help offered, Christoph Haag and Thomas Lenormand

Christoph Haag CNRS-UMR5175 CEFE Centre d'Ecologie Fonctionnelle et Evolutive 1919, route de Mende 34293 Montpellier cedex 5 France

E-mail : christoph.haag@cefe.cnrs.fr

"Christoph.HAAG@cefe.cnrs.fr"
<Christoph.HAAG@cefe.cnrs.fr>

NSF SystBiodiversity RotatingProgOfficer

EvolDir -for announcement section Reply-To: "Chakrabarty, Prosanta" <pchakrab@nsf.gov>

ProgramOfficer.SystematicsBiodiversity.NationalScienceFoundation

The Systematics and Biodiversity Sciences Cluster of the Division of Environmental Biology at the National Science Foundation is searching for a Program Director to serve on a temporary (rotating) basis. <https://www.nsf.gov/pubs/2016/bio16001/-bio16001.jsp?org=BIO> DEB supports fundamental research on populations, species, communities, and ecosystems. <https://www.nsf.gov/div/index.jsp?org=DEB> The Systematics and Biodiversity Science Cluster supports research that advances our understanding of the diversity, systematics, and evolutionary history of organisms in natural systems.

Cheers and thanks, Prosanta

Prosanta Chakrabarty, Ph.D. Program Director Systematics & Biodiversity Sciences Cluster Division of Environmental Biology National Science Foundation Office: 703-292-5190 Email: pchakrab@nsf.gov

“Chakrabarty, Prosanta” <pchakrab@nsf.gov>

PeerCommunity in EvolutionaryBiology

Dear EvoDir members,

We are pleased to announce the launch of the Peer Community in Evolutionary Biology (PCI Evol Biol) website: <https://evolbiol.peercommunityin.org>. This website will host free, open and transparent reviews and recommendations of preprint (i.e. prereview) articles deposited in open archives, such as bioRxiv (biorxiv.org) as well as recommendations of postprint (i.e. reviewed) articles. Several recommendations for postprint articles are already available on the home page of the website.

We warmly invite you to submit your preprint articles to PCI Evol Biol for evaluation and recommendation by this community.

PCI Evol Biol is currently supported by more than 160 researchers (evolbiol.peercommunityin.org/public/recommenders) and we expect to be joined by many more.

Details about the aims, structure and functioning of PCI Evol Biol can be found on the websitehelp page (evolbiol.peercommunityin.org/about/help_generic).

Briefly, PCI Evol Biol is the first community of the parent project Peer Community In (peercommunityin.org). The Peer Community In project is driven by a desire to establish a high-quality, free, public system for identifying high-quality articles through specific recommendations recognized initially within, and subsequently beyond the community, including by funding and research agencies. This recommendation system will offer a free alternative to all those uncomfortable with the current evaluation and editing process of scientific journals, which is very costly for research institutions.

Using PCI Evol Biol as an example, we will call for the establishment of other specific communities of researchers (e.g. PCI Ecology, PCI Entomology) reviewing and recommending articles in their fields. In the long term, this project could, therefore, lead to the development of an entirely new system of scientific publication, in which articles are deposited in free open archives, and, if appropriate, are reviewed and awarded a recommendation providing a public guarantee of their scientific quality.

We hope you will appreciate this project and will provide it with your support, by submitting preprints of high quality. Please tell your colleagues all about PCI Evol Biol and its website.

Thomas Guillemaud, Benoit Facon, Denis Bourguet and the Managing Board of PCI Evol Biol.

<https://evolbiol.peercommunityin.org> contact@evolbiol.peercommunityin.org

tguillemaud <thomas.guillemaud@inra.fr>

PLE Pennsylvania SchwartzCareerFellowship

PLE Schwartz Early Career Fellowship Pymatuning Laboratory of Ecology Summer 2017

The University of Pittsburgh's Pymatuning Laboratory of Ecology (PLE) is pleased to offer the Frank J. Schwartz Early Career Research Fellowship of up to \$10,000 plus up to three months of station fees and residency costs for the primary investigator (PI). PLE is a vibrant research and education facility located on Lake Pymatuning in Northwest Pennsylvania. PLE's research facilities are spread across 350 acres and include access to a variety of aquatic and terrestrial ecosystems. Its 10,000+ square feet of laboratory facilities include a field laboratory adjacent to an open field that can be used for large-scale replicated experiments, a modern molecular laboratory for ecological or evolutionary research, and facilities for animal, plant and aquatic studies.

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

For more information about the fellowship program or research opportunities at PLE, please contact the Director,

Dr. Cori Richards-Zawacki (cori.zawacki@pitt.edu).

Applicants should submit a single .pdf file including their CV, a 2-3 page proposal outlining the proposed research, a budget detailing how the fellowship funds will be spent, and planned dates of residence to cori.zawacki@pitt.edu, placing the words “PLE Schwartz Early Career Fellowship” in the subject line of the email. Review of proposals will begin February 10, 2017.

–

Corinne L. Richards Zawacki, Ph.D. email: cori.zawacki@pitt.edu <email%3Acori@tulane.edu> Associate Professor, Department of Biological Sciences and Director, Pymatuning Laboratory of Ecology University of Pittsburgh

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

“cori.zawacki@pitt.edu” <cori.zawacki@pitt.edu>

PLE Pennsylvania SummerRes

The Pymatuning Laboratory of Ecology (PLE) invites applications for McKinley/Pape/Darbaker/ Grants in Aid of Research. PLE is a vibrant research and education facility located on Lake Pymatuning in Northwest Pennsylvania. PLE’s research facilities are spread across 350 acres and include access to a variety of aquatic and terrestrial ecosystems (<http://www.biology.pitt.edu/facilities/pymatuning/research>). Its 10,000+ square feet of laboratory facilities include a field laboratory adjacent to an open field that can be used for large-scale replicated experiments, a modern molecular laboratory for ecological or evolutionary research, and facilities for animal, plant and aquatic studies.

McKinley/Pape/Darbaker Grants are intended to support researchers in the early stages of their ecological and evolutionary research programs at PLE. Grant proposals are submitted each year in February and several awards are made, generally not exceeding \$3,500. Most awards go to graduate students, but consideration will be given to recent Ph.D.’s and more senior researchers interested in initiating new work at PLE. The due date for 2017 grant proposals is February 10, 2017.

Please visit our website for further details about the application process:

<http://www.biology.pitt.edu/facilities/pymatuning/>-

research-grants=E2=80A –

Corinne L. Richards Zawacki, Ph.D. email: cori.zawacki@pitt.edu <email%3Acori@tulane.edu> Associate Professor, Department of Biological Sciences and Director, Pymatuning Laboratory of Ecology University of Pittsburgh

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

“cori.zawacki@pitt.edu” <cori.zawacki@pitt.edu>

QUBES FacultyMentoring

iDigBio (via the Education and Outreach Working Group), Kurator, AIM-UP!, and BLUE in partnership with QUBES are pleased to offer a unique networking and professional development opportunity for teaching faculty interested in incorporating real natural history collections data into their lessons and data literacy skills into their curricula. Anticipated involvement runs from April through the fall semester of 2017. During this Faculty Mentoring Network we will be testing, customizing, and extending a series of biodiversity collections-based modules that address fundamental biological principles using real data. These modules have been developed by members of AIM-UP and BLUE (visit here to see the featured modules). Participants will work in a team to optimize and implement selected materials that complement their specific curriculum.

Who Should Apply: We are looking for engaged and enthusiastic faculty and instructors of undergraduate biology who want to bring real collections-based data into their classrooms. We are especially keen to introduce new people to the biodiversity collections community, so if you are not yet familiar with natural history collections, and their associated data, we welcome your interest and potential participation.

The majority of the network activities will take place virtually, but there will be a 2-day kick-off workshop in Gainesville, Florida, May 24-25. All accepted applicants must be available to attend the workshop, commit to the length of the FMN, plan to implement a module in their fall 2017 classroom, and share developed materials. Lodging and meals for the workshop will be provided. Some funding is available to offset travel to the May meeting, but we encourage participants to acquire additional funds.

Requirements:

1. Be teaching in a college biology (or other related classes like ecology, evolution, taxonomy...) course for fall 2017. 2. Incorporate at least one of the modules into their course during the fall 2017 semester. 3. Be able to commit 1-2 hours every week to the project. This includes virtual meetings April - December 2017. 4. Attend the entire kickoff workshop in Gainesville, Florida, May 24-25, 2017. 5. Be willing to share modified resources created during the network. 6. Participate in evaluation of the network.

Benefits of Participation:

- Develop, implement, and assess effective materials and innovative pedagogical practices for teaching with collections data and incorporating data literacy skills into the classroom. - Build collaborations with experts in biodiversity collections data and data literacy skills. - Work as a community of practice with diverse colleagues at both an in person meeting in Gainesville, FL and through a 9 month collaboration in a FMN.

All teaching faculty and instructors are encouraged to apply. Faculty from community colleges, two-year institutions, and Minority-Serving Institutions (MSIs) are especially encouraged to apply.

Ready to apply now? Visit: <https://qubeshub.org/groups/nhc.fmn> Questions? Attend the Informational Webinar on January 26, at 1:00 pm ET at <https://idigbio.adobeconnect.com/eo> Contacts: Molly Phillips (mphilips@flmnh.ufl.edu) or Anna Monfil (monfilak@cmich.edu)

“Hale, Alison” <HaleA@CarnegieMnh.Org>

ReedWarbler BloodSamples

Dear list members,

I am a PhD student at the University of Oslo, Norway, investigating range shifts and adaptation in the Eurasian reed warbler (*Acrocephalus scirpaceus*). I would be very interested to hear from anyone that had blood samples of reed warblers that I could use for DNA analyses.

If you do have samples and are interested in contributing/collaborating, I would be very happy to hear from you.

All the best, Camilla?

“c.l.c.satre@ibv.uio.no” <c.l.c.satre@ibv.uio.no>

SouthAfrica VolResAssist CooperativeBehaviour

Volunteer Research Assistant position Causes of individual variation in cooperative investment in the Damaraland Mole-Rat

I am a PhD student at the University of Cambridge and I'm looking for a volunteer research assistant to carry out exciting experiments with captive Damaraland mole-rats, *Fukomys damarensis*. The study site is at the Kuruman River Reserve, in the South African Kalahari Desert.

My research, investigates the causes of individual variation in cooperative behaviour. I am particularly interested in whether and how varied social experiences throughout life can generate differences in development and behavioural profile. Further information about the experiments will be provided on interview.

I am looking for applicants available for a period of 6 to 12 months starting as soon as possible. Applicants should be hardworking, enthusiastic, physically fit, and prepared for long hours in the laboratory. Successful applicants will be responsible to run experiments and will be involved in data collection and management (behavioural observations and collection of blood, and urine samples). Other general tasks related to animal handling (hormone injections and implants) and husbandry and data handling will also be expected. Working weeks will not exceed 45 hours.

This position is particularly suited, but not exclusively, for people aiming to carry on their academic education or a management position in a research project. Successful applicants can expect to gain invaluable experience in animal handling procedures and conducting and managing experiments on a daily basis. They will be trained to work with the software ObserverXT and Microsoft Access.

Costs of food and accommodation while at the project will be covered.

If you are interested in this position send your CV and cover letter stating your availability to Philippe Vulliouid (philippe.vulliouid@gmail.com).

Shortlisted applicants will be invited for a Skype interview.

Deadline: 05/February/2017 (the position will remain

open until filled)

philippe.vullioud@gmail.com

SouthAfrica VolResAssist SocialMoleRats

SouthAfrica.VolResearchAssistant.SocialMoleRats

Cooperative breeding in Damaraland mole-rats (*Fukomys damarensis*).

We are looking for voluntary research assistants to help with our research on the completely subterranean, highly social Damaraland mole-rat (*Fukomys damarensis*) in the Kalahari. Starting between March and July 2017 for 6 months

Position 1: Behaviour and Physiology - mainly laboratory based

This position entails assisting in several studies on social evolution and hormonal effects on social behaviour of mole-rats. We are interested in the effects of hormonal variation on allo-parental care and the effects variation in the social environment on behaviour and physiology in mole-rats. The research assistant will be involved in all steps of the experiments and will mainly work in the laboratory with our captive mole-rats which are housed in large semi-natural tunnel systems. The responsibilities include behavioural observations, hormonal measures (blood sampling, urine sampling), obtaining morphological measures by X-Ray, and hormonal manipulations. The laboratory is situated in the Kuruman River Reserve in the southern Kalahari, Northern Cape province of South Africa.

The successful applicant will work in a team of 5-10 persons and will receive extensive training to acquire the skills needed for the above mentioned data collection. The research station is also the home of several other projects studying meerkats (www.kalahari-meerkats.com), cape ground squirrels, pied babblers, forktailed drongos and hornbills resulting in a stimulating scientific environment. Around 20-30 research assistants are based at the station year round. Research assistants will learn a range of skills such as remote sensing of behaviour, endocrine sampling techniques, behavioural observations, data handling and management.

Applicants should be enthusiastic, willing to work hard and keen to get involved in a research project in a remote location.

Position 2: Ecology - mainly field based

We are conducting a capture-mark and recapture study in which the voluntary research assistant can play an important role. Entire groups of mole-rats will be captured and individually marked. Morphological measurements and tissue samples will be obtained before the release of the animals. The field work is physically demanding (long hours, heavy digging to capture mole-rats) and weather conditions are very challenging (heat during the day, very cold during the night). Field work will make trapping during the night necessary. The assistant will mostly be working along one more experienced scientist but will need to work independently at times. This position requires working in a very small team in a remote location on free ranging animals and the trapping season will last for 3 months (starting in March or April 2017)

In both positions accommodation is provided, and research assistants are paid a monthly allowance to cover their personal costs and food. Domestic travel to the field site can be covered but we cannot provide an international airfare, travel insurance, or visa fees for applicants from overseas.

Applications received until the 22nd of January 2017 are ensured full consideration. Later applications may be considered. Please indicate whether you apply for position 1 or 2 or both positions.

Please apply to or contact for further information:

Markus Zottl, University of Cambridge,
mz338@cam.ac.uk

Markus Zoetl <mz338@cam.ac.uk>

SystematicsResearchFund

The call for the 2016/17 round of the Systematics Research Fund is now open.

The Councils of the Linnean Society of London and the Systematics Association jointly administer the Systematic Research Fund.

Typical activities supported include contributions to 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 contributions to publication costs (although we are unable to support article processing charges). Projects of a more general or educational nature will also be considered, provided that

they include a strong systematics component. Typical activities not supported include attendance at scientific meetings and contributions to student maintenance or tuition fees. The fund does not provide payments 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.

The application form may be found at:

<http://www.systass.org/awards/srf.shtml> and

<https://www.linnean.org/the-society/medals-awards-prizes-grants/systematics-research-fund> The deadline for applications is 15th February 2017.

Please read the “Guidelines for applying for SRF funding” before completing the online application form. Please note that only applications made using the online form are acceptable.

Questions about the application procedure can be sent to the SRF Administrator (srf@systass.org).

Mark Carine <M.Carine@nhm.ac.uk>

UCaliforniaRiverside Trinidad ResearchInternships

Research Internships - Evolutionary Biology

Research interns are needed to assist in a multi-disciplinary, multi-investigator, experimental study of the interactions between ecology and evolution in Trinidad. The research is led by Professor David Reznick at the University of California, Riverside in collaboration with Joseph Travis (Florida State), Tim Coulson (Oxford), Paul Bentzen (Dalhousie U.), Andres Lopez-Sepulcre (L'Ecole Normal Superieure, Paris) and Ron Bassar (Oxford). We seek to integrate multiple biological fields for the study of these interactions in experimental populations of guppies in Trinidad. Duties include assisting in monthly censuses of guppy populations in montane streams. The monthly censuses include long hours in the field and laboratory. There will also be 12 days off between each census when interns can pursue an independent project.

Qualifications: We seek interns who are entertaining the possibility of pursuing graduate studies in some area

of ecology and evolution and who wish to gain some additional field research experience before doing so. Research will take place in semi-remote areas of Trinidad sometimes under bad weather conditions. Applicants must be able to live and work well with others. Research will involve carrying heavy packs over slippery and steep terrain. Applicants must be in good physical condition and be able to meet the demands of field research under these conditions. Ability to drive a standard transmission vehicle is desirable but not required. Applicants with first-aid/first responder training, skills in automobile maintenance, and construction skills are highly desirable. Please address these skills when applying.

Interns will be required to spend a minimum of 3-months in Trinidad, with possibility of extension. Starting dates are as early as May 2017. We will cover all travel and living expenses and provide housing.

Please see our website <cnas.ucr.edu/guppy> for more information on the project and access to reprints. Our video menu includes a “guppy censuses” submenu that details the main tasks associated with the internship.

Applicants should send cover letter, CV and the names and e-mail addresses of three or more professional references to David Reznick (gupy@ucr.edu). At least two of the references should be academics.

Joshua Goldberg <jgold011@ucr.edu>

UKansas EEB REU program

Applications are now open for our NSF funded Research Experience for Undergraduate (REU) program, Models in Evolution, Ecology and Systematics. —The program will take place May 22-July 28 2017 in the Department of Ecology and Evolutionary Biology at the University of Kansas. In this ten week program, students will participate in mentored, independent research and receive training in research support skills.— “Models” is broadly interpreted to include not only building of theoretical models, but also testing of models (empirical work). More information on projects is available at <http://eebreu.ku.edu> . Students will be provided with a generous stipend, housing and meals, and travel to the program. Review of applications begins February 15, 2017 and will continue until all positions are filled. Students must have completed one semester of college level work (including community college), must plan to be enrolled in an undergraduate program during the fall of 2017, and be US citizens or permanent

residents.—Biology, math and computer science majors are encouraged to apply.

Former students have been highly successful at continuing on to graduate school and obtaining the NSF Graduate Research Fellowship.— Review of applications begins February 15 and will continue until all positions are filled.— Questions may be addressed to eebreu@ku.edu.

Dr. Jennifer Gleason Program Director Associate Professor Ecology and Evolutionary Biology University of Kansas Lawrence, KS 66045

jgleason@ku.edu

UMichiganBiolStation SummerRes

The University of Michigan Biological Station (UMBS) is now accepting applications for its Research Experience for Undergraduates (REU) program, “Climate Change in the Great Lakes Region.”

Our REU summer program runs for nine weeks (June 20 - August 19, 2017) at the U-M Biological Station on Douglas Lake in beautiful northern Michigan. Each REU participant will:

- Work closely with a research mentor on a project of mutual interest.
- Design, conduct, analyze, and report on their research project with guidance from the mentor and the two program co-directors.
- Participate in workshops and group discussions designed to provide the background knowledge and technical tools needed to carry out interdisciplinary scientific research.
- Contribute to the body of knowledge that can help address many of Earth’s most important environmental challenges.

COMPENSATION: Participants receive: a stipend of \$5,000; free room and board at the Station; and a travel allowance.

DEADLINE: The deadline to apply is Wednesday, March 1, 2017.

Application and details at: [*http://lsa.umich.edu/content/michigan-lsa/umbs/en/students/research-opportunities/reu-program.html*](http://lsa.umich.edu/content/michigan-lsa/umbs/en/students/research-opportunities/reu-program.html) The University of Michigan Biological Station is located on Douglas Lake near Pellston, Michigan at the tip of the lower peninsula. Surrounded by more than 10,000 acres of undeveloped university-owned property, Students have quick access to many unique habitats in the region including dune,

alvar, bog, and old-growth forest. UMBS also has two atmospheric gas sensing towers for monitoring forest and atmospheric gas. More information is available at <http://www.lsa.umich.edu/umbs> . *Stephanie Fortino* Recruitment and Outreach Coordinator, University of Michigan Biological Station (734) 763-8574 | safort@umich.edu | lsa.umich.edu/umbs

“safort@umich.edu” <safort@umich.edu>

UOxford VolResAssist Seabirds

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 2017. The work will involve several research projects coordinated by Prof Tim Guilford at Oxford’s Department of Zoology (see the OxNav website). We utilise state-of-the-art tracking technologies (miniature GPS, geolocators, time-depth recorders, etc) on several species of seabirds but mainly on Manx shearwaters. Most work will involve assisting doctoral students with the day-to-day monitoring of breeding birds and with deploying and retrieving 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. The role will also involve monitoring Atlantic puffins tracked with geolocators and helping with their recapture (with some work to be carried out at dawn) as part of a project led by Dr Annette Fayet.

Unfortunately we cannot provide a stipend but (shared and basic) accommodation on Skomer will be provided. 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 due to 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. 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.

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, and who can work with us between April and September 2017 (with some flexibility for the start and end dates). 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).

How to apply: 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 (with oliver.padget@zoo.ox.ac.uk, james.evry@wadh.ox.ac.uk and annette.fayet@zoo.ox.ac.uk in cc). Please note that providing names of referees is not enough, the candidate needs to arrange for their referees to email us a reference (unfortunately we do not have time to contact each referee individually). The deadline for submitting applications (including reference letters) is the 12th February 2017. We will interview the best candidates on Skype shortly after and we expect to make a decision by the end of February.

PDF link: <https://goo.gl/V8YKAF> James Evry <james.evry@wadh.ox.ac.uk>

US govt scientists

Governmental scientists employed at a subset of agencies have been forbidden from presenting their findings to the public. We have drafted the following response

for distribution, and encourage other scientists to post it to their websites, when feasible.

Graham Coop Professor of Evolution and Ecology UC Davis

Michael B. Eisen Professor of Molecular and Cell Biology UC Berkeley

Molly Przeworski Professor of Biological Sciences Columbia University

—

In Defense of Science

We are deeply concerned by the Trump administration's move to gag scientists working at various governmental agencies. The US government employs scientists working on medicine, public health, agriculture, energy, space, clean water and air, weather, the climate and many other important areas. Their job is to produce data to inform decisions by policymakers, businesses and individuals. We are all best served by allowing these scientists to discuss their findings openly and without the intrusion of politics. Any attack on their ability to do so is an attack on our ability to make informed decisions as individuals, as communities and as a nation.

If you are a government scientist who is blocked from discussing their work, we will share it on your behalf, publicly or with the appropriate recipients. You can email us at USScienceFacts@gmail.com.

Molly Przeworski <molly.przew@gmail.com>

UTexasAustin SummerUndergraduateRes PlantGenetics

Switchgrass (*Panicum virgatum*) is emerging as an important biofuel candidate in the United States. Our labs (see list of collaborators below) collectively study the ecology, genetics/genomics, physiology and agronomy/plant breeding of Switchgrass. We are seeking a talented and diverse group of undergraduate students interested in conducting a variety of research in Switchgrass biology across the US.

Program description: This program is an opportunity for undergraduate students to participate in mentored independent research on the biology of Switchgrass. The program is funded through the NSF Research Experience for Undergraduates (REU) program and is associated

with our ongoing interdisciplinary work on the ecology, physiology, and genomic responses of switchgrass to future climate change. Summer students will be immersed in research and learn basic and applied biology through active participation in primarily field-based work. Working as part of our research team, they will contribute to group research projects, design short research projects, and present their work in an end-of-summer student symposium.

Each position is supported for 8-10 weeks beginning the first week of June. Students are awarded a \$4500 stipend, plus a housing and food allowance, and some funds to help defray the cost of traveling to the designated University.

Who Should Apply: Undergraduates that are not in their senior year (typically 1st to 3rd year students), who are either U.S. citizens or permanent residents studying in the U.S.

Application process: The application deadline is February 19, 2017. Applicants should submit a 1-page cover letter describing any relevant research experience, along

with their motivation for joining our research group, and include a copy of their current transcript (unofficial transcript or screenshots are acceptable). Applicants should also ensure that two letters of recommendation are submitted on their behalf. Only applications that are complete will be considered. Applications and requests for further information should be directed to:

Dr. Brandon Campitelli e-mail: brandon.campitelli@utexas.edu Subject: Switchgrass REU 2017

For more information regarding this opportunity, and ongoing research, please visit our website: https://sites.cns.utexas.edu/juenger_lab/summer-research-opportunities – Brandon E Campitelli | PhD Postdoctoral Researcher | Dept. of Integrative Biology | College of Natural Sciences Clinical Assistant Professor | Biology of Biofuels | Freshmen Research Initiative University of Texas at Austin | (512) 471-9920 | Patterson Labs 638

brandon.campitelli@utexas.edu

PostDocs

Barcelona GenomicsMachineLearning	99	Ottawa EvolutionBeePathogens	107
Budapest CancerEvolution	100	ParisCollege de France ModelsGenomicsDiversification	107
CharlesU Prague PolyploidEvolution	101	Paris SimilarityNetworks	108
CornellU ConservationBiology	102	PurdueU PlantEvolutionaryGenetics	109
CSIRO ArmidaleNSW LivestockPopGenetics	102	SLU Sweden QuantGenBreeding	109
Dartmouth MicrobialEvolution	102	StellenboschU AntarcticPlantPhylogenomics	110
Hungary FungalEvoluitonaryGenomics	103	UArizona EvolutionaryEcologicalGenomics	111
IndianaU Phylogenomics	104	UBasel PathogenEvolutionGenomics	111
ISTAustria PopulationGenomics	104	UCalifornia Berkeley InfectiousDiseasePopGenomics	112
Luzern Biodiversity	105	UCalifornia Davis EvolutionGeneFunction	112
Madrid ComputationalBiology	105	UCalifornia Santa Cruz PopulationGenomics	113
ManchesterU KlebsiellaGenomics	106	UCIrvine FunctionalMolecularEvolution	113
MonashU Influenza phylodynamics	106		
OhioStateU ExperimentalMicrobiomeResearch ...	107		

UCopenhagen IranianForestPhylogeography	114	ments	118
UGeorgia CropWildIntrogression	115	UOslo PopulationGenetics	119
ULaval FishPopulationGenomics 2	115	UOslo PopulationGenomics	120
ULondon EvolutionaryAnalysisCancer	116	UOxford EvolutionDosageComp	121
UMassachusetts Amherst DawinFellow	116	UWarwick AncientPathogens	122
UmeaU 5PDF and 5PhD Metagenomics	117	Vienna StatisticalGenomics	122
UMinnesota PhyloComparativeMethods	118		
UNorthCarolina Charlotte ChromosomeRearrange-			

Barcelona GenomicsMachineLearning

We offer a 22 month postdoc to work in the machine learning area. The profile is ample, from identifying selective sweeps to genomic selection and individual interests can be discussed. Gross salary is about 30k euro / year. The details are below. Interested candidates please send a letter of motivation letter, CV and emails of contact persons.

Miguel Perez-Enciso ICREA professor Centre for Research in Agricultural Genomics (CRAG) and Facultat de Veterinaria UAB Campus Universitat Autonoma Barcelona Bellaterra E-08193 Spain Tel: +34 935636600 ext 3346 Fax: +34 935636601 miguel.perez@uab.es <http://www.icrea.cat/Web/ScientificStaff/Miguel-Perez-Enciso-255> <http://bioinformatics.cragenomica.es/numgenomics/> Machine learning tools to combine sequence and biologically heterogeneous data

Research project

Big data are characterized not only by their size but also by their heterogeneity and noisiness. These features apply in particular to genomic data: their size has been increasing exponentially with the advent of new sequencing technologies, but also their complexity. We aim at combining several available sources of information, not only the phenotypes and sequence data, but also, e.g., annotation features or metabolic pathways. An important goal is not only to provide efficient predictors but also tools to biologically interpret the results. We will explore machine learning tools such as ensemble methods or deep learning to investigate two main problems (i) genomic prediction, and (ii) inference of selective sweeps.

Job description

We are looking for a PhD with a computational profile and an interest in biological applications.

Required

- Programming ability and experience in python.
- Quantitative and/or population genetics background

Valued

- Experience in machine learning area

We offer a 22 month year postdoc contract (extendable up to three years if funding is available).

Group description

The numerical genomics group (<http://bioinformatics.cragenomica.es/numgenomics/>) at Centre for Research in Agricultural Genomics (CRAG, www.cragenomica.es) is primarily interested in the use of high throughput sequencing technology (NGS) for population and statistical genomics. Topics of particular interest are studying the footprint of domestication and artificial selection and the use of sequence for genomic selection. CRAG was recently awarded a Severo Ochoa project for excellence centres in Spain.

Group leader

Miguel Perez-Enciso

ICREA professor

miguel.perez@uab.es

<https://bioinformatics.cragenomica.es/numgenomics/>
<https://www.icrea.cat/Web/ScientificStaff/Miguel-Perez-Enciso-255/> Miguel Perez Enciso
 <1136012@uab.cat>

Budapest Cancer Evolution

A postdoctoral position is available to join the recently established Evolutionary Genomics Research Group funded in 2016 under a highly competitive 5 year grant from the Hungarian Academy of Sciences' "Momentum" program as well as an ERC Starting Grant starting in 2017.

Research Topic:

Cancer is a genetic disease fuelled by somatic evolution. Despite advances in the molecular biology of cancer associated genes and the recent surge in the amount of DNA sequences available for different cancers, our understanding of the evolutionary mechanisms that lead to cancer is limited and cancer mortality rates have changed little in the last few decades. Until we unravel cancer's basic principles, the battle against it can only progress in inches, rather than in miles.

To address the problems quantitatively, a new field called the "physics of cancer" has emerged. In the context of this emerging field the Evolutionary Genomics Research Group works to understand the evolutionary process that leads to the breakdown of the hierarchical organisation of healthy tissues and the emergence of tumours, using evolutionary models, computer simulations, and sequence analysis. We do this with the aim of developing models that can predict how cancers respond to treatment depending on their functional and genetic diversity and guide us toward developing novel treatment strategies and improving existing ones. In our most recent work (Derényi & Szöllősi 2017) we asked how tissues generate large numbers of cells while at the same time minimising the accumulation of mutations and the risk of cancer.

To answer the question we introduced a general model of hierarchically organised self-renewing tissue and derived the lower limit of lifetime divisional load of a tissue. We showed that hierarchically differentiating tissues can approach this limit, and that this depends on uneven divisional rates across the hierarchy. We are looking for a postdoctoral researcher to build on these results and work with us in exploring the evolutionary process that lead to breakdown of hierarchical organisation of healthy tissues. The questions that we want to answer include: Under what conditions do hierarchically differentiated tumours, i.e. "cancer stem cells", evolve? Which kind of mutation lead to cancer and in what combination, e.g.

do mutations that increase symmetric vs. asymmetric cell division rate drive tumour progression or vice versa?

Derényi, I & Szöllősi, GJ Hierarchical tissue organization as a general mechanism to limit the accumulation of somatic mutations Nature Communications in press (2017) <https://doi.org/10.1101/098129> Position Details:

The successful candidate will either have a PhD in Evolutionary or Computational Biology or come from a strong quantitative background such as Physics, Applied Mathematics or Statistics with the ambition to pursue research in Evolutionary Biology.

The position is for up to 2 years with the possibility of extension and a salary of up to 2,000 EUR per month conditional on experience (adjusting for cost of living this corresponds to approx. EUR 3,000 in Berlin, 3,300 in Vienna and 4,200 in Paris [numbeo.com]).

The research group is lead by Dr. Gergely Szollosi (<https://scholar.google.hu/citations?user=sPrYT-oAAAAJ>) and Prof. Imre Derenyi (<https://scholar.google.hu/citations?user=kDEAL-wAAAAJ>).

The research group is hosted at Eotvos University's Institute of Physics. The Institute of Physics has been included in the Excellence Group of European Universities, and has achieved top placement in the number of citations, the number of ERC grants, the time available for PhD research and the gender balance of masters students in the CHE Excellence Ranking. The research group is associated to the Depts. of Biological Physics and Complex Systems composed of several interdisciplinary research groups including those of Prof. Imre Derenyi, Prof. Tamas Vicsek, and Prof. Istvan Csabai.

Please direct all enquiries to Dr. Gergely Szollosi (ssolo@elte.hu). First round of applications closes March 1st 2017. Please include a CV with list of publications (preferably referencing a google scholar profile) and a motivation letter addressing the research topic described above.

Dr. Gergely J Szöllősi

MTA-ELTE „Lendület“ Evolutionary Genomics Research Group ERC "GENECLOCKS" Research Group head researcher <http://ssolo.web.elte.hu> Tel: 00 36 30 725 35 32

Gergely J Szöllősi <sszolo@gmail.com>

CharlesU Prague PolyplloidEvolution

Short-term postdoc position at the Department of Botany, Faculty of Science, Charles University in the working group of Population ecology *(option for a PhD position)*

Consequences of polyploidization: from single traits to population dynamics

Understanding the consequences of polyploidization is a major step in the attempt to understand species diversification. The project addresses critical gaps in our knowledge on the role of polyploidization in the genesis and maintenance of plant diversity. It describes differences in single traits and population dynamics between diploids, tetraploids and newly synthesized tetraploids by using multiple species and comparing performance of plants coming from different evolutionary lineages (defined by their haplotype profiles). The results will allow the identification of general differences between tetraploids and diploids. It will be one of the first studies to compare i) different cytotypes from the same evolutionary lineage with different lineages within the same cytotype, ii) differences between neo-polyploids (synthetically created polyploids) and their established counterparts and iii) full life cycles of diploids, tetraploids and neo-tetraploids under natural conditions.

*We seek *a highly motivated independent postdoc interested in the evolution of polyploids. The postdoc will use the existing data of the team, analyze the data and prepare publications. Ideas for new analytical approaches are most welcome. Candidates will be expected to produce peer-reviewed publications in high impact factor international journals based on these data and present their results at an international conference. We welcome candidates interested to start their independent research projects within our group and stay with us past the postdoc period. A PhD position within the framework can also be discussed.

At the moment, we dispose of a large amount of data waiting to be analyzed and published. Specifically, we have data on:

1) the difference of natural diploids and natural and synthetic tetraploids in photoprotective and antioxidative enzymes. These data can be combined with data on plant fitness (a manuscript on the fitness data alone is

about to be submitted). This is a unique opportunity to study the effects of polyploidization without subsequent evolution and between population variation in the enzyme production patterns.

2) seed damage in natural diploids and natural and synthetic tetraploids and diploid offspring of synthetic tetraploid mothers. These data come from a two-year survey and can be combined with data on plant phenology (repeated census per individual) and fitness. This is a unique opportunity to study the effects of polyploidization without subsequent evolution but also to account for colchicine effects in the second generation after the treatment and for between population variation of seed damage.

3) pollinator communities and a range of pollinator related traits e.g. phenology, nectar production, pollen production from several diploid-polyploid pairs from multiple populations studied in control conditions.

4) pairwise competitive interactions between different cytotypes in two species using plants of different phylogenetic origin.

5) interactions of the same species in mixture of the two cytotypes allowing to study the development of mixed ploidy populations using material of different sources cultivated under different soil conditions.

6) performance (fitness related traits) of different cytotypes belonging to different evolutionary lineages allowing to study the relative importance of cytotype and lineage for species performance.

The applicant will be selected based on their past publication record, ideas on the subject and additional skills. The successful applicant is expected to bring new expertise to the group. We will also consider candidates interested in pursuing a PhD within the project.

Application and project duration. The application is opened until being filled. The postdoc position is for a maximum of 9 months and has to finish by December 31st 2017. The position may be prolonged by application for a subsequent project. Conditions for the PhD. will be explained individually.

We offer a young, friendly, working group broadly interested in plant population biology and genetics with many PhD and Master students involved in the research, a competitive salary (by Central European standards) and freedom to direct your work according to your interests within the broad topic of our research. Candidates will enjoy working in a collaborative team but must be highly self-motivated and work well independently.

Location. The post-doc will be primarily based at the Charles University in the center of Prague

(www.natur.cuni.cz). It will, however, be partly associated with the Botanical Institute situated in a large UNESCO heritage

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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>

CornellU ConservationBiology

POSTDOCTORAL POSITION IN COASTAL CONSERVATION BIOLOGY

David Lodge Lab, Cornell University

A postdoctoral research position is available to pursue collaborative research that would inform the management and policy of coastal marine ecosystems, with a focus on invasive species and their interactions with other drivers of global change. Experience with environmental DNA (eDNA) or related genetic methods and/or coastal marine ecosystems would be especially valuable. The postdoctoral fellow would join an interdisciplinary team of researchers, and lead one or more efforts within an NSF Coastal SEES project that includes a global network of collaborators working in coastal environments. Subprojects might focus on one or more of the following: metagenetic characterization of freshwater and marine communities with eDNA; quantitative analysis to forecast species dispersal and range changes caused by shipping and other vectors, and interactions with climate change; quantification of the ecological and economic impacts of invasions; and management and policy of invasive species at local, national or global scales. Intellectual leadership would be expected, with the choice of topic(s) depending on experience and interests. Opportunities for collaborations exist with other biologists, big data scientists, economists, and policy experts. The postdoc would assist with the organization and administration of projects, including organizing eDNA sampling with collaborators around the world, 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 (spring 2017). Salary and benefits will be competitive. The postdoc would be supervised by David Lodge. Collaborations with other researchers at Cornell, Notre Dame, and other universities will be encouraged. 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 (DML356@cornell.edu). The subject line of the email should read “Coastal SEES Postdoctoral Application 2017.”

“Andres, Jose” <jose.andres@usask.ca>

CSIRO ArmidaleNSW LivestockPopGenetics

Applications are invited for a 2 year CSIRO Postdoctoral Fellowship in Population Genetics, to work on a project funded by Meat & Livestock Australia (MLA). The Postdoctoral Fellow will work with genome sequence data from the parasite *Haemonchus contortus* to develop a high throughput platform for assaying genetic variants (SNP and/or INDEL). Accompanying the development, the Postdoctoral Fellow will perform genetic selection and genetic mixing experiments, analyses of genetic structure in populations and detection of divergence between isolates. The outcomes of the work will be aimed at developing a practical tool for population monitoring within the Australian sheep industry.

Applications should be submitted at the website:

<https://jobs.csiro.au/job/Armidale%2C-NSW-Postdoctoral-Fellowship-in-Population-Genetics/-381615500/> Peter Hunt

CSIRO McMaster laboratory,

Armidale, NSW, Australia

Phone +61 2 6776 1321

Fax +61 2 6776 1333

email peter.hunt@csiro.au

“Peter.Hunt@csiro.au” <Peter.Hunt@csiro.au>

Dartmouth MicrobialEvolution

A postdoctoral researcher position is available in the lab of Olga Zhaxybayeva (a.k.a. the lab of OZ) in the Biological Sciences Department of Dartmouth College in Hanover, NH to study evolution of gene transfer agents

and microbial adaptations to temperature and salinity. The research approaches include comparative omics analyses, mathematical modeling, population genetics and phylogenetics.

Qualified applicant must have a Ph.D. in bioinformatics, applied mathematics, computer science, statistics, biology, microbiology, or a related field with strong interest in molecular evolution and at least some programming experience.

The successful candidate will join a vibrant research and educational environment of Dartmouth College, will have the opportunities to establish his/her own independent projects and participate in professional development programs offered via Dartmouth's Postdoctoral Association. More information about Zhaxybayeva's lab is available at <http://www.dartmouth.edu/~ecglab/>. Review of applications will begin immediately and continue until the position is filled. Start date is negotiable. Interested applicants should send a single PDF file containing CV, one-page statement of research interests and contact information of three referees to Olga Zhaxybayeva at ECGLabJobs@gmail.com.

Dartmouth offers competitive salary and benefits along with the opportunity to live in a picturesque rural region that offers year-round recreational activities and is located near the culturally vibrant cities of Boston, Montreal, and New York.

Dartmouth College is an equal opportunity/affirmative action employer with a strong commitment to diversity and inclusion. We prohibit discrimination on the basis of race, color, religion, sex, age, national origin, sexual orientation, gender identity or expression, disability, veteran status, marital status, or any other legally protected status. Applications by members of all underrepresented groups are encouraged.

– Olga Zhaxybayeva, Ph.D. The Simons Foundation Investigator and Assistant Professor Department of Biological Sciences Dartmouth College 333 LSC 78 College Street Hanover, NH 03755 USA

Office: (603) 646-8616 Lab: (603) 646-9397 Email: olgazh@dartmouth.edu Web: <http://www.dartmouth.edu/~ecglab/> <http://dartmouth.edu/faculty-directory/olga-zhaxybayeva> “Olga.Zhaxybayeva@dartmouth.edu” [<Olga.Zhaxybayeva@dartmouth.edu>](mailto:Olga.Zhaxybayeva@dartmouth.edu)

Hungary

FungalEvolutinaryGenomics

POSITIONS IN EVOLUTIONARY GENOMICS OF FUNGAL PLANT PATHOGENS

We are seeking talented and motivated postdoc (research associate) and PhD student (research assistant) candidates in the Fungal Genomics and Evolution Lab within the Synthetic and Systems Biology Unit of the Biological Research Center, with experience in molecular biology, microbiology, light microscopy or bioinformatics.

The successful candidate will be responsible for studying the evolution of the interaction between pathogenic fungi and host plants in the context of multicellular development using a wide range of high-throughput techniques, including single-cell transcriptomics, comparative genomics and bioinformatics. Candidates are welcome for both bioinformatics and wet-lab projects (please specify).

The successful Candidate has: - PhD/Msc or equivalent in biology with specialization in molecular biology, functional genomics, bioinformatics or microbiology - Solid skills in molecular biology assays, microscopy and/or basic microbiological methods - Experience or interest in bioinformatics, phylogenetics - Fluency in English - Good team player traits

We offer: - Top notch projects and instrumentation - International environment - Competitive salaries (420000 HUF, equivalent to EUR 3400 in Paris when adjusted to cost of living in Szeged [numbeo.com]) - Extensive collaborator network

Preferred candidates will have diverse research interest, high motivation, excellent communication skills and willingness to work both independently and as part of a team. For more details on our research see the lab website:

<http://group.szbk.u-szeged.hu/sysbiol/nagy-laszlo-lab-index.html> Related Publications: Kohler A, Kuo A, Nagy LG, et al. (2015) *Nature Genetics* 47:410-5.

Nagy GL, Ohm R, et al. (2014) *Nature Communications* 5:4471

Contact and application If interested, send a motivation letter along with your CV to Laszlo Nagy (cortinarius2000@gmail.com).

László Nagy <cortinarius2000@gmail.com>

IndianaU Phylogenomics

Postdoc in Phylogenomics

An NSF-funded postdoctoral position is available in the lab of Matthew Hahn in the Department of Biology and School of Informatics and Computing at Indiana University, Bloomington. The work will use phylogenomic methods to study gene gain and loss across large species trees. Our lab has developed the statistical and computational tools necessary to study these phenomena, and we are looking for a motivated individual to extend these methods to studies involving hundreds to thousands of genomes. The postdoctoral candidate will also be encouraged to carry out independent work in the lab.

There is a wide variety of research going on in the lab in addition to the current project. For a summary of work in the lab, please see: <http://www.indiana.edu/~hahnlab/> The candidate must have a Ph.D., preferably in phylogenetics, population genetics, statistical genetics, or computer science. The position requires skills in the more computational areas of biology, and a strong record of research in these areas.

To apply, please submit (i) a letter of application, (ii) a full CV, (iii) a brief statement of research interests, and (iv) contact information for three references electronically to <http://indiana.peopleadmin.com/postings/3398>. Review of applications will start immediately and will continue until the position is filled. The exact start date is flexible, but best consideration to those applying before February 24, 2017. Inquiries about the position can be directed to Matthew Hahn (mwh@indiana.edu; 812-856-7001; 1001 E. 3rd St., Bloomington, IN 47405).

Indiana University has a large and active group in evolutionary genetics, and considerable resources computational resources. Bloomington is situated in scenic, hilly southern Indiana, near several parks and wilderness areas. The cultural environment provided by the University is exceptionally rich in art, music, and theater.

Indiana University is an Equal Employment and Affirmative Action employer and a provider of ADA services. All qualified applicants will receive consideration for employment without regard to age, ethnicity, color, race, religion, sex, sexual orientation or identity, national origin, disability status, or protected veteran status.

Matthew Hahn Professor Department of Biology & School of Informatics and Computing 1001 E. 3rd St. Indiana University Bloomington, IN 47405 Phone: (812)856-7001 <http://www.bio.indiana.edu/facultyresearch/faculty/-Hahn.html> <http://www.indiana.edu/~hahnlab> “Hahn, Matthew William” <mwh@indiana.edu>

ISTAustria PopulationGenomics

A postdoctoral position in population and evolutionary genomics is available in the Vicoso group at the Institute of Science and Technology, Austria. The general focus of the lab is the evolution of sex chromosomes, which we investigate 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 work on an ERC-funded project investigating the influence of sex-specific selection on genome evolution. This will entail a combination of comparative genomics and population genetics in sexual and asexual species of the brine shrimp *Artemia*. Candidates wishing to develop theoretical models of sex-specific selection and genome 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: - population genetics - comparative genomics - molecular evolution - bioinformatics The initial appointment is for two years, with the possibility of extension and a minimum salary of 49,070 Euros per year (gross).

IST Austria (www.ist.ac.at) is a young and vibrant institute dedicated to basic research, with a strong focus on evolutionary biology (other EB groups include those of Nick Barton and Sylvia Cremer) and ties to several evolutionary groups in the area (www.univie.ac.at/evolvienna/). We are located on the outskirts of Vienna, and the official language of the institute is English.

To apply, send a short summary of research interests, a CV, up to three relevant publications/manuscripts, and the names and contact information for three references

to Beatriz Vicoso (bvicoso@ist.ac.at). The review of applications will start on February 1st and continue until the position is filled. The start date is flexible, but an earlier start would be preferable.

More information on the lab is available at: <http://pub.ist.ac.at/~bvicoso/index.html> “bvicoso@ist.ac.at” <bvicoso@ist.ac.at>

Luzern Biodiversity

The Eawag Department of Fish Ecology & Evolution invites applications for a CEEB Synthesis Postdoc. The CEEB (Eawag Center for Ecology, Evolution & Biogeochemistry) is situated in Kastanienbaum near Luzern.

CEEB and its Department of Fish Ecology and Evolution provide a very dynamic research environment, unique in its operational structure as well as its physical settings on the shores of Lake Lucerne. Its core is a cluster of research groups dedicated to the integration of evolutionary biology and ecosystem sciences. The Center is well networked with the Eawag headquarters in Dübendorf, the Institute of Ecology & Evolution at the University of Bern and the ETH Zürich. It aspires to contribute to the growing synthesis between evolutionary biology and ecosystem science.

You may visit our homepages here <http://www.eawag.ch/en/department/fishec/main-focus/> and here <http://www.eawag.ch/en/research/water-for-ecosystem/ecosystems/ceeb/>. The Postdoc will develop concepts and outline scenarios, review literature from currently weakly connected fields, and lead the writing of a paper about relationships between diversification, biodiversity and biomass across scales. The Postdoc will be supported by all group leaders in the department.

We are looking for an ecologist or evolutionary biologist within the first 3 years of their PhD with a solid background in biodiversity research, excellent proven writing skills, and a strong drive to develop synthesis.

The period of appointment is limited to 12 months, starting no later than 1 April 2017.

Additional information: Eawag offers a unique research and working environment and is committed to promoting equal opportunities for women and men and to support the compatibility of family and work. Applications from women are especially welcome. For more information about Eawag and our work conditions please consult www.eawag.ch and www.eawag.ch/en/aboutus/

[working/employment](#). For further information please contact Prof. Ole Seehausen (ole.seehausen@eawag.ch).

The closing date for applications is 31 January 2017.

Very important: Please submit your application (including CV, motivation letter, and copies of academic qualifications, and the names and contact information of three references) via the Eawag Jobs & Career webpage, any other way of applying will not be considered. This link will take you directly to the application form <https://apply.refline.ch/673277/0492/pub/1/index.html>. We look forward to receiving your application.

“Ole.Seehausen@eawag.ch” <Ole.Seehausen@eawag.ch>

Madrid ComputationalBiology

A 1-year postdoctoral position in Computational Biology/Bioinformatics/Evol. Biology/Statistics is available in Madrid, Spain.

Brief description: Simulation and analysis of evolutionary processes in cancer.

Requirements:

- Postdoc younger than 30 years.
- Be registered as resident (“estar empadronado”) in Madrid, Spain, since 08-August-2016.
- Be registered in the “Fichero del Sistema Nacional de Garantía Juvenil” (<http://www.empleo.gob.es/es-garantiajuvenil/accesoJovenes.html>).
- Full details of requirements are available, in Spanish, at http://www.madrimasd.org/uploads/documents/bases_reguladoras_en_bocm_contratos_pre_y_post_pej.pdf.

Further information is available from the official resolution from: https://www.bocm.es/boletin/-CM_Orden_BOCM/2017/01/16/BOCM-20170116-4.PDF

- Ideally, candidates should have experience with R (and possibly also C++ programming) and be interested in at least some of the areas dealt with in the project (evolutionary biology, statistics, computational biology).

Procedure:

- Given that the deadlines are extremely tight I'd suggest interested candidates to contact me directly (ramon.diaz@iib.uam.es or rdiaz02@gmail.com) as soon as possible.

- Ramon Diaz-Uriarte Department of Biochemistry, Lab

B-25 Facultad de Medicina Universidad Autónoma de Madrid Arzobispo Morcillo, 4 28029 Madrid Spain

Phone: +34-91-497-2412

Email: rdiaz02@gmail.com ramon.diaz@iib.uam.es

<http://ligarto.org/rdiaz> rdiaz02@gmail.com

ManchesterU KlebsiellaGenomics

Postdoc in Manchester, UK on Klebsiella genomics / phage depolymerases. Would suit microbiologist / bioinformatician / genomics bod.

<http://bit.ly/2iNlpPr?> Mark C. Enright, Professor of Medical Microbiology, Room E206a, John Dalton Building, Manchester Metropolitan University, Chester Street, Manchester, M1 5GD, United Kingdom.

Term-time office hours Tuesdays and Thursdays 2.00 - 3.30pm.

Email M.Enright@mmu.ac.uk

Tel +44 (0) 161 247 1147 / 1153

Web http://www.shs.mmu.ac.uk/staff_list/-staffbiog/default.asp?StaffID=1220 Mark Enright <M.Enright@mmu.ac.uk>

MonashU Influenza phylodynamics

Postdoctoral position in influenza phylodynamics at Monash University, Melbourne, Australia.

The Infectious Disease Dynamics Laboratory (www.vjlab.io) is seeking to appoint a postdoctoral fellow in Influenza Phylodynamics.

The research project involves implementing and applying phylogenetic, statistical and bioinformatics methods to understand the fundamental processes governing the evolution and epidemiology of human and animal influenza viruses. This will entail conducting independent and high quality scientific research using pathogen genome data generated within the group as well as hospitals and national and international health systems. You will work with the group head and members of the infectious disease dynamics laboratory to incorporate

sequence and associated metadata within the phylodynamics framework and apply these methods to research problems in the evolution of influenza.

You will be expected to contribute to and develop research projects within the research group and produce high quality and impact publications. Our research is highly interdisciplinary and involves substantial global collaboration with experimental virologists, immunologists and clinicians to better understand their evolutionary dynamics, and to inform control strategies.

A PhD and track record in biology, statistics, mathematics, computer science, or computational biology is essential. The ideal candidate will have strong programming and data analysis skills and experience in the curation and analysis of large genome datasets generated through Next-Generation Sequencing.

This role is a full-time position; however, flexible working arrangements may be negotiated.

The job description, complete with the position description, and instructions on how to apply, can be found at: <http://careersmanager.pageuppeople.com/513/cw/en/job/555868/research-fellow-microbiology-medicine?> Please direct enquiries to Assoc. Prof. Vijaykrishna Dhanasekaran

vijay.dhanasekaran@monash.edu

Application closes on Tuesday 24 January 2017, 11:55pm AEDT

Information about Monash University and the lab. Currently ranked 74th in the Times Higher Education World University Rankings, Monash University is a member of Australia's "Group of Eight" a coalition of research-intensive universities, and is internationally recognised for excellence in research and teaching. The Infectious Diseases Dynamics Laboratory (www.vjlab.io) is within the School of Biomedical Sciences (<http://www.med.monash.edu.au/sobs/>) and part of the new Monash Biomedicine Discovery Institute (<http://www.monash.edu/medicine/discovery-institute>).

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

"vijay.dhanasekaran@monash.edu"

<vijay.dhanasekaran@monash.edu>

OhioStateU ExperimentalMicrobiomeResearch

Postdoctoral Research Position in Experimental Microbiome Research at The Ohio State University

Project: Examining the role of endemic gut bacteria in gut epithelial tissue development and differentiation in an invertebrate insect model.

Position is funded for two years and set to begin on or after March 15th 2017.

Location: Department of Evolution, Ecology and Organismal Biology, The Ohio State University, Columbus, Ohio, USA

Qualifications: - PhD with a strong bioinformatics and molecular biology and/or microbiology background (which will be assessed as part of the interview) - strong experience with transcriptome sequencing and analysis - excellent writing and communication skills - must have co/authored an average of 1 paper for every 18 months of graduate work - successful experience with grant writing - strong teaching and mentoring experience

OSU is an equal opportunity employer with a strong commitment to ethnic, gender, racial, lifestyle and religious diversity. We prohibit discrimination on the basis of race, color, religion, sex, age, national origin, sexual orientation, gender identity or expression, disability, veteran status, marital status, or any other legally protected status. Applications by members of all under-represented groups are encouraged.

Eligible applicants should send a single PDF including CV and a one-page research statement to Zakee L. Sabree (sabree.8@osu.edu) and include [ExpMicrobiome] in the Subject heading for correct mail routing.

Zakee L. Sabree | Assistant Professor Dept. of Evolution, Ecology and Organismal Biology The Ohio State University office addy: 318 W. 12th Avenue, Room 300, Columbus, OHIO, USA, 43210 lab: (614) 292-2452 | office: (614) 688-1590 | fax: (614) 292-2030 website: <https://u.osu.edu/sabreelab/> email: sabree(dot)8(at)osu(dot)edu

“Sabree, Zakee L.” <sabree.8@osu.edu>

Ottawa EvolutionBeePathogens

A research team at Agriculture and Agri-Food Canada is seeking a postdoctoral researcher to join the group in Ottawa, Ontario to study pathogens in native bees as part of a larger collaborative project investigating the health of bee pollinators in Canadian agricultural landscapes. The postdoctoral researcher would be responsible for conducting an RNAseq analysis on already collected native and commercial bee samples from sites across Canada to detect bee pathogens. These samples have already been screened for 8 pathogens using a multiplexed 2 step RT-PCR approach as part of a study looking for interactive effects between land-use, pesticides and pathogens on native bee diversity and abundance. The postdoc would have the opportunity to participate in the analysis of this data as well as the new data collected through their RNAseq work. A Phd in a related field with expertise in either preparing libraries for next-gen sequencing, or in the bioinformatics analysis of data produced via next-gen sequencing is required. The position is available for one year. Salary is dependent on experience and will follow the SE-RES-1 annual rates of pay. For more information or if interested in applying, contact Sophie Cardinal Sophie.cardinal@agr.gc.ca.

scardina44@gmail.com

ParisCollege de France ModelsGenomicsDiversification

A postdoctoral position in mathematical/computational evolutionary biology is available to work on project “Genomics of Diversification” in collaboration with the three following research groups located in Paris

Amaury Lambert <http://www.lpma-paris.fr/smile>
Anton Crombach <http://www.college-de-france.fr/site/en-cirb/crombach.htm> H el ene Morlon <http://www.biologie.ens.fr/phyloeco/index.html> The project aims at mixing models of species diversification with models of genome evolution, in order to infer tempo and modes of diversification from multi-species genomic data.

We are looking for a highly motivated post-doc with interest in probabilistic models of species diversification and in individual-based simulations of genome evolution. Applicants should have solid mathematical and computational skills. A background in evolutionary genetics/speciation genomics would be welcome. Excellent written, verbal, and interpersonal skills are desired. Speaking French is not mandatory.

The project is funded by MemoLife, a scientific association between CIRB (Center for Interdisciplinary Research in Biology - Collège de France) and IBENS (Institute of Biology of Ecole Normale Supérieure), two of the French most competitive research centers, both located in the Latin Quarter in downtown Paris. The position is initially for one year, renewable once. It will be hosted at Collège de France.

Salary will be commensurate with experience and will range from 25 to 30 K euro /yr (free of charge but before income tax) - schools and healthcare in France are cheap when not free.

Starting date is flexible but should be prior to December 2017. Review of applications starts immediately and will continue until position is filled. Questions should be sent to Amaury Lambert <amaury.lambert@college-de-france.fr

To apply please submit i) a cover letter summarizing research interests and expertise; ii) a CV; iii) a list of publications; and iv) names and contact information of two references, all in a single pdf document sent to the three of us

Amaury Lambert <amaury.lambert@college-de-france.fr
Anton Crombach <anton.crombach@college-de-france.fr
Hélène Morlon <morlon@biologie.ens.fr>

Amaury Lambert, professeur UPMC <http://www.lpma-paris.fr/pageperso/amaury> SMILE group <http://www.lpma-paris.fr/smile> Stochastics & Biology group <http://www.lpma-paris.fr/~psb> amaury.lambert@ens.fr

Paris Similarity Networks

Dear colleagues, Please find below the description of a postdoctoral position in statistics and evolution to “improve the comparative framework based on similarity networks”. The EVOLUNET project, funded by the ERC, is enhancing the use of similarity networks, adapted to evolutionary biology questions (<http://www.evol-net.fr/index.php/fr/evolunet>). Such net-

works, inspired by the studies on social and regulatory networks, allow mainly for fast inclusive comparative analyses of both (highly) divergent and conserved molecular sequences from living organisms, mobile genetic elements, that were obtained either from lab cultures or from environmental samples, or both. These networks allow in particular to detect chimeric genes (i.e. genes made of parts with different evolutionary histories) and therefore to investigate the evolution of genes; and to detect lateral gene transfer, and therefore to investigate the evolution of genomes and microbial communities. Moreover, similarity networks also allow to compare diverse data, gathered by experts from different evolutionary fields, such as historical linguistics and paleontology. The EVOLUNET project already implemented various methods and applied them to different evolutionary questions. Now, network comparison becomes the next important development for network analyses. In particular, network comparison should be most useful to test whether different similarity networks (i.e. constructed from samples from different locations and/or different time periods) have resulted from similar (or from distinct) evolutionary processes. To further develop network comparisons, especially networks of sequences from environmental microbiomes, our lab is now looking for a post-doctoral fellow in bio-informatics, graph theory or evolutionary biology with a strong background in programming, who will be funded for up to 2 years by an ERC grant (for an approximate salary of 2,727 euros/ month before taxes). The candidate will take advantage of the properties of many of the real-life networks constructed in the lab, of our original microbiome data, and of algorithms from network sciences for: -1) Developing and comparing network-based diversity indices -2) Constituting a comparative framework between real-life sequence similarity networks and sequence similarity networks generated based on various models of sequence evolution The first task implies exploring various network-based diversity measures to compare labelled weighted networks that harbor millions of nodes and dozens of millions of edges. Such networks are often too large to be directly compared by graph matching algorithms. However, they contain precious information regarding genetic diversity of the investigated datasets. While diversity measures have been developed for phylogenetic trees or phylogenetic networks, sequence similarity networks provide an additional kind of distances among biological objects (sequences, genomes, environments) that can be investigated taking advantages of the network topological properties, and therefore the comparison of similarity networks should provide new insights about the evolution of genetic diversity.

The second task relies upon descriptions of large net-

works by various topological indices (diameter, clustering, distribution of motifs of a given size, ...) and by the diversity indices considered above. These descriptions will be used to test whether two networks exhibit the same properties or not. The postdoctoral fellow will first test if real-life similarity networks share the same properties as networks generated from sequences evolved under a given model to determine whether the data fit that particular model. Such comparisons will help the postdoctoral fellow to determine what a real-life network properties usually are, and thus help him/her build better null model similarity networks, specifically designed for evolutionary studies (as opposed to the random networks often used in the graph literature that do not always fit the properties of real-life networks). The postdoctoral fellow will also develop test statistics to compare the topological and diversity indices of real-life similarity networks with those of carefully simulated networks. Such statistics will allow classifying genes and proteins into sets that show a diversity that can be relatively simply explained (e.g. displaying indices compatible with known processes and evolutionary models), or require other explanations (e.g. surprisingly extremes rates of divergence, fusion, or recombination). Ultimately, the postdoctoral fellow will determine which simulated networks best fit with real-life networks and develop a random graph model specifically designed for evolutionary studies, so that this model might be further exploited by

— / —

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>

PurdueU PlantEvolutionaryGenetics

Postdoc: Plant ecological and evolutionary genetics

A postdoctoral position is available study the genetic basis of adaptation in native populations of the model plant *Arabidopsis thaliana*. This research is part of a NSF funded collaborative project on the genetic basis of fitness tradeoffs across environments, focusing on freezing tolerance as a key adaptive trait. We use a combination of field experiments in the native environments, experiments in controlled growth chambers, and -omic data to investigate, across environments, the links between genotype, phenotype, and fitness. Additional research in the

lab is focused on the evolutionary ecology and genetic basis of heterosis and outbreeding depression in *Arabidopsis*. Resources available in the lab include a large collection of lines from natural *A. thaliana* populations spanning latitudinal and altitudinal gradients, recombinant inbred lines and near isogenic line populations for genetic mapping, and engineered lines (transgenic and CRISPR-CAS9) for candidate genes. Development of new research directions building on these themes and resources is encouraged.

Research activities will include (but are not limited to): Leading growth chamber experiments to estimate freezing tolerance, lifetime fitness, and patterns of global gene expression; field planting and harvesting of experiments at sites in Italy (near Rome) and northern Sweden (three to four trips per year, ~10 days each); overseeing development of near isogenic lines (for fine mapping), and the production and genotyping of two new recombinant inbred line populations; data analysis; and manuscript preparation.

A PhD in biology or related discipline is required and preference will be given to candidates with a strong background in plant evolutionary biology. Previous experience with the analysis of genomic data is strongly preferred. This is initially a one-year appointment, with the possibility of an extension of 1-2 years dependent on funding and performance. A start date of April 1, 2017 or sooner is preferred, but this is negotiable.

Applicants should send (as a single PDF attachment) a CV, a letter summarizing research interests, accomplishments, and objectives, and the names and contact information for two professional references. Review of applications will begin February 4, 2017 and will continue until a suitable candidate is found.

Chris Oakley oakleyc at purdue dot edu

“Oakley, Christopher G” <oakleyc@purdue.edu>

SLU Sweden QuantGenBreeding

We are looking for a highly motivated person that will work within a newly started project focused on climate-adapted poplars (*Populus* spp.) for Swedish and Baltic regions (CLAP, <https://www.slu.se/clap>). The postdoc (24 months fixed term employment) will do work in association genetics and quantitative genetics to study the genetic architecture of phenology traits as bud burst, bud set and growth cessation with the overall aim to

develop molecular markers for breeding poplars varieties for use at northern latitudes. The applicant will conduct work in the lab, in the field and use genomic and phenotypic data for different types of quantitative genetic analyses.

Successful candidates will have a PhD degree in genetics or equivalent field. As postdoctoral appointments are career-developing positions for junior researchers, we are primarily looking for candidates with a doctoral degree that is three years old at most. The candidate should have proven expertise in genetics and be used to handle large genomic and/or phenotypic datasets. Prior experience of working with computational and/or statistical analyses in a quantitative genetics framework is thus highly desirable. Excellent proficiency in English is required, as English is the working language in the research group. A driving license is preferable, as the work will involve some fieldwork in remote areas. The project involves working within a larger research team of around ten researchers, so candidates should have an easy time working with others but also the ability to work independently with your own research topics. Creativity and drive are personal characteristics that are desirable due to the knowledge-driven aspect of the project. The PhD position is housed at the Department of Plant Biology, Swedish University of Agricultural Sciences in Uppsala, Sweden.

For more information and instructions of how to apply see:

<http://www.slu.se/en/about-slu/jobs-vacancies/read-more/?eng=1&Pid=2923> The Swedish University of Agricultural Sciences (SLU) is a research-intensive university that also offers unique degree programmes in for example rural development and natural resource management, environmental economics, animal science and landscape architecture. SLU has just over 3,000 employees, 5,000 students and has recently invested heavily in a modern, attractive environment on its campuses in Alnarp, Umeå and Uppsala.

Pär K. Ingvarsson Professor, Plant genomics and breeding Department of Plant Biology Uppsala BioCenter Swedish University of Agricultural Sciences PO-Box 7080 SE-750 07 Uppsala, Sweden

Pär Ingvarsson <par.ingvarsson@slu.se>

StellenboschU AntarcticPlantPhylogenomics

An exciting postdoctoral position to investigate Antarctic terrestrial plant phylogenomics is available at Stellenbosch University (<http://academic.sun.ac.za/cib/team/-academic/jleroux.asp>) and the University of Johannesburg (<http://www.molzoolab.co.za/>), South Africa. The successful applicant will be based at Stellenbosch University, but will be expected to spend some time at the University of Johannesburg. The envisaged research will address a major question in modern biology: how has plant life evolved and spread around the Antarctic region, both in the past and currently? This research forms part of an international collaboration: “A Functional Biogeography of the Antarctic (AFBA, see <http://antarcticbiogeography.org>)” as part of the Antarctic Circumnavigation Expedition (ACE). ACE involves 22 projects, 55 researchers and 19 countries and is the first project of the newly created Swiss Polar Institute.

The successful candidate will be responsible for plant phylogenomic research on selected taxa from the Antarctic and Southern Ocean Islands. Using the latest phylogenomic and analytical approaches, the research aims to shed light on the history of plant life in the region, how it will respond to environmental change, and what can be done to secure its future.

Only candidates with demonstrable (i.e. published) skills in next generation sequencing data analyses with an emphasis on phylogenomics will be considered. Preference will be given to candidates with previous postdoctoral research experience 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 to 2 years depending on satisfactory performance. An attractive annual bursary will be offered along with additional expenses for research, international travel and subsistence, and conference attendance. Individuals from all nationalities are eligible.

To apply, please send a CV, contact details for at least two academic references, and a brief outline of research interests to Prof. Jaco Le Roux (jleroux@sun.ac.za) and Prof. Bettine van Vuuren (bettinevv@uj.ac.za) by 28 February 2017. Informal inquiries are welcome. Review of applications will begin immediately after the closing date, and short-listed candidates will be contacted to

set up phone/Skype interviews. The envisaged start date for the project would be March/April 2017.

Professor Jaco Le Roux Associate Professor | Department of Botany and Zoology Core Team Member | Center for Invasion Biology Stellenbosch University Associate Editor | Biological Invasions Associate Editor | Conservation Genetics

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jleroux@sun.ac.za

UArizona EvolutionaryEcologicalGenomics

The Matzkin Lab at the University of Arizona, Department of Entomology is currently recruiting a postdoc to work on a variety of possible projects on the evolutionary ecological genomics of adaptation and speciation in cactophilic *Drosophila*. I am seeking a highly motivated and creative individual with strong quantitative & evolutionary genetics, molecular and/or computational biology skills to join our evolutionary and ecological genomics lab. Good writing and communication skills will be required for this position. Prior experience working with *Drosophila* is not necessary, but a plus. Postdoc will be based at The University of Arizona, Department of Entomology and will have the opportunity to interact with investigators at the BIO5 Institute and Department of Ecology and Evolutionary Biology.

The postdoc will be involved in all research aspects of the assigned projects, and would have the possible opportunity to develop projects in consultation with Dr. Matzkin. Critical and independent thinking is very important for this position, as well as having the ability to analyze data, write manuscripts and proposal writing.

PhD in evolutionary biology, evolutionary genetics/genomics, entomology or related field is required. A background in quantitative and evolutionary/ecological genetics and/or molecular and computational biology desired. Postdoc must have excellent writing, communication and critical thinking skills with at least 1-3 publications (in print or submitted). Prior experience working with *Drosophila* a plus but not necessary. Background working with CRISPR/Cas9 in model or

non-model system also a plus, but not necessary.

Apply at <http://uacareers.com/postings/15931>. You will need to submit a 1) cover letter briefly outlining the candidate's fit to the position and future goals 2) curriculum vitae 3) contact information (email and phone) for three references, preferably including doctoral advisor and/or postdoctoral advisor (if relevant) and 4) no more than three relevant publication PDFs. Please contact Luciano Matzkin (lmatzkin@email.arizona.edu) if you have additional questions about the position or visit our lab page, www.matzkinlab.org Outstanding UA benefits include health, dental, vision, and life insurance; paid vacation, sick leave, and holidays; UA/ASU/NAU tuition reduction for the employee and qualified family members; access to UA recreation and cultural activities; and more! The University of Arizona has been recognized on Forbes 2015 list of America's Best Employers in the United States and has been awarded the 2015 Work-Life Seal of Distinction by the Alliance for Work-Life Progress! For more information about working at the University of Arizona, please www.whyua.com. Dr. Luciano M. Matzkin Associate Professor Department of Entomology BIO5 Institute University of Arizona (520) 621-1955 www.matzkinlab.org "Matzkin, Luciano Matias - (lmatzkin)" <lmatzkin@email.arizona.edu>

UBasel PathogenEvolutionGenomics

A postdoctoral position (full time) is available in the newly established research group of Richard Neher (<http://neherlab.org>) at the Biozentrum of the University of Basel. Our group works on genomics of pathogenic viruses and bacteria with a focus on intra-patient HIV evolution and prediction of seasonal influenza virus evolution. Research in our group combines mathematical modeling, bioinformatics, next-generation sequencing, and methods from statistical physics to understand the complex dynamics of host-pathogen interactions. Our group is a co-developer of the real-time virus tracking tools nextflu.org and nextstrain.org. We have recently started to extend our real-time tracking efforts to bacterial populations.

Possible projects include (i) extension of our recent results on influenza virus evolution to use all genomic segments, (ii) genome evolution of bacteria or (iii) real-time tracking applications for bacteria. The exact scope of the projects is flexible and can be tailored to the applicants interest and skills.

We are looking for: a creative and collaborative person with a genuine interest in evolution and with * either: - PhD in physics, applied math, bioinformatics, computer science and strong interest in biology - a life science degree and strong quantitative skills * scientific computing and programming experience (ideally in python and C/C++) * firm background in probability theory and statistical methods

In addition, the following skills are desirable: * experience with next-generation sequencing data * population genetic models/phylogenetic inference * data visualization and experience with javascript/d3

Application: Please send your cover letter, statement of research interests (max one page), CV, publication list, and contact information of three references as one pdf file to Richard Neher (richard.neher@unibas.ch). Please state clearly in your cover letter what you want to do and why this fits with our research. For informal inquiries, contact Richard Neher.

Environment: The Biozentrum of the University of Basel is one of the leading institutes worldwide for molecular and biomedical basic research and teaching. It is home to more than 30 research groups with scientists from over 40 countries. Research at the Biozentrum focuses on the areas of Cell Growth & Development, Infection Biology, Neurobiology, Structural Biology & Biophysics and Computational & Systems Biology. With its more than 500 employees, the Biozentrum is the largest department at the University of Basel's Faculty of Science.

Basel is a very international city and a center of life science research, with many life science research companies in the area, including Novartis and Roche. Several other academic institutions are also in the city, including the Friedrich Miescher Institute, the ETH Zurich Biosystems Science and Engineering department, and the Swiss Tropical Institute. The city is less than 5km from both France and Germany and an hour and a half from the Swiss Alps.

"richard.neher@tuebingen.mpg.de"
<richard.neher@tuebingen.mpg.de>

UCalifornia Berkeley InfectiousDiseasePopGenomics

A postdoctoral researcher position for a highly motivated young scientist is available in the group of Rodrigo

Almeida in the Department of Environmental Science, Policy and Management, at the University of California, Berkeley, to study the dynamics of plant pathogen epidemics and host adaptation and specialization. The position is funded by a Horizon 2020 collaborative project dedicated to the emerging plant pathogen *Xylella fastidiosa*. Within the broad scope of the project, developing novel research questions will be encouraged.

Requirements Applicants must have a Ph.D. in an area related to microbial genomics, evolution, or population genetics; computational, programming, and quantitative skills are required. The successful candidate will be independent and have good writing skills, yet be able to work in an interdisciplinary environment where collaboration and synergistic interactions are expected.

Responsibilities Researcher will be responsible for experimental design, data analyses, preparation of research manuscripts and project reports. Post-doctoral researchers in our group are also expected to help mentor and work with students and peers when necessary.

Appointment One year renewable to two years based on satisfactory performance. Salary commensurate to experience; starting annual salary for UC Berkeley post-doctoral researchers immediately after obtaining a PhD is US\$48,216 salary scale follows NIH/NRSA stipend. Start date is negotiable, but strong preference will be given to candidates that can start by early Summer 2017.

Application Prepare a single PDF with i) a 2-page CV that lists publications and computational skills, ii) a research statement (up to 2 pages), and iii) three references who could be contacted. Position will remain open until filled; applications will be reviewed immediately upon receipt. We hope to close the position by February 17. Send PDF directly to Rodrigo Almeida: email- rodrigoalmeida@berkeley.edu.

"rodrigoalmeida@berkeley.edu"
<rodrigoalmeida@berkeley.edu>

UCalifornia Davis EvolutionGeneFunction

I am looking for a postdoctoral fellow to work on the genetics, cell biology, and biochemistry of young *Drosophila* de novo genes. An ideal candidate would have experience in *Drosophila* functional biology and an interest in evolution. However, evolutionary geneti-

cists enthusiastic about learning and doing fly functional biology are also encouraged to apply. There may be opportunities to participate in other lab projects.

The Department of Evolution and Ecology at UC Davis is the home of many evolutionary biologists and population geneticists, and has a strong *Drosophila* evolutionary genetics group. The floor on which the Begun lab is located also houses the laboratories of Graham Coop, Chuck Langley, Michael Turelli, Artyom Kopp, and Susan Lott. The laboratory of Joanna Chiu is in the same building.

Applicants should send a CV with a brief statement of research interests, and names and email addresses of three references. I will be attending the fly meeting this year and would be happy to meet and discuss the position. I can be contacted at djbegun@ucdavis.edu. Compensation for this position will follow NIH guidelines.

“djbegun@ucdavis.edu” <djbegun@ucdavis.edu>

UCalifornia Santa Cruz PopulationGenomics

The Corbett-Detig lab at UC Santa Cruz is hiring a postdoctoral fellow to work on computational population genomics. Projects in the lab are flexible. For example, research could focus on chromosomal inversions or admixture genetics. There will also be many opportunities to collaborate on other lab projects. An ideal candidate would have experience in genetics, analysis of next-generation sequencing data, and would be proficient in at least one programming language. Molecular biology experience is a big plus. The most important prerequisite is to be excited about working on interesting problems in evolution by developing and applying computational tools to sequence data.

Santa Cruz is a fantastic place to live and do research. UCSC has a strong research community with lots of interest in high throughput computing and evolutionary genomics. The hiking, mountain biking, surfing, and scuba diving “basically anything outdoors, really” are all phenomenal.

Interested candidates are encouraged to contact Russ Corbett-Detig at rucorbet@ucsc.edu. Please send a CV and a statement describing your research experiences, interests, and goals. The target start date is flexible, but ideally the candidate would begin on or before July

1st, 2017. Compensation for this position will follow NIH guidelines.

russcd@gmail.com

UCIrvine FunctionalMolecularEvolution

Postdoctoral Scholar - Briscoe Lab

Job #JPF03835

Francisco J. Ayala School of Biological Sciences - Ecology & Evolutionary Biology

Recruitment Period

Open date: January 18th, 2017

Next review date: February 17th, 2017 Apply by this date to ensure full consideration by the committee.

Final date: March 15th, 2017 Applications will continue to be accepted until this date, but those received after the review date will only be considered if the position has not yet been filled.

Description

A NSF-funded postdoctoral scholar position is immediately available in the laboratory of Dr. Adriana Briscoe at University of California, Irvine. Research in the Briscoe lab is aimed at understanding the molecular basis of color vision evolution in butterflies. The lab has recently developed a new method for expressing invertebrate rhodopsins at levels suitable for functional characterization of rhodopsin absorption spectra (see Frentiu et al. 2015 *Molecular Biology and Evolution*). The lab is seeking a postdoctoral scholar who will extend this method to develop further insights into the molecular basis of spectral tuning, a form of adaptation to the light environment. To accomplish this, the postdoctoral researcher will use homology modeling, western blot analysis, and functional expression of opsins in HEK293 cells to identify the amino acid residues responsible for the tuning of butterfly rhodopsins across an adaptive radiation.

Successful candidates will collaborate with a dynamic team of behaviorists, electrophysiologists, and evolutionary biologists at UC Irvine and other institutions.

Required qualifications include a Ph.D. in molecular biology, biochemistry, or related fields and demonstrated proficiency with cell culture, western blot analysis, and immunoaffinity purification. Desirable qualifications in-

clude expertise in immunohistochemistry, qPCR, and DNA sequence analysis; a strong publication record and excellent writing/communication skills.

Duration of position is dependent upon performance (annual appointments, with potential for renewal), and salary will be on an NIH payscale, commensurate with experience. Applications submitted by February 17, 2017 will be given full consideration, although applications will be reviewed until the position is filled.

Qualified candidates should submit curriculum vitae, a one-page statement of research interests, and names and contact information for three references to the following on-line recruitment URL:

<https://recruit.ap.uci.edu/apply/JPF03835> For more information about this position contact Dr. Adriana Briscoe at abriscoe@uci.edu

Frentiu FD, Yuan F, Savage WK, Bernard GD, Mullen SP, Briscoe AD. 2015. Opsin clines in butterflies suggest novel roles for insect photopigments. *Molecular Biology and Evolution*, 32:368-79. doi: 10.1093/molbev/msu304

The University of California, Irvine is an Equal Opportunity/Affirmative Action Employer advancing inclusive excellence. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age, protected veteran status, or other protected categories covered by the UC nondiscrimination policy.

Adriana Briscoe Professor Department of Ecology and Evolutionary Biology 321 Steinhaus Hall Irvine, CA 92697 University of California, Irvine Irvine, CA 92697

Adriana Briscoe <abriscoe@uci.edu>

UCopenhagen IranianForestPhylogeography

Postdoc in phylogeography and evolutionary genetics of trees from the Caspian Forests of Iran Department of Geosciences and Natural Resource Management (IGN) Faculty of Science University of Copenhagen

The postdoc will primarily work with phylogeography and evolutionary genetics of a range of tree species growing in the Caspian forest of northern Iran. The forests contain tree species which are also indigenous in Europe - for example beech, ash, oak, maple, lime, wild cherry, elm and hornbeam. The Caspian forests date back to

before the Pleistocene, i.e. more than 2.6 million years, and have thus existed continuously during all the glacial and interglacial periods in the current ice age. The overall project, to which the postdoc will be affiliated, aims to test to which extent the Caspian forests in Iran contain genetic potential for our European forests and their ability to adapt to future challenges in terms of climate change, new diseases and pests. This will imply establishment of field trials in Denmark and Iran with Iranian provenances and the following 6 species have been selected as study objects: 1) *Fagus sylvatica* subsp. *orientalis*, 2) *Fraxinus excelsior*, 3) *Acer velutinum*, 4) *Quercus castaneifolia*, 5) *Carpinus betulus* and 6) *Alnus subcordata*. The project includes a DNA work package, which will study the population genetic structure and evolutionary genetics of the selected species in Iran and compare genetic diversity between the Caspian and Danish/European forests. This will be the main subject for the post doc.

The ideal candidate may already have postdoctoral experience, and should have an expertise in one or ideally several of the following areas: population and evolutionary genetics, bioinformatics and handling of next-generation-sequencing data, DNA-marker development, phylogeny and forest genetics. The applicant should be familiar with working in a molecular genetics lab as well as be able to do independent field work in remote areas of Iran for periods of up to 1-2 months.

The postdoc's duties will include research within phylogeography and evolutionary genetics as well as teaching. The post may also include performance of other duties.

Further information on the Department is linked at <http://www.science.ku.dk/english/about-the-faculty/-organisation/>. Inquiries about the position can be made to Associate Professor Ole K. Hansen - okh@ign.ku.dk; telephone + 45 35 33 16 47. The position is open from May 1 2017 or as soon as possible thereafter and has a duration of 3 years.

Terms of employment The position is covered by the Memorandum on Job Structure for Academic Staff. Terms of appointment and payment accord to the agreement between the Ministry of Finance and The Danish Confederation of Professional Associations on Academics in the State. The starting salary is currently up to DKK 408,730 including annual supplement (+ pension up to DKK 69,893). Negotiation for salary supplement is possible.

The application, in English, must be submitted electronically by going to the following link: <http://-employment.ku.dk/faculty/?show=882632> Please include - Curriculum vita - Diplomas (Master and PhD degree or equivalent) - Complete publication list - Sepa-

rate reprints of 3 particularly relevant papers - Research plan - description of current and future research plans.

In relation to the latter, the applicant is requested to make an outline - based on the information given above - of the studies and analyses he/she would recommend. Please, include brief descriptions of technical and analytical methodology. Due to number of studied species, cost-effective methods using cutting-edge DNA methodology will be especially appreciated. The outline should be of maximum 250 words. The deadline for applications is March 15 2017, 23:59 GMT +1.

After the expiry of the deadline for applications, the authorized recruitment manager selects applicants for assessment on the advice of the Interview Committee.

You can read about the recruitment process at <http://-employment.ku.dk/faculty/recruitment-process/>. Interviews will be held in the first week of April 2017.

Ole Kim Hansen <okh@ign.ku.dk>

UGeorgia CropWildIntrogression

A postdoctoral position studying the genomic consequences of crop-wild hybridization in sunflower is available in the Burke lab at UGA. This position will involve population genomic analyses aimed at documenting genome-wide patterns of introgression over the history of sunflower cultivation in North America. The results of this research will thus provide insight into the long-term fate of crop alleles/traits in the wild. Moreover, when coupled with the results of prior studies of selection in experimental hybrid populations, this work will enable an investigation of the reliability of experimental studies for predicting long-term, real-world evolutionary outcomes.

The ideal candidate will have a strong background in population genetics and experience handling and analyzing large, genome-scale datasets. Funds are currently available to support this position for up to three years, and the successful candidate will also be given the opportunity to develop independent lines of inquiry.

To apply, please send your CV, a brief statement of research interests, and contact information for three references to: jmburke@uga.edu

Informal inquiries are also encouraged. Applications will be reviewed on an ongoing basis until the position is filled.

Information on the plant science research community at UGA can be found at:

<https://plantcenter.uga.edu/> Information about the UGA Department of Plant Biology can be found at:

<http://plantbio.uga.edu/> And information on the Burke lab can be found at:

<http://www.theburkelab.org/> – John M. Burke, Ph.D. Tel: 706.583.5511 <(706)%20583-5511> Fax: 706.542.1805 <(706)%20542-1805> <http://-www.theburkelab.org/> University of Georgia Department of Plant Biology Miller Plant Sciences Athens, GA 30602

“jmburke@uga.edu” <jmburke@uga.edu>

ULaval FishPopulationGenomics 2

The Bernatchez's Lab at University Laval (Québec City, Canada) is currently searching for a postdoctorate researcher to be involved in our ongoing research program pertaining to the comparative and population genomics of fishes. This research program is very well supported from multiple funding agencies (Natural Sciences and Engineering Research Council of Canada, Canadian Research Chair Program, Genome Canada, Genome Québec, Fonds nature et Technologie Québec) and involves numerous collaborators, both national and international from over 20 countries. Our research program aims to enhance fundamental knowledge pertaining to the evolutionary processes responsible for generating and maintaining genetic diversity within populations of aquatic animals, with relevance for management and conservation.

Depending on his/her specific expertise and qualifications, the selected candidate can be involved in one or several of the specific projects currently conducted including either marine (Halibut, Capelin), anadromous/catadromous (Salmon, Eel) or freshwater (Trout, Whitefish), among others. Details of specific ongoing projects can be found on our website (see below).

Required Qualifications: We are primarily searching for a prospective candidate with strong and demonstrated bioinformatics skills in whole genome assembly who is also familiar with scripting and programming. The ideal candidate should also be familiar with population genomics analyses of data sets derived from whole genome resequencing, high density SNP chips, RADseq/GBS genotyping, as well as epigenome (methylation) data

sets. Candidates must be fluent in English, both written and spoken.

The position is available now and for 2 years, likely renewable for a third year, and to be filled as soon as possible. Salary is established according to local University standards.

To apply, please send a cover letter describing your research interests and qualifications, a complete CV and names of three references by e-mail to Louis.Bernatchez@bio.ulaval.ca

Do not hesitate to contact me directly for any further details or questions.

To learn more about.

Our lab, research program, publications, people: The Canadian Research in Genomics and Conservation of Aquatic Resources https://www.bio.ulaval.ca/~louisbernatchez/research_programs.htm Laval University : <https://www.ulaval.ca/en/research.html> Québec City : <http://www.quebecregion.com/en/> Louis Bernatchez, Canadian Research in Genomics and Conservation of Aquatic Resources Institut de Biologie Intégrative et des Systemes, Pavillon Charles-Eugene Marchand, Université Laval, Québec, QC G1V 0A6 Canada

Tel: 1 418 656-3402 Fax: 1 418 656-2043 Courriel: Louis.Bernatchez@bio.ulaval.ca

Louis Bernatchez <Louis.Bernatchez@bio.ulaval.ca>

U London Evolutionary Analysis Cancer

We are seeking postdocs interested in using an evolutionary perspective to forecast the progression and treatment of cancer. We have open positions to join our dynamic interdisciplinary teams (Andrea Sottoriva at the ICR, Trevor Graham at Barts) that combines molecular methods with mathematical modelling to measure and predict cancer evolution.

We're looking for people either with bioinformatic and/or mathematical modelling expertise, or excellent wet-lab skills (genetics or cell biologists, particularly those experimentalists excited about Big Data). Our groups are highly interdisciplinary (mix of mathematicians, physicists, evolutionary theorists, cell biologists, geneticists and clinicians) and we perform theory-led experiments to understand and predict cancer evolu-

tion. Genomic analysis and Bayesian inference are our methodologies of choice. The positions are funded by Cancer Research UK, the Wellcome Trust and the MRC, and are part of a close collaboration between Trevor Graham's lab at the Barts Cancer Institute, and Andrea Sottoriva's lab at the Institute of Cancer Research (ICR), and postdocs are available at both institutes.

More on the roles details are here: <https://sites.google.com/site/nottrevorgraham/home> And our recent publications are here: <https://sites.google.com/site/nottrevorgraham/publications> <http://www.sottorivalab.org/-publications.html>

Interested people should feel free to get in touch with me <t.graham@qmul.ac.uk> and they can apply here: (Graham - Barts) <https://webapps2.is.qmul.ac.uk/-jobs/job.action?jobRef=3DQMUL9908> (Sottoriva - ICR) <http://tinyurl.com/jss289p> Trevor Graham

richard.alan.nichols@googlemail.com

UMassachusetts Amherst DawinFellow

The Graduate Program in Organismic and Evolutionary Biology at University of Massachusetts Amherst announces a two-year postdoctoral FELLOWSHIP/lectureship. OEB draws together more than 90 faculty from the Five Colleges (University of Massachusetts Amherst and Smith, Hampshire, Mount Holyoke and Amherst Colleges), offering unique training and research opportunities in the fields of ecology, organismic and evolutionary biology. Our research/lecture position provides recent PhD's an opportunity for independent research with an OEB faculty sponsor, as well as experience mentoring graduate students and teaching a one-semester undergraduate biology course. To be qualified, a candidate must have a recent PhD in a field relevant to ecology, organismic or evolutionary biology and proven teaching skills. Position subject to availability of funds.

To apply online, please go to <https://umass.interviewexchange.com/-jobofferdetails.jsp?JOBID=80061> and submit a CV, statements of research and teaching interests, and contact information (email) for 3 professional references. Also please arrange to have a letter from your proposed OEB faculty sponsor sent to oeb@bio.umass.edu. A list of OEB faculty and additional information is available at www.bio.umass.edu/oeb. Applicants should apply

by the priority deadline of January 20, 2017 in order to ensure consideration. The position is expected to start in August 2017. Questions about this search may be sent to: oeb@bio.umass.edu

More information about the search can be found at: <http://gpls.cns.umass.edu/oeb/darwin-fellows> The Darwin Fellow Program, founded in 1995, brings promising young postdoctoral researchers to UMASS Amherst. The two-year position provides a unique combination of teaching and research responsibilities and is excellent preparation for academic positions. The fellowship program embodies the interdepartmental collaboration that characterizes the OEB Graduate Program. Darwin Fellows are active participants in OEB, acting as mentors to graduate students, conducting research, leading seminar courses, and teaching courses in the Biology Department.

“caicedo@bio.umass.edu” <caicedo@bio.umass.edu>

UmeåU 5PDF and 5PhD Metagenomics

The Department of Ecology and Environmental Science, Umeå University, Sweden, invites applicants for 5 postdoc and 5 PhD positions in ecology, biogeochemistry, paleolimnology, environmental genomics and modelling of northern lakes

In a five-year project, “Climate change induced regime shifts in Northern lake ecosystems” at Umeå University, Sweden, funded by the Knut and Alice Wallenberg Foundation, we are recruiting 5 postdocs (2- year fellowships) and 5 PhD students (4-year positions). Below we list each position with a short title indicating the focus of the position, the name of the primary advisor/mentor, application deadline, and a web link to the full text of the advertisement. The full advertisements are also appended as separate pdf files for all PhD positions and all postdoc fellowships, respectively.

Project description Effects of climate change on ecological communities are expected to be particularly strong at northern latitudes. The collaborative project “Climate change induced regime shifts in northern lake ecosystems” addresses two major, climate-dependent drivers of northern lakes: (i) altered thermal regimes, and (ii) increased input of terrestrial dissolved organic matter (tDOM). In a series of interconnected work packages we will use experimental, comparative, paleo-ecological,

environmental genomics and modeling approaches to study the impact of temperature and tDOM on ecosystem processes ranging from primary production and greenhouse gas dynamics to fish production and food web dynamics. We expect responses to these drivers to be highly nonlinear.

PhD positions

1. Greenhouse gases in lakes (advisor Jan Karlsson, deadline 20 February 2017) <https://umu.mynetworkglobal.com/en/what:job/-jobID:133460/>
2. Effects of climate change on fish production (advisor Pär Byström, deadline 20 February 2017) <https://umu.mynetworkglobal.com/en/what:job/jobID:133528/>
3. Primary production in lakes (advisor Ann-Kristin Bergström, deadline 20 February 2017) <https://umu.mynetworkglobal.com/en/what:job/jobID:133628/>
4. Modelling lake ecosystems (advisor Sebastian Diehl, deadline 9 March 2017) <https://umu.mynetworkglobal.com/en/what:job/-jobID:133564/>
5. Long term climate and environmental changes (advisor: Richard Bindler, deadline 20 February 2017) <https://umu.mynetworkglobal.com/en/what:job/jobID:133685/>

Postdoctoral Fellowships

1. Climate impact on fish production and consumer resource interactions (mentor Pär Byström, deadline 27 February 2017) <http://www.umu.se/english/about-umu/news-events/grants/6-75-17>
2. Climate Impacts on Benthic Processes of Northern Lakes (mentor Ryan Sponseller, deadline 27 February 2017) <http://www.umu.se/english/about-umu/news-events-grants/6-77-17>
3. Climate impact on C cycling in lakes (mentor Jan Karlsson, deadline 27 February 2017) <http://www.umu.se/english/about-umu/news-events-grants/6-76-17>
4. Climate impact on methane cycling in lakes (mentors David Bastviken and Jan Karlsson, deadline 27 February 2017) <http://www.umu.se/english/about-umu/news-events/grants/6-78-17>
5. Environmental genomics in northern Swedish lakes (mentor Xia-Ru Wang, deadline 27 February 2017) <http://www.umu.se/english/about-umu/news-events-grants/6-79-17> Xiao-Ru Wang

Xiao-Ru Wang, PhD Dept. of Ecology and Environmental Science Umeå University SE-901 87 Umeå, Sweden xiao-ru.wang@umu.se

Xiao-Ru Wang <xiao-ru.wang@umu.se>

UMinnesota PhyloComparativeMethods

Postdoctoral Position at the University of Minnesota, Twin Cities

A postdoctoral researcher is sought to develop phylogenetic comparative methods and apply them to studies of plant macroevolution. This project is a collaboration between the labs of Emma Goldberg at the University of Minnesota (where the position will be based), Itay Mayrose at Tel Aviv University, and Tracy Heath at Iowa State University. The postdoc will additionally work closely with Heath Blackmon at UMN, with a postdoc and software engineer at TAU, and with graduate and undergraduate students at UMN and TAU. More information about our labs is available at < <http://www.umn.edu/~eeg> >, < <http://www.tau.ac.il/~itaymay> >, < <http://phyloworks.org> >, and < <http://coleoguy.github.io> >.

The work will focus on improving and applying phylogenetic methods for testing the influence of traits on lineage diversification. One line of attack is developing new model-based phylogenetic comparative methods, targeting known weaknesses in existing approaches. The other is creating tools for more robust testing, to stabilize the use of existing and future methods; this includes designing benchmark test suites and tests of model adequacy. For all topics, the goal is to create products that are intellectually stimulating and practically useful, and to facilitate their adoption by the broader community. Empirical work will make use of extensive datasets on plant reproductive systems and chromosome counts, and it has the potential to make one of the strongest cases yet for the importance of species selection. The postdoc will also contribute to new workshops teaching phylogenetic comparative methods, to be held in the Midwest US and in Israel.

Relevant skills and knowledge include: macroevolution of reproductive systems and genome structure; phylogenetic comparative methods use and development; mathematics of stochastic processes; computational statistics; database and user interface design; programming in R, RevBayes, and C++; software tools for reproducible research workflows; writing clearly for both technical and general readers; and teaching in a computer lab setting. Expertise is not required in all these areas, however! We are generally looking for a biologist with macroevo-

lutionary interests and technical problem-solving skills.

Initial appointment will be for one year with competitive salary (compliant with FLSA) and benefits. Renewal for up to two more years is possible, pending excellent performance and mutual agreement. The start date is flexible. To apply, please assemble (i) a 1-3 page cover letter that highlights how your research interests and skills fit with this project, (ii) a CV, and (iii) names and contact information for three professional references. Materials should be submitted online at < <http://www1.umn.edu/ohr/employment/> > (Job Id #315262). Review of completed applications will begin on March 1, but candidates will be considered until the position is filled. Informal inquiries are welcome, directed to Emma Goldberg <eeg@umn.edu>.

The Twin Cities campus of the Univ Minnesota is home to a diverse set of local collaborators, expertise, and resources, particularly within the departments of Ecology, Evolution & Behavior <cbs.umn.edu/eeb> and Plant and Microbial Biology <cbs.umn.edu/plantbio>, the Bell Museum <bellmuseum.umn.edu>, and the Minnesota Supercomputing Institute <msi.umn.edu>. The campus is located in the heart of the Minneapolis-Saint Paul metropolitan area, which is rich in cultural and natural attractions (and ice skating rinks).

The University of Minnesota is committed to the policy that all persons shall have equal access to its programs, facilities, and employment without regard to race, color, creed, religion, national origin, sex, age, marital status, disability, public assistance status, veteran status, or sexual orientation.

Emma E. Goldberg Assistant Professor Dept. of Ecology, Evolution and Behavior University of Minnesota – Twin Cities email: eeg@umn.edu <http://www.umn.edu/~eeg> “eeg@umn.edu” <eeg@umn.edu>

UNorthCarolina Charlotte ChromosomeRearrangements

The Rogers lab at UNC Charlotte is hiring a postdoc to work on evolutionary genetics of genome structure. The lab is interested in duplications and chromosomal rearrangements, their role in creating new gene sequences, and the ways that selection acts on new genetic material. We will survey genome structure changes in a variety of organisms including *Drosophila* and humans to determine the importance of these mutations in evolu-

tion. More info at <http://evolscientist.com/>. The ideal candidate will have a thorough understanding of genetics, statistics, and bioinformatics. Experience working with Illumina short read sequencing and PacBio long molecule sequencing will be advantageous. Experience working with *Drosophila* will be beneficial. Applicants should have working familiarity with at least one programming language, with a strong preference for Python. Molecular biologists who wish to learn bioinformatics or quantitative scientists interested in genetics are encouraged to contact the PI and discuss their research interests.

Target start date is July 2017. Some flexibility exists, depending on circumstances. The Rogers lab supports diversity in science. We are committed to a positive working environment for LGBTQ individuals, underrepresented minorities, and women in science.

Applications should include a CV, a brief summary of research interests, proposal for how their work will fit with the lab, and three references to be contacted on request. Applications received by March 31st will be given full consideration. Later applications will be considered if the position remains available. Materials can be emailed to Rebekah.Rogers@uncc.edu. Minimum salary will follow NIH recommendations.

Charlotte, NC is a diverse city with an excellent symphony, theater, and performing arts scene. Charlotte also offers a thriving arts scene and live music in NoDa, excellent restaurants surrounding the Downtown, and family-friendly programs in local museums. The cost of living is very affordable, providing a comfortable lifestyle for postdocs.

rroger26@uncc.edu

UOslo PopulationGenetics

Postdoctoral Research Fellow in Population Genetics and Biogeography

Application Deadline: 6 February 2017

Apply at: <https://uio.easycruit.com/vacancy/-application/fba371fd81b6380fd91c79df8bcfb645/-1773755/96323?iso=gb> Position as postdoctoral research fellow available at University of Oslo, Department of Biosciences, Section for Genetics and Evolutionary Biology (EVOGENE)

The fellowship period is two years. Within the frame-

work of the position duties may be assigned. Starting date no later than 01.04.2017. No one can be appointed for more than one fixed-term period at the same institution.

Project description

The post-doctoralfellow will work within the framework of iGran, a Norwegian Research Councilfunded project examining the ecology and evolutionary history of *Lophodermium piceae**, a near ubiquitous endophytic fungus associated with spruce species worldwide. The lifecycle of the fungus is tightly linked to its host, although horizontal transmission of the fungus can occur. The iGran project aims to characterize the nature of the interaction between *L. piceae** and its hosts, its role in the leaf microbiome of spruce needles, as well as the role of both geography and historical events in shaping the genetic structure of European populations of the fungus. The post-doctoral researcher will be responsible for a pan-European survey of the genetic structure of *L. piceae** populations to examine the effects of the last glacial maxima on the organism's evolutionary history. The successful candidate will also undertake small-scale investigations of the role of natural dispersal barriers in shaping the genetic structure of these fungal populations. The project will use NGS-based approaches to generate data for SNP detection and population genetic/genomic analysis.

Qualifications:

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

The candidate must have a PhD or other corresponding education equivalent to a Norwegian doctoral degree in molecular ecology, biogeography, or population genetics. The research group working language is English. A good oral command of the language is mandatory and strong writing skills are highly desirable.

We seek a highly motivated and skilled person who is able to work independently as a contributor to a collaborative team. Background knowledge in mycology is desirable, but not essential. The post doctoral fellow will be responsible for a pan-European assessment of populations of a specific endophytic fungus and will be required to manage and execute all steps of the project including fieldwork, lab work, data analysis, and writing. The main purpose of post-doctoral research fellowships is to qualify researchers for work in top academic positions within their disciplines.

Essential qualifications include:

-wet lab experience with DNA extraction and NGS or RADSeq library preparation

-demonstrated knowledge and skills in bioinformatics and statistical analysis for population genetics including knowledge of software such as Stacks, Structure, Arlequin, poppr, or similar platform

-experience analyzing large-scale genetic/genomic datasets (ex/ SNP data)

Desirable qualifications include:

-good knowledge of fungal biology and biostatistics

-experience with fungal culturing'

-valid driver's license.

The main purpose of post-doctoral research fellowships is to qualify researchers for work in top academic positions within their disciplines.

Please also refer to the regulations pertaining to the conditions of employment for post-doctoral fellowship positions:

<http://www.uio.no/english/about/regulations/-personnel/academic/regulations-employment-conditions-postdoc.html>

Salary:

Position code 1352, NOK 486 100 - 567 100 per year, depending on qualifications and seniority.

The application must include:

-Application letter

-CV (summarizing education, positions, administrative experience and other qualifying activities)

-Copies of educational certificates, transcript of records, letters of recommendation

-A complete list of publications and up to 5 academic papers that the applicant wishes to be considered by the evaluation committee

-Names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number) Please remember that all documents should be in English or a Scandinavian language

Marie Davey <davey.marie@gmail.com>

UOslo PopulationGenomics

Department of Biosciences

Researcher in population and landscape genomics

Position as research fellow available at Department of Biosciences, Section for Genetics and Evolutionary Biology (EVOGENE).

This researcher position will begin as soon as April 2017, but the start date can be flexible. Initial appointment is for two years.

Job description/ Project description:

The Kausrud's Lab at the University of Oslo is seeking a motivated Researcher to be part of an ongoing collaborative project investigating the effect of forest fragmentation on the genetic variation of wood-decay fungi throughout Fennoscandia. The research programme FunGen, aims to enhance fundamental knowledge pertaining to the evolutionary processes responsible for generating and maintaining genetic diversity within populations of fungi in order to provide baseline information for improved forest management practices and conservation initiatives. This project is funded by the Research Council of Norway (NFR), under the programme Miljøforsk.

For further information please visit our webpage:

http://www.mn.uio.no/ibv/english/research/sections/-evogene/projects/fun_gen/

Depending on her/his specific expertise and qualifications, the selected candidate would be responsible for:

- the analysis of a RAD sequencing data set generated from several populations of a wood-decay fungal species. The corresponding genome has been sequenced in collaboration with the Joint Genome Institute. This data set is available and the postdoc/researcher will carry out the bio-informatics & population genomics analyses (Task1).

- both the wetlab and computational analysis of other polypore species sampled on a macro landscape-scale. In this subproject, the postdoc/researcher will work in close collaboration with other partners (NINA, NIBIO and SLU) involved in the landscape analyses (Task 2).

The candidate will also have opportunities for implementing her/his scientific ideas in different subprojects.

Qualifications:

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

The candidate must have obtained by the start date a PhD or other corresponding education equivalent to a

Norwegian doctoral degree in ecology, population genetics, evolutionary genomics or bioinformatics. We seek a highly motivated and skilled person who is able to work independently, to take own initiatives and to have a strong interest in producing high quality research and writing scientific publications. Good writing and communication competencies along with excellent team working traits are highly desirable. The ideal candidate would have experience in preparing libraries for next-gen sequencing (RADseq/GBS), demonstrated bioinformatics skills in 'Big-data' analytical approaches and high expertise in population genetics analyses. The candidate should be familiar with programming languages like Unix and Python/Perl and have advanced statistical skills, preferably in R. Knowledge of the Norwegian language is not required.

A good command of English is required.

Salary:

Position code 1109, Salary NOK 486 100 - 567 100 per year (pay grade 57 -65), depending on qualifications and seniority.

The application must include: * Application letter * CV (summarizing education, positions, pedagogical experience, administrative experience and other qualifying activity) * Copies of educational certificates, transcript of records and letters of recommendation * A complete list of publications and up to 5 academic works that the applicant wishes to be considered by the evaluation committee * Names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number)

Please remember that all documents should be in English or a Scandinavian language.

In accordance with the University of Oslo's equal opportunities policy, we invite applications from all interested individuals regardless of gender or ethnicity.

UiO has an agreement for all employees, aiming to secure rights to research results a.o.

- * Region: * Oslo
- * Job type: * Contract
- * Working hours: * Full-time
- * Working days: * Day
- * Application deadline: * 17 February, 2017
- * Location: * Oslo
- * Reference number: * 2017/1655
- * Company homepage: * <http://www.mn.uio.no/ibv/> *
- Contacts: * Sundy Maurice Telephone: +47 22845918
- * Questions regarding EasyCruit, contact HR Officer

Torunn Standal Guttormsen Telephone: +47 22 85 42 72

Sundy Maurice Researcher Mycology Group Section for Genetics and Evolutionary Biology University of Oslo Norway sandym@ibv.uio.no

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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>

UOxford EvolutionDosageComp

Postdoctoral Research Assistant - University of Oxford, United Kingdom Project: Evolution of Dosage Compensation on Recently Evolved Sex Chromosomes

Postdoc grade 7: 31,076 - 38,183 UK pounds per annum; initially a 1-year contract (extendable to 3 years)

Start date: on or shortly after 1st April 2017

Location: Department of Plant Sciences, University of Oxford, South Parks Road, Oxford OX1 3RB United Kingdom

The Department of Plant Sciences of the University of is seeking to recruit a Postdoctoral Research Assistant to work on a project devoted to evolution of sex chromosomes in plants, with the focus on evolution of dosage compensation on recently evolved sex chromosomes in *Silene latifolia* (see refs below). The postdoc on this project will be responsible for evolutionary genetic analysis of high-throughput genome and transcriptome sequence data and preparation of papers for publication. Most of the data will be available on or soon after the start date, so it is expected that wet lab work will be minimal and the bulk of the work will be computer-based. The postholder should have or be expected to obtain a PhD or equivalent and publication record in a relevant area (evolutionary genetics/genomics, bioinformatics). Significant experience in population genetic and genetic high throughput data analysis will be essential for this project. It will be advantageous for the successful applicant to have previous work experience related to sex chromosome evolution, such as work with transcriptome sequence data focused on dosage compensation, as well as extensive experience in computational and statistical analysis of biological data and expert knowledge of one or more scripting or programming

languages (e.g. Perl, Python, Ruby, C++ or Java etc.). The successful applicant will have high motivation with intellectual curiosity and rigour, ability to work independently and manage multiple tasks, ability to manage the day-to-day running of a research project and excellent oral and written communication skills.

Informal enquiries should be directed to: dmitry.filatov@plants.ox.ac.uk. The closing date for applications is 12.00 noon (London time) on Friday 24 February 2017. To apply formally please use vacancy ID 126994 at <https://www.recruit.ox.ac.uk/> Relevant recent publications: Kazama et al (2016) A new physical mapping approach refines the sex-determining gene positions on the *Silene latifolia* Y-chromosome. *Sci Rep.* Jan 8;6:18917. doi: 10.1038/srep18917

Papadopulos et al (2015) Rapid Y degeneration and dosage compensation in plant sex chromosomes. *Proc Natl Acad Sci U S A.* Oct 20;112(42):13021-6. doi: 10.1073/pnas.1508454112.

Dmitry A. Filatov, PhD Professor of Evolutionary Genetics, Department of Plant Sciences, University of Oxford, South Parks Road, Oxford OX1 3RB United Kingdom

Dmitry Filatov <dmitry.filatov@plants.ox.ac.uk>

UWarwick AncientPathogens

4 Year Research Fellow in Ancient Pathogen Statistical Genomics (78464-117), Warwick Medical School, University of Warwick (Closing 15th February 2017)

This four-year fellowship will focus on the development of novel statistical tools and analysis pipelines for ancient DNA metagenomes. The post is associated with a five year, 2M Wellcome Trust Investigator award to determine: How old are bacterial pathogens, and what evolutionary steps have they undergone? The research fellow will address these key questions through the analysis of hundreds of ancient metagenomes generated from human associated fossils during this project. Statistical problems to be addressed include: inference of ancient transmission dynamics between different hosts and geographical areas, de novo reconstruction of pathogen genomes and abundances directly from metagenomes, applications of the fossilised-birth-death process to improve placement of ancient pathogens on ancestral branches within time calibrated phylogenies and applications of Bayesian non-parametrics to incor-

porate time varying rates of evolution into phylogenies. It will be co-supervised by an international team of experts headed by Prof Achtman (WMS). This will consist of Dr Christopher Quince (WMS - metagenomics), Prof Tanja Stadler (ETH Zurich - computational evolution) and Prof Philippe Lemey (KU Leuven - Bayesian phylogenetics). The ideal candidate will have a background in statistics or computational biology or a related quantitative discipline such as theoretical physics. Expertise in quantitative data analysis is essential as is either theoretical or applied experience, as evidenced by high quality publications, in at least one of the following areas: phylogenetic inference, metagenomics, statistical genomics, stochastic processes and Bayesian non-parametrics. The closing date for applications is the 15th February 2017 for a start date of 1st March 2017 although later starts are possible. Applications should be through the University of Warwick website job id 78464-117 (<http://bit.ly/2jQv3fT>) and enquiries sent to Prof. Mark Achtman (achtmanmark@gmail.com) or Dr Christopher Quince (c.quince@warwick.ac.uk).

“Christopher.Quince@glasgow.ac.uk”

Vienna StatisticalGenomics

THREE YEAR POSTDOC POSITION IN STATISTICAL GENOMICS

The postdoctoral position will be part of a joint project between the groups of Carolin Kosiol (University of St. Andrews / Vetmeduni Vienna, <https://www.vetmeduni.ac.at/en/population-genetics-research/research-groups/kosiol-lab/>), Gergely Szöllösi (Etvös University Budapest, <http://solo.web.elte.hu/>), Asger Hobolth (Aarhus University, <http://www.daimi.au.dk/~asger/>). The recent sequencing of genomes of closely related species and of many individuals from the same species enables the study of speciation and the inference of the history of populations. Standard phylogenetic methods reduce entire populations to single points in genotypic space by modelling evolution as a process in which a single gene mutates along the branches of a phylogeny. Recently, we have developed new approaches that allow the inclusion of population genetics such as the Wright-Fisher model (Tataru et al, *Syst Biol* 2016; Hobolth, *JTB* 2015), that are polymorphism-aware phylogenetic models (PoMo, Schrempf et al., *JTB* 2016, DeMaio et al., *Syst Biol* 2015), and model gene duplication transfer and loss (DTL, Szöllösi et al., *Syst*

Biol 2015; Scornavacca et al., Bioinformatics 2015) for species tree estimation. We envisage developing new theory and software to tackle the problem of species tree estimation and molecular dating genome-wide. Applications will include mammalian genomes to study the Cambrian explosion as well as contributions to international genome consortia.

The postdoc will be based in Vienna. Visits to Budapest and Aarhus for close collaboration are planned. The project is funded for three years by Wiener Technology and Science Fund (WWTF) through the “Maths and ..” Call (<http://www.wwtf.at/programmes/ma/>). It also includes a PhD student and a programmer position that will be advertised separately.

Candidates will be expected to have completed a PhD in Computational Biology, Mathematics, Statistics, Computer Science or a related field. Prior experience with

either phylogeny, population genetics or comparative genomics is essential. Preferably the candidate will have experience in C or C++ and a scripting language such as Python or Perl.

The position will be hosted by the Institute of Population Genetics at the Vetmeduni Vienna. Vienna has developed into an international center in evolutionary biology (<http://www.evovienna.at>, <http://www.popgen-vienna.at/>). In addition to a stimulating scientific environment, Vienna is also a quite liveable city with affordable housing, good public transport and an exciting cultural life.

Please send informal inquires and applications to Carolin Kosiol ck202@st-andrews.ac.at or carolin.kosiol@vetmeduni.ac.at. Deadline for application is the 15th March.

Carolin Kosiol <carolin.kosiol@vetmeduni.ac.at>

WorkshopsCourses

Barcelona MorphometricsPhylogeny Sep11-15	124	MaxPlanckInst EvolBio GraduateMeeting Coevolution	
Berlin DataAnalysisInHighThroughputBiology May29- June2	124	Deadline Jan15	135
Berlin DatavizWithPython March13-17	125	Naples EMBOPopulationGenomics May18-26	136
Berlin LinuxForBiologists July31-Aug4	126	NHM London BotanicalTaxonomicPrinciples Mar6-10	136
Berlin Metabarcoding Apr3-7 updated	127	NHM London IntroductoryMolecPylogenetics May8-12	137
Cameroon UndergradTropicalConservation Jul5-27	128	NordU Norway NGSOOfNonModelOrganisms May31- Jun1	137
HarvardU DevelopmentEvolInnovation Mar3-5 . . .	129	Paris CoevolutionFitnessLandscapesEpistasis Mar1-3	138
HarvardU microMORPH Mar3-5	130	Pconos FunctionalGenomics May25-26	138
Hungary EvolutionSexRoles Apr6-9 RegistrationOpen	130	Portugal Nature Mar20-24	139
Hungary SexRoleEvolution Apr6-9	132	UCalifornia Davis AppliedPhylogenetics Mar11-18	139
Knoxville SpeciesRangeShifts May3-5	133	UCalifornia Davis AppliedPhylo Mar11-18	140
Konstanz AdaptiveEpigenomics Jul24-25	133	UCalifornia Davis Phylogenetics Mar11-18	141
Lisbon CommunityEcol Feb13-17	134	UCalifornia LosAngeles ConservationGenomics . .	142
Mantua Italy InsectConservation May24-26	134	UEdinburgh 4 PythonLinux Apr10-Jul28	143
MaxPlanck GraduateMeeting EvolBiol Deadline Jan15	135		

UK LandscapeGeneticsAnalysisUsingR Nov6-10 ..	144	UWashington EvolQuantGenetics Jun5-9	146
UK TwoPythonCourses Nov27-Dec1	145		
UMichigan NextProf May2-5	146		

Barcelona MorphometricsPhylogeny Sep11-15

Dear colleagues,

The 8th edition of the course GEOMETRIC MORPHOMETRICS AND PHYLOGENY has open registration. Basic knowledge of Geometric Morphometrics is required.

INSTRUCTOR: Prof. Chris Klingenberg (University of Manchester, UK).

DATES: September 11th - 15th, 2017.

PLACE: Facilities of the Centre of Restauració i Interpretació Paleontològica, Els Hostalets de Pierola, Barcelona (Spain).

Testimonials of previous editions: <http://www.transmittingscience.org/courses/gm/gm-and-phylogeny/#Testimonials> PROGRAM,

1. Phylogeny, trees and phylogenetic reasoning. 2. Brief review of geometric morphometrics (Procrustes fit, PCA, etc.). 3. Mapping traits onto phylogenies: squared-change parsimony. 4. Practice: making/editing Nexus files, mapping morphometric data onto the tree (Mesquite, MorphoJ). 5. Phylogenetic signal, morphometric traits and estimating phylogeny. 6. Comparative methods: independent contrasts. 7. Application in morphometrics: evolutionary allometry and size correction. 8. Practice: comparative methods (MorphoJ). 9. Application of comparative methods: morphological integration. 10. Multi-level analyses of integration: inferring evolutionary mechanisms. 11. Application of comparative methods: partial least squares (ecomorphology, etc.). 12. Practice; comparative methods (cont.). 13. Morphometrics, phylogenies and qualitative characters. 14. Disparity and diversification. 15. Presentations of group work.

More information: <http://www.transmittingscience.org/courses/geometric-morphometrics/geometric-morphometrics-phylogeny/> or writing to courses@transmittingscience.org

Organized by: Transmitting Science, the Institut Català de Paleontologia Miquel Crusafont and the Council of Hostalets de Pierola.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Soledad De Esteban-Trivigno, PhD. Scientific Director Transmitting Science www.transmittingscience.org Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.org>

Berlin DataAnalysisInHighThroughputBiology May29-June2

Data analysis in high throughput biology <https://www.physalia-courses.org/courses/course3/> >From the 29th of May to the 2nd of June 2017 in Berlin, Germany (<https://www.physalia-courses.org/courses/course3/>).

Instructor: Dr. January Weiner (Max Planck Institute for Infection Biology; <https://www.physalia-courses.org/instructors/t14/>).

Course overview

High throughput (HT) techniques such as transcriptomics or metabolomics are of great significance in many areas of biology. With the standard techniques becoming more affordable and new techniques being introduced all the time, the amount of data sets generated is staggering. However, statistical and computational analysis of HT data sets present many challenges. In this course, the students will gain the ability to independently process and analyse HT data sets, select the appropriate tools, functionally interpret the results as well as learn the paradigms of computational biology and statistics which will allow them to efficiently communicate with computational biologists.

Intended audience

In general, the course is aimed at biologists who would like to take their data analysis in their own hands. While an aptitude for computational work is necessary, the main goal of the course is the application of biological and statistical knowledge to HT sets with as little effort as necessary.

* basic computer skills (a rudimentary knowledge of programming principles in any language is recommended, but not mandatory) * basic understanding of statistics * basic understanding of molecular techniques for generating high throughput data

The students should be comfortable with using a computer and have at least a rudimentary understanding of computer programming. However, no specific skills are necessary; the students will learn basic R programming in this course.

Basic skills in statistics are necessary. The students should understand the concepts of statistical hypothesis testing and p-values. However, an in-depth introduction to these concepts will also be provided.

Target student skills

* overview of commonly used high-throughput data types
 * techniques for data clean-up and preparation for analysis
 * understanding of computational problems associated with high-throughput data analysis
 * statistical problems and solutions in analysis of HT data
 * practical skills in analysis methods of HT data: - basic differential analysis (limma, DESeq, alternative and non-parametric techniques) - set enrichment techniques (GSEA, gene ontologies, metabolic profiling and more) - multivariate approaches to data analysis (PCA / ICA, PLS, multiple correspondance analysis) - basic approaches in machine learning: cross
 * Communication skills in statistics and computational biology

After the course, the student should be able to prepare, analyse and interpret a HT data set, including multivariate and machine learning techniques.

Teaching format

On each day, the course will consist of four parts:

* Lecture: theoretical introduction to the days focus
 * Hands-on guide: guided practical session in R where students replicate the analysis performed by the teacher. While the lecture is general, here specific R techniques and R packages are introduced
 * Guided self-study: students are given exercises and problems to solve and work on them individually under the guidance of the teacher
 * Individual project work: each student will receive a transcriptomic (RNASeq or microarray) data set to analyse throughout the course
 * Lecture: wrap-up and side notes; preparation for the following day

Venue

Botanischer Garten und Botanisches Museum (BGBM) Berlin-Dahlem/Freie Universität Berlin, Königin-Luise-Straße 6-8, 14195 Berlin

Course plan

* Day 1: Introduction to statistical reasoning and R
 Lecture: “Statistics gone wrong: basics of statistical problems in HT applications”
 o Hands-on guide: working with R: first steps
 o Guided self-study: using R for data loading and basic statistical calculations
 o Individual project work: loading data for the individual project
 o Lecture: “On the importance of lab books - documentation and organization in computational projects”

* Day 2: Data preparation and basic differential analyses
 o Lectures: + “Steps in HT data analysis and overview of HT techniques” + “Differential analysis in transcriptomics”
 o Hands-on guide: documentation with knitr, data pre-processing, QC
 o Guided self-study: creating self-documenting R code; basic steps in transcriptomic analyses
 o Individual project work: basic analysis of the individual data sets
 o Lecture: “So you have a list of thousand gene names: why do we do HT analyses?”

* Day 3: Functional analysis, gene set enrichments and biological interpretation

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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>

Berlin DataVizWithPython March13-17

Dear all,

we still have a few places available (first come, first served) for the “Data Manipulation and Visualization with Python” Workshop, 13-17 March 2017 in Berlin (Germany) <http://www.physalia-courses.org/courses/-course10/> Application deadline:

February 24th 2017.

Instructor:

Dr Martin Jones (Founder, Python for Biologists <http://pythonforbiologists.com>) <http://www.physalia-courses.org/instructors/t1/> Course overview:

One of the strengths of the Python language is the availability of mature, high-quality libraries for working with scientific data. Integration between the most popular libraries has led to the concept of a “scientific Python stack”: a collection of packages which are designed to work well together. In this workshop we will see how

to leverage these libraries to efficiently work with and visualize large volumes of data.

Workshop format:

The workshop is delivered over ten half-day sessions. Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizer's discretion. Each session uses examples and exercises that build on material from the previous one, so it's important that students attend all sessions. The last two sessions will be kept free for students to work on their own datasets with the assistance of the instructor. A description of the sessions can be found at the bottom of this page.

Who should attend:

This workshop is aimed at researchers and technical workers who are dealing with large datasets and don't know how to investigate them to make publishable graphics.

Requirements:

Students should have enough biological/bioinformatics background to appreciate the example datasets. They should also have some basic Python experience (the Introduction to Python course will fulfill these requirements). Students should be familiar with the use of lists, loops, functions and conditions in Python and have written at least a few small programs from scratch. Students will require the scientific Python stack to be installed on their laptops before attending; instructions for this will be sent out prior to the course.

Venue

Botanischer Garten und Botanisches Museum (BGBM) Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Straße 6-8, 14195 Berlin.

Curriculum

Monday 13th - Classes from 09:30 to 17:30

Session 1 - Introduction and datasets

Jupyter (formerly iPython) is a programming environment that is rapidly becoming the de facto standard for scientific data analysis. In this session we'll learn why Jupyter is so useful, covering its ability to mix notes and code, to render inline plots, charts and tables, to use custom styles and to create polished web pages. We'll also take a look at the datasets that we'll be investigating during the course and discuss the different types of data we encounter in bioinformatics work.

Session 2 - Introduction to pandas

In this session we introduce the first part of the scientific Python stack: the pandas data manipulation

package. We'll learn about Dataframes the core data structure that much of the rest of the course will rely on and how they allow us to quickly select, sort, filter and summarize large datasets. We'll also see how to extend existing Dataframes by writing functions to create new columns, as well as how to deal with common problems like missing or inconsistent values in datasets. We'll get our first look at data visualization by using pandas' built in plotting ability to investigate basic properties of our datasets.

Tuesday 14th - Classes from 09:30 to 17:30

Session 3- Grouping and pivoting with pandas

This session continues our look at pandas with advanced uses of Dataframes that allow us to answer more complicated questions. We'll look two very powerful tools: grouping, which allows us to aggregate information in datasets, and pivoting/stacking, which allows us to flexibly rearrange data (a key step in preparing datasets for visualization). In this session we'll also go into more detail about pandas indexing system.

Session 4- Advanced manipulation with pandas

In this final session on the pandas library we'll look at a few common types of data manipulation binning data (very useful for working with time series), carrying out principal component analysis, and creating networks. We'll also cover some features of pandas designed for working with specific types of data like timestamps and ordered categories.

Wednesday 15th - Classes from 09:30 to 17:30

Session 5-Introduction to seaborn

This session introduces the seaborn charting library by showing how we can use it to investigate relationships between different variables in our datasets. Initially we concentrate on showing distributions

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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>

**Berlin LinuxForBiologists
July31-Aug4**

Dear all,

We are happy to announce that we will be holding the second edition of the “Introduction to Linux and workflows for biologists” in Berlin (Germany) from the 31th July to the 4th August 2017.

Instructor:

Dr Martin Jones (Founder, Python for Biologists <http://pythonforbiologists.com>) <http://www.physalia-courses.org/instructors/t1/> Overview

Most high-throughput bioinformatics work these days takes place on the Linux command line. The programs which do the majority of the computational heavy lifting genome assemblers, read mappers, and annotation tools are designed to work best when used with a command-line interface. Because the command line can be an intimidating environment, many biologists learn the bare minimum needed to get their analysis tools working. This means that they miss out on the power of Linux to customize their environment and automate many parts of the bioinformatics workflow. This course will introduce the Linux command line environment from scratch and teach students how to make the most of its tools to achieve a high level of productivity when working with biological data.

Intended audience

This workshop is aimed at researchers and technical workers with a background in biology who want to learn to use the Linux operating system and the command line environment. No previous experience of Linux is required.

Venue

Botanischer Garten und Botanisches Museum (BGBM) Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Straße 6-8, 14195 Berlin.

Course Programme

<https://www.physalia-courses.org/courses/course1/-curriculum/> Monday 31th - Classes from 09:30 to 17:30

Session 1 - The design of Linux

Session 2 - System management

Tuesday 1sh - Classes from 09:30 to 17:30

Session 3 - Manipulating tabular data

Session 4 - Constructing pipelines

Wednesday 2nd - Classes from 09:30 to 17:30

Session 5 - EMBOSS

Session 6 - Using a Linux server

Thursday 3rd - Classes from 09:30 to 17:30

Session 7 - Combining methods

Session 8 - Combining methods

Friday 4th - Classes from 09:30 to 17:30

Session 9 - Customization

Session 10

The afternoon of Friday 18th is reserved for finishing off the next- gen workflow exercise, working on your own datasets, or leaving early for travel.

Application deadline is June 30th 2017.

Available packages:

- 1) “only-course” (580 euros VAT included) includes refreshments, lunch and course material;
- 2) “all-inclusive” (795 euros VAT included) includes refreshments, course material, accommodation and meals (breakfast, lunch, dinner).

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator

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Berlin Metabarcoding Apr3-7 updated

Dear all,

here’s an updated version of the syllabus for the “16S rRNA gene Metabarcoding” workshop, 3-7 April 2017 in Berlin (Germany).

<https://www.physalia-courses.org/courses/course8/> Instructor: Dr. Alexandre de Menezes (National University of Ireland Galway) <https://www.physalia-courses.org/instructors/t5/> Course overview

The 16s rRNA gene has become the standard marker for prokaryote phylogenetic analysis, and combined with high-throughput sequencing technologies it is widely used to infer the structure and composition of microbial communities. Due to the continuous improvements in sequencing technologies and bioinformatics tools, there is a wide choice of methods for sequencing and analysing 16S rRNA gene assemblies. This workshop is designed

to give students the necessary background and practical experience of the strategies for the analysis of the diversity and structure of prokaryote communities, covering i) experimental design and primer choices; ii) wet-lab and library preparation options; iii) sequence quality control and analysis and iv) statistical analysis of microbial community data. The many sequencing and analysis options will be discussed, whereas a more in-depth tutorial using real sequence data will provide an opportunity for the student to practice 16S rRNA sequence analysis from raw sequence files to ecological interpretation. Course material, such as presentation slides and necessary model data, will be provided to the students.

Targeted audience and assumed background

This workshop is intended for students and researchers interested in microbial ecology but who are not yet very familiar with the techniques involved. Choosing the appropriate primers, library preparation kits, sequencing methodologies and bioinformatics pipelines can be quite daunting to the uninitiated. This workshop will allow researchers interested more confidence in their methodology and analyses choices. The target audience include students of animal or plant microbiomes as well as those studying environmental microbial communities. It is assumed that the workshop attendees are interested in performing 16S rRNA metabarcoding using the Illumina MiSeq platform, although other sequencing technologies will be discussed during the workshop.

Knowledge of Linux and R or familiarity with working in the command line will be helpful, but for those new to the area detailed instructions will allow students to follow the workshop. Students will need to have a computer running either on Linux or a Linux virtual machine running on MacOX/Windows computers. Contact the instructor at ademez@gmail.com if in doubt about computational requirements.

Workshop structure

The workshop will consist of both lectures and practical classes. Background information will be provided to help workshop attendees choose the appropriate experimental design, primers, sequencing library preparation kits and to contextualise the bioinformatics and statistical analysis methods. Practical tutorials will be conducted on a step-by-step basis to guide the student from when receiving data from a sequence provider to obtaining plots and tables describing microbial community diversity, structure and relationships to environmental variables or host data.

Venue

Botanischer Garten und Botanisches Museum (BGBM)

Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Straße 6-8, 14195 Berlin.

Session contents

Monday 3rd-Classes from 10:00 to 18:00

Session 1: the 16S rRNA gene

The use of the 16S rRNA gene as a marker for prokaryote phylogenetics will be discussed to introduce the students to the concept of conserved and hypervariable regions. The student will learn about the history of this molecular marker and why it is the choice for prokaryote diversity studies. The primer combinations used to target the different hypervariable regions will be discussed, as well as what is known regarding their advantages and disadvantages. The pros and cons of PCR-based 16S rRNA gene sequencing versus PCR-free shot-gun metagenomics will also be discussed.

This session will also include an overview of current sequencing technologies, and the Illumina MiSeq platform will be contrasted with other sequencing technologies (Ion Torrent, MinIon, PacBio and Moleculo).

Session 2: sequencing experimental design and initial hands-on exercises

Focusing on the MiSeq platform, experimental design considerations will be discussed and topics discussed will include sequence depth, replication, contamination and the use of appropriate controls and mock communities. Other topics that will be taught include: metadata collection, DNA extraction and RNA-cDNA sequencing. Demo sequence data will be used to check that the appropriate tools are installed correctly for subsequent practical work, and students will perform exercises in the

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Cameroon UndergradTropicalConservation Jul5-27

The Central African Biodiversity Alliance (CABAl-
liance) is pleased to announce a three-week undergradu-
ate field course in tropical biology and conservation that

will run from July 5th to 27th, 2017 in Cameroon. This field course will be hosted by Drexel University, UCLA, and the Congo Basin Institute (Yadoundé, Cameroon). Classroom and field instruction will be given on site in Yaoundé and Mbam and Djerem National Park by scientists from collaborating institutions including Drexel University, UCLA, University of Buea, University of Hong Kong, University of Halle-Wittenberg.

Course information and application forms can be found on the Drexel Study Abroad Website: http://studyabroad.drexel.edu/index.cfm?FuseAction=Programs.ViewProgram&Program_ID=47722 Application deadline: March 1, 2017

More information on CABalliance can be found at: www.caballiance.org Course objectives: The overall aim of this program is to provide training in the fundamentals of tropical field research. A total of 20 undergraduate students will participate in this course, half of which will be from U.S. institutions and the other half from Cameroonian and Equato-Guinean universities. Students will work collaboratively in teams to:

- Design an independent research project in tropical ecology
- Collect data and analyze results
- Write a report in the format of a scientific publication summarizing the aims, methods, results and conclusions of the research project
- Present project findings to participants and instructors at the end of the course

By participating in this program, students will:

- Understand the basic principles of conservation biology and evaluate how these principles are applied to problems in conservation
- Read the assigned literature and be able to critically assess the key concepts in a discussion and written format
- Demonstrate how to research data, work through spread-sheet exercises and manipulate software applicable to solving conservation problems
- Co-design an original research project and work effectively as a team member in a group environment
- Demonstrate an ability to effectively communicate research findings and key concepts through both oral and written presentation

Requirements: - Currently registered as an undergraduate at a U.S. institution - Participate in mandatory 3-week online seminar prior to the program - One semester of college-level French (Recommended) - Hold a valid passport - Obtain all necessary vaccinations - Enjoy working in a multi-cultural setting - Able to work under physically strenuous conditions - All travel expenses (flight, lodging, meals) will be covered

This course is optionally available for two credits (applicable course fees apply). All successful applicants will be required to pay a \$500 commitment fee which will

be refunded upon completion of the program.

For more information, please contact: Dr. Matthew Mitchell (mwmitchell@drexel.edu) or Dr. Katy Gonder (gonder@drexel.edu) This project is funded through NSF award OISE 1243524

Matt Mitchell <mwmitche@gmail.com>

HarvardU DevelopmentEvoInnovation Mar3-5

microMORPH Workshop 2017 - The Developmental Basis of Evolutionary Innovation

March 3-5, 2017, at the Arnold Arboretum of Harvard University, Boston, MA.

microMORPH INTERDISCIPLINARY WORKSHOPS bring together small groups of graduate students, post-doctoral researchers, 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.

We are accepting applications from graduate students (at all stages of their dissertation research) and post-doctoral researchers. Eight student/postdoctoral participants will be chosen to attend, give presentations on their research (which should address some aspect of evolutionary innovation in plants), and engage in the discussions.

microMORPH will fund travel, accommodations, and meals for selected participants who are U.S. citizens or who are associated with a U.S. institution/university. Non-U.S. citizens that are not associated with a U.S. institution are welcome to participate but will have to fund their own travel and accommodations.

Participating Faculty Include: Jeff Doyle (Cornell University), Spencer Barrett (University of Toronto), Robin Hopkins (Harvard University), Elizabeth (Toby) Kellogg (Donald Danforth Center), Lionie Moyle (Indiana University), Günter Theißen (Friedrich-Schiller-University Jena), Carolyn Wessinger (University of Kansas), Pamela Diggle (University of Connecticut), William (Ned) Friedman (Harvard University).

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>).

Questions or Comments? Contact Becky Povilus at RCNmicromorph@gmail.com, or visit our website at <http://projects.iq.harvard.edu/micromorph> . Application deadline extended: Applications must be submitted by 11:30 pm January 23rd, 2017.

Pamela Diggle

Professor Department of Ecology and Evolutionary Biology University of Connecticut

860-486-4788 <tel:860-486-4788>

diggle@colorado.edu

HarvardU microMORPH Mar3-5

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Pamela Diggle

Professor Department of Ecology and Evolutionary Biology University of Connecticut

860-486-4788 <tel:860-486-4788>

diggle@colorado.edu

Hungary EvolutionSexRoles Apr6-9 RegistrationOpen

EVOLUTION OF SEX ROLES

Dear Colleagues

Glad to announce that our Wshop just launched a website: www.congressline.hu/evolution2017 The Registration document is downloadable from the website.

See you soon in Tihany.

Best wishes, Tamas Szekely on behalf of the organisers
 ===WORKSHOP INVITATION SEX-ROLE EVOLUTION: INTEGRATING NEURAL, BEHAVIOURAL AND PHYLOGENETIC APPROACHES

We are glad to invite you to our Workshop that will take place between 6th April 2017 and 9th April 2017 in Tihany, Hungary. The event will start with wine-tasting on Thursday 6 April, will include 2 full days for research talks by top scientists, post-docs and students, and an optional excursion on Sunday to a hot spa (Heviz) and/or the historic Festetics Palace in Keszthely.

Theoretical, experimental, phylogenetic, demographic and neuro-genomic studies of sexual selection, mating systems, pair-bonding, parenting and reproductive behaviours are rapidly advancing. The objectives of the workshop are to overview recent developments in sex roles and associated behaviours, and allow scientists and students to develop new ideas. The Workshop will take place at the guesthouse of the Hungarian Academy of Sciences at Lake Balaton. The guest-

house offers a great venue for up to 60 participants, see www.blki.hu/vendeghaz/index_en.html Balaton is a major tourist destination in Central Europe (see <http://balaton.gotohungary.com/>), and the Workshop will be before the peak tourist season; so we'll have all the scenery, folklore and tradition without the crowd. Balaton is one of the best wine-growing regions in Hungary famous for white wines including the Szurkebarat and Juhfark.

The Workshop will focus on three main themes: (i) behavioural variations in sex roles and their ecological and demographic causes, (ii) phylogenetic analyses of sex role variations, and (iii) neuro-genomic regulation of sex roles.

In each theme there will be seminars by invited speakers and contributions by young scientists, post-docs and PhD students. We will also discuss the future of sex role research: what are the outstanding questions, what techniques will need to be developed, and how should the field as such develop. The combination of different research skills and variety of model organisms will provide outstanding opportunities to synthesize major research directions.

Confirmed invited speakers include:

1. Variations in sex roles

Professor Franjo Weissing

University of Groningen, Groningen

Dr Franziska Lemmel-Schadelin

University of Veterinarian Medicine, Vienna

Dr Lutz Fromhage

University of Jyvaskyla, Jyveskyla

Professor Wolfgang Goymann

Max Planck Institute, Radolfzell

Professor Jan Komdeur

University of Groningen, Groningen

2. Phylogenetic approach to sex roles

Dr Laszlo Garamszegi

Donana Biological Station, Sevilla

Dr Elina Immonen

University of Uppsala, Uppsala

Professor Jean-Michael Gaillard

CNRS-University of Lyon, Lyon

Dr Veronika Bokony

Hungarian Academy of Sciences, Budapest

3. Neuro-genomic regulation of sex roles

Dr Dora Zelena

Hungarian Academy of Sciences, Budapest

Dr Araxi Urrutia

University of Bath, Bath

Dr Clemens Kupper

Max Planck Institute, Seewiesen

Professor Hans Hofmann

University of Texas, Austin

Registration fee that includes the welcome wine-tasting on Thursday and the farewell dinner on Saturday will be 80 EUR for students and 125 EUR for non-students. Accommodation will be around 25 EUR per night in shared rooms, and 30-40 EUR per night in single rooms or apartments. Lunch and dinner will be around 10-15 EUR per meal.

Spaces are limited to 60 and we will give priority to students offering a talk. This will be an excellent training opportunity for young scientists, and we encourage senior scientists to bring along their students and post-docs. We recommend registering early, since spaces will rapidly fill up.

Application deadline: Friday, 17 February 2017. Registration will be available soon on the workshop website. For scientific details feel free contacting one of the organisers. For administrative questions and further information on the venue, please, contact Bea Golovanova, CongressLine Ltd. Address: Revay koz 2, H-1065 Budapest, Hungary. Phone: + 36 1 429 0146. E-mail: golob@congressline.hu

This will be a family-friendly event so do consider bringing along your family. CongressLine Ltd will be glad to accommodate individual requests so that you'll benefit from the off-season prices around Balaton.

We look forward to hearing from you. Best regards,

Prof Arpad Dobolyi, Hungarian Academy of Sciences, dobolyia@caesar.elte.hu, dobolyi.arpad@med.semmelweis-univ.hu

Prof Andras Liker, University of Pannonia, andras.likier@gmail.com Prof Tamas Szekeley, University of Bath, T.Szekeley@bath.ac.uk

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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>

Hungary SexRoleEvolution Apr6-9

WORKSHOP INVITATION SEX-ROLE EVOLUTION: INTEGRATING NEURAL, BEHAVIOURAL AND PHYLOGENETIC APPROACHES

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We look forward to hearing from you. Best regards,

Prof Arpad Dobolyi, Hungarian Academy of Sciences, dobolyia@caesar.elte.hu, dobolyi.arpad@med.semmelweis-univ.hu Prof Andras Liker, University of Pannonia, andras.likier@gmail.com Prof Tamas Szekely, University of Bath, T.Szekely@bath.ac.uk

Tamás Székely, Professor of Biodiversity Fellow of Wissenschaftskolleg zu Berlin 2016/17 Dept of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK 01225 383676 (phone), 01225 386779 (fax), T.Szekely@bath.ac.uk (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/evodir.html>

Knoxville SpeciesRangeShifts May3-5

Call for applications:

Please consider applying to an Investigative Workshop on Species Range Shifts to be held at the National Institute of Mathematical and Biological Synthesis (NIMBioS), University of Tennessee, Knoxville, May 3 - 5, 2017. Specifically, we will be discussing new methods for integrating niche models, [evolutionary] genetics, and fossil pollen data to understand species' range dynamics under changing climates. We hope this workshop will lead to several group papers as well as a long-term working group initiative at NIMBioS. Faculty, post-docs, and senior graduate students are welcome to apply.

For more information visit this website: http://www.nimbios.org/workshops/WS_rangeshifts If you are selected, your travel and accommodations are covered by NIMBioS.

– A. Michelle Lawing, PhD Assistant Professor Ecosystem Science and Management Texas A&M University 2120 TAMU Centeq Building B, 223 College Station, TX 77843

“alawing@tamu.edu” <alawing@tamu.edu>

Konstanz AdaptiveEpigenomics Jul24-25

We would like to welcome you to join a two-day interdisciplinary workshop on “Adaptive Epigenomics: Building a bridge between animal and human research” hosted Prof. Thomas Elbert and Prof. Axel Meyer and sponsored by the Hector Fellowship Academy. The workshop will be held in Konstanz, Germany, from July 24-25, 2017, and is organized by Dr. Amber Makowicz (post-doc research with Dr. Meyer), Daniela Conrad (PhD student with Dr. Elbert) and Maggie Sefton (PhD student with Dr. Meyer).

The goal of this 2-day workshop is to provide theoretical input on epigenetics as an evolutionary component and important mechanism in the development of (psycho)pathologies and evolutionary adaptations. In addition, providing explanations on the processing and statistical evaluation of epigenetic data, including hands-on exercises of small pseudo-datasets. The workshop shall furthermore represent a platform for the interdisciplinary exchange between biologists and psychologists using epigenetic approaches to investigate the biological underpinnings of (pathological) behavior and adaptation.

Confirmed speakers include:

- Dr. Tuncay Baubec is an SNF Professor in the Department of Molecular Mechanisms of Disease at the University of Zurich.
- Dr. Vanja Vukojevic is a postdoc in the Department of Molecular Neurosciences at the University of Basel.
- Dr. Bridgett vonHoldt is a professor in the Ecology and Evolutionary Biology Department at Princeton University.
- Dr. Robert Philibert runs the Psychiatric Genetics lab at the University of Iowa.
- Dr. Tomas Marques-Bonet leads the research group on comparative genomics at Universitat Pompeu Fabra.

We welcome any Masters and PhD students, postdocs, and any other young scientists in the fields of evolutionary biology and psychology to join us. Registration fees include a social dinner on a boat on Lake Konstanz (July 24th), and farewell dinner at the Hotel St. Elisabeth in Hegne (July 25th). Registration deadline for earlier-bird rate (50 euro) is March 31st and for the normal rate

(100 euro) is May 31st. Space is limited to 35 people, so please register as soon as possible.

Accommodations can be found at the Hotel St. Elisabeth, however, these rooms book rapidly and will require you to book well in advance (www.st-elisabeth-hegne.de/en/hotel.html). Other accommodations can be found in Konstanz with direct train connection to Hegne (~10-12 min ride).

Konstanz is a cozy town in the south of Germany, located near the border to Switzerland. With direct access to beautiful Lake Konstanz and its historical old town it is a favorite holiday destination for locals and international tourists. Furthermore, the University of Konstanz is one of the highest-ranking German universities. For many years, the University of Konstanz belongs to the German Universities Excellence Initiative, and is host to a large, international body of students from various fields.

Any questions in regards to the workshop can be found on our website (<http://adaptive-epigenomics.weebly.com/>) or emailed to epigenetics-workshop@uni-konstanz.de or directly to Amber Makowicz at amber.makowicz@uni-konstanz.de

Many thanks for your assistance.

Cheers, Amber – Amber M. Makowicz, Ph.D.

Hector Postdoctoral Fellow Room M821 Biology Department Lehrstuhl für Zoologie und Evolutionsbiologie, University Konstanz, Universitätsstraße 10, 78457 Konstanz, Germany +49 (0) 7531 884660

<http://meyerlab-konstanz.weebly.com/dr-amber-makowicz.html> Amber Makowicz
<amber.makowicz@uni-konstanz.de> Amber Makowicz
<amber.makowicz@uni-konstanz.de>

Lisbon CommunityEcol Feb13-17

Subject: Portugal-cE3c-Course Applied Methods in Community Ecology- February 13-17 2017 @ Lisbon, Portugal

cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing the Advanced Course Applied Methods in Community Ecology and Functional Ecology by Paulo A. V. Borges & François Rigal - February 13-17 2017 @ Lisbon, Portugal

Applied Methods in Community Ecology and Functional Ecology

OBJECTIVES: This five-days intensive course is mostly a practical course offering an overview on different community ecology and macroecological methods and software. These will include all steps of a research project, from the optimal sampling of communities to process inference from large-scale patterns of taxon, phylogenetic and functional diversity. Specific topics will be: (1) alpha, beta and gamma diversity; (2) estimating diversity from incomplete sampling; (3) partitioning taxonomic beta diversity; (4) community-assembly rules, (5) functional and phylogenetic diversity, (6) null models, (7) rarity and species abundance distribution. Finally, students will be asked to present own data and case studies.

See the PROGRAMME at: <http://ce3c.ciencias.ulisboa.pt/training/?cat=8> Course INSTRUCTORS: Paulo A. V. Borges (Assistant Professor at Azores University, researcher at cE3c) (<http://gba.uac.pt/team/IBBC>; <http://ce3c.ciencias.ulisboa.pt/member/paulo-a-v-borges>) and François Rigal (Assistant Professor at Environment and Microbiology Team, MELODY group, University of Pau and external collaborator of cE3c -IBBC, Azorean Biodiversity Group) (<http://ce3c.ciencias.ulisboa.pt/member/francedilois-rigal>)

INTENDED AUDIENCE This five days intensive course will be open to a maximum number of 20 participants, being directed to PhD or MSc students in Ecology, Geography or related areas, and postdocs and other professionals working in related topics. The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL, UP) and Biology and Ecology of Global Changes (BEAG UL, UA). For information of fees for other participants see the programme details.

Deadline for applications: January 16 2017 For additional details about the course and to know how to register, click here: <http://ce3c.ciencias.ulisboa.pt/training/?cat=8> For more information about the course, please contact: pborges@uac.pt

Margarida Matos <mmmatos@fc.ul.pt>

Mantua Italy Insect Conservation May24-26

LIFE MIPP EUROPEAN WORKSHOP

24-26 May 2017

Mantua, Italy

International workshop of the Life project “Monitoring Insects with Public Participation” From 24th to 26th May 2017 the concluding workshop “Monitoring of saproxylic beetles and other insects protected in the European Union” will be held in Mantua (Italy).

The project LIFE11 NAT/IT/000252 (Monitoring Insects with Public Participation - MIPP) is developing national guidelines for the monitoring of five saproxylic beetles species (*Osmoderma eremita*, *Lucanus cervus*, *Cerambyx cerdo*, *Rosalia alpina* and *Morimus asper/funereus*) listed in the Habitats Directive. One innovative method tested is the use of a “molecular dog” to detect *Osmoderma eremita*. The MIPP project is also applying a citizen science approach for the mapping of rare insects in Italy: people collaborated with scientists. The workshop is open to anyone interested in entomology and in particular in: monitoring protocols, conservation and management, habitats and biodiversity, citizen science.

The workshop is organized by the National Center for Study and Conservation of the Forest Biodiversity “Bosco Fontana” in partnership with the Universities of Roma “Sapienza” and “Roma Tre”, the Council for the Research in Agriculture, the Ministry for the Environment and the Lombardy Region. Registration is free and the workshop is open to 80 attendees.

For registration, detailed information and contacts please visit www.wsmipp2017.eu. The MIPP Project is co-funded by the LIFE financial instrument of the European Union.

Gloria Antonini <gloria.antonini@uniroma1.it>

MaxPlanck GraduateMeeting EvolBiol Deadline Jan15 2

Love the whooshing noise* of deadlines as they pass by? Here is one to remember: Registration is due Jan 15 for the

22nd Graduate Meeting in Evolutionary Biology

of the Germany Zoological Society (DZG) from 19th to 21st of April 2017 at the Max Planck Institute for Evolutionary Biology in Ploen, Germany (meeting will be in English!).

The 2017 theme of the graduate meeting will be “Antagonistic Coevolution”, but the meeting is open to all graduate/PhD students and early postdocs in evolution-

ary biology.

Please visit the meeting website for more information and registration:

<http://web.evolbio.mpg.de/coevolve> The main goal of the meeting is to foster interactions among early career evolutionary biologists and provide opportunities for presenting your work in a semi-official environment. The program includes time slots for both oral and poster presentations.

Keynote speakers: Kayla King (Oxford University)
Sylvain Gandon (CEFE Montpellier)

Local organizers: Tobias Lenz Lutz Becks

Deadline for registration is January 15th 2017.

* “I love deadlines. I love the whooshing noise they make as they go by.” - Douglas Adams, *The Salmon of Doubt*

<lenz@evolbio.mpg.de> <lenz@evolbio.mpg.de>

MaxPlanckInst EvolBio GraduateMeeting Coevolution Deadline Jan15

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Sylvain Gandon (CEFE Montpellier)

Local organizers: Tobias Lenz Lutz Becks

Deadline for registration is January 15th 2017.
 "lenz@evolbio.mpg.de" <lenz@evolbio.mpg.de>

Naples EMBO Population Genomics May18-26

One month to the deadline for registration!

EMBO, in collaboration with the Elixir-ITA, Isita and the IGB-CNR, is pleased to inform you that the applications for the upcoming training course on "Population Genomics: background and tools" are open.

IMPORTANT DATES for this Course:

Deadline for applications: 24/02/2017

Latest notification of acceptance: 10/03/2017

Course date: 18-26/05/2017

Venue: National Research Council, Institute of Genetics and Biophysics, via P. Castellino 111, 80131 Naples, Italy

A maximum of 24 candidates will be selected based on their application.

Notifications of acceptance will be sent shortly after the closing date of registration.

Full details, including the course programme and the application form,

at: <http://meetings.embo.org/event/17-population-genomics> Instructors:

Aida Andres (Max Planck Institute for Evolutionary Anthropology, Germany) Andrea Manica (University of Cambridge, UK) Andrew Clark (Cornell University, USA) Garrett Hellenthal (University College London, UK) Ida Moltke (University of Copenhagen, Denmark) Martin Sikora (Natural History Museum of Denmark, Denmark) Mathias Currat (Université de Genève, Switzerland) Olivier Delaneau (Université de Genève, Switzerland) Pascale Gerbault (University of Westminster, UK)

Course description

Study methods in population genomics have been profoundly reshaped in the last few years thanks to the growing availability of complete genomic sequences at population level. The rapid and recent growth of data and methods calls for new approaches to become routine in evolutionary genomics laboratories. The objective of

this EMBO Practical Course is to give an overview of state of the art methods in population genomics combining lecturing from outstanding experienced population geneticists and software developers. All conceptual innovation will be presented in lectures and applied in practice both individually and in group work.

Practicals includes computer exercises supervised by lecturers and training assistants. After attending the course participants will be aware of up-to-date concepts in population genetics, capable of running analyses using software based on whole genome data sequences and able to deal with basic aspects of any population genomics project. This EMBO Practical Course aims at evolutionary biologists who already have bioinformatics skills. PhD students and Post-Doc researchers will benefit the most out of this course, but applications from all candidates will be evaluated in their context.

Thank you for your interest,

The Organisers

Chiara Batini (University of Leicester, UK) Vincenza Colonna (CNR, Napoli, IT) Allegra Via (CNR, Bari, IT)

"Batini, Chiara (Dr.)" <cb334@leicester.ac.uk>

NHM London Botanical Taxonomic Principles Mar6-10

Short course on taxonomic principles and tools in botanical research 6-10 March 2017, Natural History Museum, London Applications are open for a short course on plant taxonomy and identification funded by the UK's Natural Environment Research Council (NERC).

The course is taught by NHM taxonomic specialists and makes use of the outstanding botanical collections of the Museum. Specialist training is offered in vascular plants (flowering plants and ferns), bryophytes, lichens and marine macroalgae (red, brown and green seaweeds).

The course comprises two days of lectures and demonstrations and three days of practical sessions, comprising one day in the field and two days in the herbarium/laboratory.

The course is available to environmental science researchers and PhD students. There are 25 spaces available, and priority will be given to those with NERC funding.

The deadline for applications is 17th January 2017.

For more details see: <http://www.nhm.ac.uk/our-science/courses-and-students/short-course-taxonomic-principles-botanical-research.html> Mark Carine <M.Carine@nhm.ac.uk>

NHM London
Introductory MolecPylogenetics
May 8-12

Dear Colleagues,

The Natural History Museum, London and BBSRC are offering a one-week introductory course \hat{A}^3 Integrating molecules with taxonomy and systematics: an introductory molecular phylogenetics course for species identification and evolutionary analysis \hat{A}^2 , to run from 8-12th May 2017. The course will be taught by NHM scientists and will benefit anyone wishing to gain expertise in molecular diagnostics and phylogenetic analysis for systematic, taxonomic and ecological studies. Note that this course assumes no prior experience with DNA sequence analyses and is an introductory course. As such, it is not appropriate for more advanced students. More information can be found here: <http://www.nhm.ac.uk/our-science/courses-and-students/integrating-molecules-with-taxonomy-and-systematics.html>

Summary: This one-week introductory-level course will teach participants the steps involved to produce molecular phylogenies from raw Sanger and next-generation sequence data (i.e. Illumina paired-end). A phylogeny is essential for defining species boundaries, species identifications, recognition of cryptic species, testing systematic hypotheses, identifying evolutionary and biogeographic patterns and understanding the evolution of traits. As such, knowing how to produce a robust tree is an indispensable tool for modern taxonomists, systematists and evolutionary biologists. By the time the participants have completed the course, they will have had theoretical and practical experience enabling them to i) edit raw Sanger and NGS sequence data, ii) carry out multiple sequence alignments, iii) choose appropriate models of sequence evolution, iv) carry out phylogenetic analyses (including Bayesian inference, maximum likelihood), v) interpret tree topology and nodal support, vi) produce publication ready trees, vii) work with public sequence repositories, viii) assemble and annotate next generation sequence data, and viii) recognise cryptic species.

Venue and duration: The Natural History Museum, London, UK. The course will run for one week, 9.30am-6.00pm, 8-12th May 2017.

Eligibility and how to apply: The course is available to anyone but please note that priority will be given to applicants supported by BBSRC, working on a BBSRC grant or based at a BBSRC institute. There are a maximum of 12 places available. The course is sponsored by BBSRC and the NHM and we are charging only a nominal fee of 300, which includes all course costs as well as accommodation in London and some travel costs within the UK. Lunch and light refreshments will be provided each day. To apply please use the application form provided and return by the closing date: 31 March 2017. Applications will be accepted up to the deadline and places will be decided based on merit and suitability.

Email applications to: molec.NHMBBSRC@nhm.ac.uk (Note that this is an automated email account \hat{A} do not send queries. Your application will receive a bounce back message so you know it has arrived safely). Application forms can be found here: <http://www.nhm.ac.uk/our-science/courses-and-students/integrating-molecules-with-taxonomy-and-systematics.html>

Dr Suzanne Williams Dept of Life Sciences Natural History Museum Cromwell Rd London SW7 5BD United Kingdom Tel: + 44 (0) 207 942 5351

<http://www.nhm.ac.uk/research-curation/-staff-directory/zoology/s-williams/index.html>
"s.williams@nhm.ac.uk" <s.williams@nhm.ac.uk>

NordU Norway
NGS Of Non Model Organisms
May 31-June 1

Course: NordUNorway. HighThroughputSequencingOfNonModelOrganisms. May31-June1

High throughput sequencing (HTS) technologies are being applied to a wide range of important topics in biology. However, the analyses of non-model organisms, for which little previous sequence information is available, pose specific problems. This course will address the specific strengths and weaknesses of alternative HTS technologies, the computational resources needed for HTS, and how to analyze non-model species using HTS. The course consists of practical training in preparing and running fragment libraries, HTS bioinformatics training, and lecturing/seminars of HTS approaches specifically

targeting non-model organisms.

A detailed course description is available here.

We will accept a maximum of 10 students. The closing date for applications is April 29.

If you have questions regarding the course, please contact Prof. Truls Moum at truls.b.moum@nord.no

“Alexander-Jueterbock@web.de” <Alexander-Jueterbock@web.de>

**Paris CoevolutionFitnessLandscape-
sEpistasis
Mar1-3**

Dear colleagues,

A *small* workshop entitled “co-evolution, fitness landscapes and epistasis” will take place in Paris, at the “Museum National d’Histoire Naturelle”, 1-3 March 2017.

The workshop aims at gathering scientists with various backgrounds (biologists, computer scientists, physicists and mathematicians) who work on the co-evolution within genomes, the fitness landscapes or even more generally on epistasis. The working time will be evenly split between presentations and questions / discussions. The list of confirmed speakers is provided below.

It will start on wednesday (March the 1st) at lunch and will end on friday (March the 3rd) at lunch. Workshop registration is free but mandatory (!). Meals expenses are not included but attendees will be encouraged to join common lunches in restaurants nearby as well as the diner of thursday evening. Travel and hotel expenses are also left to participants.

The number of attendees is limited to 50. Few slots are available for contributed talks.

To register to the workshop, please reply to this email (to guillaume.achaz@mnhn.fr) and fill the following form:

- Full Name : - Affiliation(s) : - Email :

If you would like to present your work (beware that only few slots are available), please also provide:

- a title - a list of the author(s) - an abstract.

** Confirmed speakers **

Thomas Bataillon (Université de Aarhus, DK) Claudia Bank (Gulbenkian Institute, Lisbonne, PT) Alessandra Carbone (UPMC, Paris, FR) Kristina Crona (Wash-

ington DC, USA) Luis-Miguel Chevin (CEPHE, Montpellier, FR) Julien Dutheil (Institut Max Planck, Plön, DE) Luca Ferretti (Pribright Institute, UK) Raphaël Guerois (CEA, Paris, FR) Joachim Krug (Université de Cologne, DE) Thomas Lenormand (CEFE, Montpellier FR) Guillaume Martin (ISEM, Montpellier, FR) Sebastian Matuszewski (EPFL, Lausanne, SW) Olivier Tenaillon (Hopital Bichat, Paris, FR) Richard Watson (Southampton University, UK) Martin Weigt (UPMC, Paris, FR) Daniel Weinreich (Brown University, Providence, US)

We hope to see you in Paris to share this exciting scientific event,

Yours sincerely,

The organizing comitee (Guillaume Achaz, Sophie Brouillet, Mathilde Carpentier, Joël Pothier and Eduardo Rocha)

“guillaume.achaz@mnhn.fr”
<guillaume.achaz@mnhn.fr>

**Pconos FunctionalGenomics
May25-26**

We are pleased to announce a “Workshop on Ecological Functional Genomics” in the Poconos, May 25-26, 2017.

See <http://www.lacawac.org/workshop-on-ecological-functional-genomics.html> for more information.

The workshop will include the following instructors: -David Liberles, Temple University -Liang Liu, University of Georgia -Ananias Escalante, Temple University -Stephanie Spielman, Temple University -Rob Kulathinal, Temple University

The intended audience for the workshop is research active undergraduates, graduate students, and postdoctoral researchers, although more senior researchers will also be accepted as space permits. There are a limited number of full scholarships available for undergraduate researchers to attend.

The workshop will include a mix of lectures and a chance to bring your own dataset and analyze it with guidance from workshop instructors.

Feel free to email with any questions. David Liberles daliberles@temple.edu

David A Liberles <tuf77157@temple.edu>

Portugal Nature Mar20-24

Course Nature-Based Design Frameworks organized by Gil Penha-Lopes and Hugo Oliveira (CCIAM, cE3c) | March 20th-24th 2017 @ Lisbon, Portugal

Objectives: The course will introduce participants to different Nature-based bodies of knowledge and experience, such as the Biomimicry, Permaculture and Resilience topics. With almost 2 days per topic, the students will get a good feeling of how these topics see, do research and implement effective and sustainable solutions targeting a wide variety of societal, ecological and economic challenges.

Course instructors Gil Penha-Lopes (Invited Assistant Professor at FCUL, Leader of the Subgroup 'Adaptation and Sustainability', CCIAM, cE3c) <http://ce3c.ciencias.ulisboa.pt/member/gil-pessanha-penha-lobes> And Hugo Oliveira (PhD student, CCIAM, cE3c) <http://ce3c.ciencias.ulisboa.pt/member/hugo-ferreira-calado-de-oliveira> Intended audience: This five days intensive course will be open to a maximum number of 24 participants, being directed to PhD or MSc students in Biology, Environmental studies, Geography or related areas, and postdocs and other professionals working in related topics. Minimal formation of students: Bachelor in Biology, Geography or related areas.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL; UP) and Biology and Ecology of Global Changes (BEAG UL; UA). For information of fees for other participants see the programme details.

Deadline for applications: February 24th, 2017 Candidates should send a short CV and motivation letter to Gil Penha-Lopes (email gppenha-lobes@fc.ul.pt) and ngela Antunes (email amantunes@fc.ul.pt).

For additional details about the course and to know how to register, click here: <http://ce3c.ciencias.ulisboa.pt/-training/?cat=8> For more information about the course, please contact: gppenha-lobes@fc.ul.pt

Margarida Matos <mmmatos@fc.ul.pt>

UCalifornia Davis AppliedPhylogenetics Mar11-18

[FINAL NOTICE] UC Davis WORKSHOP IN APPLIED PHYLOGENETICS at Bodega Marine Laboratory, Bodega Bay, California

March 11-18, 2017

Sponsored by the University of California, Davis and Bodega Marine Laboratory

website: <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 all 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 seventeenth 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 beautiful Northern California coast, which has on-site housing. The course format will involve equal parts of lecture and hands-on software training (with an emphasis on performing analyses using RevBayes: <http://revbayes.github.io/about.html>). 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 * Diagnos-

ing MCMC performance * Divergence-time estimation: relaxed clocks, fossil calibration * Species-tree estimation and species delimitation * Character evolution: ancestral-state estimation, rates of trait evolution * Lineage diversification: detecting rate shifts, testing key-innovation hypotheses

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 generally 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 11, leaving March 18) and return transportation from Davis to the Bodega Marine Labs.

Application Deadline Applications are due by January 31, 2017. 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. Students will be notified via e-mail by February 4, 2017 of acceptance.

Application Forms and Information Visit the Bodega website for additional information and to download an application form: <http://treethinkers.org/> 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 email: mikeryanmay@gmail.com

UCalifornia Davis AppliedPhylo Mar11-18

[SECOND NOTICE] UC Davis WORKSHOP IN APPLIED PHYLOGENETICS at Bodega Marine Laboratory, Bodega Bay, California

March 11-18, 2017

Sponsored by the University of California, Davis and Bodega Marine Laboratory

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Mike May Department of Evolution and Ecology 5343 Storer Hall University of California Davis Davis, CA 95616 email: mikeryanmay@gmail.com

“brianmoore@ucdavis.edu” <brianmoore@ucdavis.edu>

UCalifornia Davis Phylogenetics Mar11-18

UC Davis WORKSHOP IN APPLIED PHYLOGENETICS at Bodega Marine Laboratory, Bodega Bay, California

March 11-18, 2017

Sponsored by the University of California, Davis and Bodega Marine Laboratory

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“brianmoore@ucdavis.edu” <brianmoore@ucdavis.edu>

UCalifornia LosAngeles ConservationGenomics

UCLA/La Kretz Workshop in Conservation Genomics, 25 - 29 March, 2017 Conservation biology, genetics, and evolutionary biology have had a long and intimate relationship, and conservation constitutes one of the key applications of evolutionary analysis to real-world biological problems. The impacts of population and landscape genetics and gene expression studies have been particularly striking, and are helping to solve some of the most pressing problems in biological conservation.

As the field of conservation genetics continues to grow and mature, the availability of genome-scale data stand to make profound new contributions to our ability to identify and protect at-risk populations and recover those that are most endangered. However, genomic analyses also carry a heavy burden—data sets are enormous, often requiring diverse computational approaches for assembly, quality control and analysis.

The La Kretz annual workshop provides a comfortable, rigorous, but informal training environment for a small group of motivated graduate students to explore how conservation problems can best be addressed with genomic-level data. Our goal is to provide hands-on experience in the efficient collection, troubleshooting, and analysis of large data sets for conservation-relevant problems. One of the highlights of our workshop is active participation from members of several governmental agencies who are at the forefront of endangered species protection and management, providing a forum for exploring the most relevant aspects of conservation genomics to managers.

The UCLA/La Kretz workshop is held at the La Kretz Field Station (<https://www.ioes.ucla.edu/santa-monica-mountains-research/>) and Stunt Ranch Reserve (<http://stuntranch.ucnr.org/>) in the heart of the Santa Monica Mountains. Only 30 miles from UCLA and the LAX airport, but nestled in the relatively undeveloped 160,000 acre Santa Monica Mountains National Recreation Area, the Field Station/Stunt Reserve provides an ideal location to explore new developments in genomic science and pressing needs in conservation and management together in a single setting.

Our current instructor list, drawn from UCLA faculty and several other partner institutions, includes: Ben

Fitzpatrick (U. Tennessee Knoxville) Kirk Lohmueller Evan McCartney-Melstad Ian Wang (UC Berkeley, tentative) Brad Shaffer Victoria Sork Bob Wayne Ying Zhen Erin Toffelmier Alice Mouton/Devaughn Fraser Emily Curd/Zach Gold Agency partners represented include: USGS BLM USFWS CDFW

Topics covered include: Overview of traditional conservation genetics Next generation platforms: the best tool for the job Data management pipelines: Quality Control Data storage Data organization Data types and analyses: SNPs Sequences Exploring very large data sets Functional genomic data RNA-seq RADseq pipelines, from raw reads to analyzing data Genomic data and GIS Visualizing geographic structure and demographic history Admixture, clines, and hybridization Detecting adaptive variation RNAseq in a conservation context eDNA as an emerging tool Prerequisites: Available housing limits course enrollment to ~20 students. Preference will be given to masters and doctoral candidates who are in the early to middle stages of their thesis research, and who have some familiarity with using a command line interface or programming languages (i.e. Perl, python etc.). We also welcome applications from postdocs, faculty, and government researchers, although our top priority is graduate student applicants. We encourage applications from women, minorities, and individuals from under-represented demographics in the sciences.

Admission and Fees: Applicants will be admitted based on academic qualifications and appropriateness of research interests. The course fee is \$425. This includes food and lodging at the La Kretz Field Station, as well as any incidental fees, for the duration of the course (arriving Saturday March 25, departing Thursday March 30).

This year, the workshop is co-sponsored by a UC Catalyst program grant, which will provide some student support and staffing. University of California students from any campus may apply for partial support (up to \$225) from the newly awarded Conservation Genomics Consortium (<https://uconservationgenomics.eeb.ucla.edu/>) funded under the UC Catalyst program. To do so, simply note in your application that you would like to apply for this partial support.

UCLA students are encouraged to take the La Kretz Workshop for graduate credit. Other UC students may also be able to take the course for credit.

Application Forms and Information: Visit the UCLA/La Kretz Center for California Conservation Science website for additional information:

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To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evodir.html>

UEdinburgh 4 PythonLinux Apr10-Jul28

ADVANCED PYTHON FOR BIOLOGISTS

DATE: Monday 24 - Friday 28 July 2017 VENUE: The King's Buildings, The University of Edinburgh, Edinburgh, Scotland, UK REGISTRATION DEADLINE: Monday 10 July 2017 noon CANCELLATION DEADLINE: Monday 17 July 2017 noon PLACES: 20 (first come, first served) REGISTRATION FEE: pounds 525 (includes coffee/tea, but no lunch) INFORMATION: Bert Overduin (bert.overduin@ed.ac.uk), Martin Jones (martin@pythonforbiologists.com)

TO REGISTER: <http://genomics.ed.ac.uk/services/advanced-python-biologists> Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at people who already have a basic knowledge of Python and are interested in using the language to tackle larger problems. In it, we will look in detail at the parts of the language which are particularly useful in scientific programming, and at the tools Python offers for making development faster and easier. The workshop will use examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) take advantage of the advanced language features in their own programs and (2) use appropriate tools when developing software programs.

“Just what I needed to start writing more complex code.” (August 2015)

“I also liked the fact that Martin spent a good amount of one on one time talking to people helping explain specific concepts and giving people advice on their personal academic projects.” (July 2016) INSTRUCTORS

Dr. Martin Jones (Founder, Python for Biologists) Dr. Bert Overduin (Training and Outreach Bioinformatician, Edinburgh Genomics)

WORKSHOP FORMAT

The workshop is delivered over ten half-day sessions. Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at

the organiser's discretion. Each session uses examples and exercises that build on material from the previous one, so it's important that students attend all sessions. A description of the sessions can be found at the bottom of this page.

WHO SHOULD ATTEND

This workshop is aimed at researchers and technical workers with a background in biology and a basic knowledge of Python.

Note that we are also offering a workshop Data Manipulation and Visualisation with Python. The Advanced course is aimed at people who want to develop bigger or more complicated programs in Python, or to learn more about the language, or to explore different approaches (object-oriented, functional) to programming. The material covered is very general purpose and can be applied to any kind of problem. The Dataviz course is about using a set of Python libraries that are specifically designed for data exploration and visualisation. In the Dataviz course, we're going to concentrate on using these tools to explore patterns in data, but the actual code that we write will be very simple - mostly we will be calling the functions and methods in these libraries.

To summarise: if you want to learn more about the language, build more complicated programs, or need to work with existing complicated programs, attend the Advanced course. If you want to explore datasets, find patterns, produce figures and charts, attend the Dataviz course.

REQUIREMENTS

Students should have enough biological/bioinformatics background to appreciate the examples and exercise problems (i.e. they should know what a protein accession number, BLAST report, and FASTA sequence is). They should also have basic Python experience (the Edinburgh Genomics Introduction to Python for Biologists course will fulfil these requirements). Students should be familiar with the use of lists, loops, functions and conditions in Python and have written at least a few small programs from scratch. During the workshop students will use their own laptops. Instructions for any software to be installed will be sent out prior to the course.

SESSION CONTENT

1. Data structures in Python

In this session we will briefly recap Python's basic data structures, before looking at a couple of new data types “tuples and sets” and discussing where each should be used. We will then see how we can combine these basic types to make more complex data structures for

solving specific problems. We'll finish our discussion by looking at specialized data types that are found in the Python core library. This session will also be our first introduction to benchmarking as we talk about the relative performance of different data types. In the practical session we'll learn how to parse an input file into a complex data structure which we can then use to rapidly query the data. Core concepts introduced: tuples, sets, higher-order data structures, default dicts, Counters, big-O notation.

2. Recursion and trees

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UK LandscapeGeneticsAnalysisUsingR Nov6-10

“Landscape (population) genetic data analysis using R”

Delivered by Dr. Rodney Dyer

<http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg02/> This course will run from 6th - 10th November 2016 at Margam Discovery Centre, Wales.

The term 'landscape genetics' has been applied studies that integrate ecological context and intervening landscape into population genetic analyses of contemporary processes such as gene flow and migration. This course will cover the basics of both quantitative landscape ecology and population genetics, focusing on how we develop and evaluate spatial/genetic analyses using the R platform

Course content is as follows Day 1 - Spatial & Ecological Data - Installation & configuring R & RStudio - Acquiring spatial data, projections, and visualization - Vector and raster data

Day 2 - Genetic markers and basic analyses - Genetic markers and sampling - Genetic distance, diversity, and structure - Ordination techniques based upon genetic markers

Day 3 - Integrating spatial and genetic data - Barrier detection & population division - Resistance Modeling

- Mantel and distance regressions - Remote sensing - LiDAR and Hyperspectral data

Day 4 - Integrating spatial and genetic data - Spatial autocorrelation - Network Approaches - PCMN & Redundancy

Day 5 - Adaptive Genetic Variance - Outliers & gradients - Quantitative genetics, why we should care. - Chromosome walking

Please email any inquiries to oliver-hooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

Upcoming courses - email for details oliver-hooker@prstatistics.com

1. ADVANCED PYTHON FOR BIOLOGISTS (February 2017) #APYB <http://www.prstatistics.com/course/advanced-python-biologists-apyb01/>
2. STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR USING R (February 2017) #SIMM <http://www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm03/>
3. NETWORK ANALYSIS FOR ECOLOGISTS USING R (March 2017) #NTWA <http://www.prstatistics.com/course/network-analysis-ecologists-ntwa01/>
4. ADVANCES IN MULTIVARIATE ANALYSIS OF SPATIAL ECOLOGICAL DATA (April 2017) #MVSP <http://www.prstatistics.com/course/advances-in-spatial-analysis-of-multivariate-ecological-data-theory-and-practice-mvsp02/>
5. INTRODUCTION TO STATISTICS AND R FOR BIOLOGISTS (April 2017) #IRFB <http://www.prstatistics.com/course/introduction-to-statistics-and-r-for-biologists-irfb02/>
6. ADVANCING IN STATISTICAL MODELLING USING R (April 2017) #ADVR <http://www.prstatistics.com/course/advancing-statistical-modelling-using-r-advr05/>
7. GEOMETRIC MORPHOMETRICS USING R (June 2017) #GMMR <http://www.prstatistics.com/course/geometric-morphometrics-using-r-gmmr01/>
8. MULTIVARIATE ANALYSIS OF SPATIAL ECOLOGICAL DATA (June 2017) #MASE <http://www.prstatistics.com/course/multivariate-analysis-of-spatial-ecological-data-using-r-mase01/>
9. TIME SERIES MODELS FOR ECOLOGISTS USING R (JUNE 2017) (#TSME)
10. BIOINFORMATICS FOR GENETICISTS AND BIOLOGISTS (July 2017) #BIGB <http://www.prstatistics.com/course/bioinformatics-for-geneticists-and-biologists-bigb02/>
11. SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R (August 2017) #SPAEC <http://www.prstatistics.com/course/spatial-analysis-ecological-data-using-r-spaec05/>

12. ECOLOGICAL NICHE MODELLING (October 2017) #ENMR <http://www.prstatistics.com/course/-ecological-niche-modelling-using-r-enmr01/> 13. INTRODUCTION TO BIOINFORMATICS USING LINUX (October 2017) #IBUL

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UK TwoPythonCourses Nov27-Dec1

Two Python courses: INTRODUCTION TO PYTHON FOR BIOLOGISTS DATA VISUALISATION AND MANIPULATION USING PYTHON (below)

INTRODUCTION TO PYTHON FOR BIOLOGISTS

<http://www.prstatistics.com/course/introduction-to-python-for-biologists-ipyb04/> This course is being delivered by Dr Martin Jones, an expert in Python and author of two text books,

Python for Biologists [<http://www.amazon.com/-Python-Biologists-complete-programming-beginners/-dp/1492346136/>] Advanced Python for Biologists [<http://www.amazon.com/Advanced-Python-Biologists-Martin-Jones/dp/1495244377/>]. Course overview: Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at complete beginners and assumes no prior programming experience. It gives an overview of the language with an emphasis on practical problem-solving, using examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackle problems in their own research and (2) continue their Python education in a self-directed way. Intended audience:

This workshop is aimed at all researchers and technical workers with a background in biology who want to learn programming. The syllabus has been planned with complete beginners in mind; people with previous programming experience are welcome to attend as a refresher but may find the pace a bit slow. Teaching format:

The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizer's discretion. There will also be plenty of time for students to discuss their own problems and data.

Assumed background: Students should have enough biological background to appreciate the examples and exercise problems (i.e. they should know about DNA and protein sequences, what translation is, and what introns and exons are). No previous programming experience or computer skills (beyond the ability to use a text editor) are necessary, but you'll need to have a laptop with Python installed.

Curriculum: Day 1: Module 1 - Introduction Module 2 - Output and text manipulation

Day 2: Module 3 - File IO and user interfaces Module 4 - Flow control 1: loops

Day 3: Module 5 - Flow control 2: conditionals Module 6 - Organizing and structuring code

Day 4: Module 7 - Regular expressions Module 8 - Dictionaries

Day 5: Module 9 - Interaction with the file system Module 10 - Optional free afternoon to cover previous modules and discuss data

Please email any inquiries to oliver-hooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

Other bioinformatics courses

ADVANCED PYTHON FOR BIOLOGISTS (February 2017) #APYB <http://www.prstatistics.com/course/-advanced-python-biologists-apyb01/> BIOINFORMATICS FOR GENETICISTS AND BIOLOGISTS (July 2017) #BIGB <http://www.prstatistics.com/course/bioinformatics-for-geneticists-and-biologists-bigb02/> INTRODUCTION TO BIOINFORMATICS USING LINUX (October 2017) #IBUL <http://www.prstatistics.com/course/introduction-to-bioinformatics-using-linux-ibul02/> DATA VISUALISATION AND MANIPULATION USING PYTHON (December 2017) #DVMP <http://www.prstatistics.com/course/data-visualisation-and-manipulation-using-python-dvmp01/> Other evolutionary statistics courses

INTRODUCTION TO STATISTICS AND R FOR BIOLOGISTS (April 2017) #IRFB <http://www.prstatistics.com/course/introduction-to-statistics-and-r-for-biologists-irfb02/> ADVANCING IN STATISTICAL MODELLING USING R (April 2017) #ADVR

<http://www.prstatistics.com/course/advancing-statistical-modelling-using-r-advr05/> GEOMETRIC MORPHOMETRICS USING R (June 2017) #GMMR

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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>

UMichigan NextProf May2-5

*NextProf** Science - Future Faculty Workshop *

We would like to invite interested evolutionary biologists to the NextProf Future Faculty Workshop at the University of Michigan. *NextProf Science *will be held May 2-5, 2017 and is a workshop designed to encourage talented scientists and mathematicians with a demonstrated commitment to diversity to consider academia as a career. The workshop is aimed at helping participants develop strategies that will strengthen their ability to pursue academic careers. The workshop is targeted at scholars ready to make take the next step –postdoctoral fellows and very advanced doctoral students. Underrepresented minorities and women are especially encouraged to apply. Travel, lodging, and meals will be provided for those selected to participate. Deadline for submission of all application materials is February 15, 2017. Learn more at: sites.lsa.umich.edu/nextprof-science.

Best wishes,

Gina Baucom

Regina S Baucom Assistant Professor 2059 Kraus Natural Science Building 830 North University Dept of EEB University of Michigan Ann Arbor, MI 48109 (734) 647-8490 <http://sites.lsa.umich.edu/baucom-lab> rsbaucom@umich.edu

UWashington EvolQuantGenetics Jun5-9

Evolutionary Quantitative Genetics Workshop

Friday Harbor Laboratories, University of Washington, 5-9 June 2017

Non-credit workshop. Participants arrive at Friday Harbor Labs on Sunday, June 4, lectures and exercises occur June 5-9, and participants depart on Saturday, June 10, 2017.

Application deadline March 1, 2017. Application forms and details here: <http://tinyurl.com/-EQG2017> Web page: <http://depts.washington.edu/fhl/studentSummer2017.html#SumB-genetics> Instructors:

Dr. Joe Felsenstein Department of Genome Sciences University of Washington, Seattle joe@gs.washington.edu

Dr. Stevan J. Arnold Department of Integrative Biology Oregon State University, Corvallis stevan.arnold@oregonstate.edu

Previous versions of this 5-day workshop were given at the National Evolutionary Synthesis Center (NES-CENT) at Duke University in Durham, North Carolina from 2011-2013, and then at the National Institute for Mathematical and Biological Synthesis (NIMBioS) at the University of Tennessee in Knoxville from 2014-2016. Like past versions, the Friday Harbor version will review the basics of theory in the field of evolutionary quantitative genetics and its connections to evolution observed at various time scales. The aim of the workshop is to build a bridge between the traditionally separate disciplines of quantitative genetics and comparative methods.

Quantitative genetic theory for natural populations was developed considerably in the period from 1970 to 1990 and up to the present, and it has been applied to a wide range of phenomena including the evolution of differences between the sexes, sexual preferences, life history traits, plasticity of traits, as well as the evolution of body size and other morphological measurements. Textbooks have not kept pace with these developments, and currently few universities offer courses in this subject aimed at evolutionary biologists. Evolutionary biologists need to understand this field because of the ability to collect large amounts of data by computer, the development of statistical methods for changes of traits on evolutionary trees and for changes in a single species through time, and the realization that quantitative characters will not soon be fully explained by genomics. This workshop aims to fill this need by reviewing basic aspects of theory and illustrating how that theory can be tested with data, both from single species and with multiple-species phylogenies. Participants will use R, an open-source statistical programming language, to build and test evolutionary models.

The workshop involves lectures and in-class computer exercises. You can consult the 2016 tutorial website for examples, it will be found at <http://www.nimbios.org/-tutorials/TT.eqg2016> The intended participants for this

tutorial are graduate students, post-docs, and junior faculty members in evolutionary biology. The workshop can accommodate up to 35 participants. Guest instructors will include:

- * Marguerite Butler, Biology, Univ. Hawai'i, Mānoa
- * Patrick Carter, Evolutionary Physiology, Washington State University, Pullman
- * Adam Jones, Biology, Texas A&M University, College Station
- * Brian O'Meara, Ecology & Evolutionary Biology, Univ. of Tennessee, Knoxville
- * Josef Uyeda, Biological Sciences,

Virginia Tech, Blacksburg

Cost: \$1000 to be paid to Friday Harbor Laboratories. This fee will cover housing and meals at FHL and all other workshop expenses, except travel. Participants who have been admitted to attend will make their payment prior to arrival at FHL. Details of payment by credit card or check will be provided once the applicant has been admitted to attend.

Joe Felsenstein <joe@gs.washington.edu>

Instructions

Instructions: To be added to the EvoDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the 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 L^AT_EX 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 \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.