
E v o l D i r

July 1, 2018

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.



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Conferences

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Edinburgh FisherCentenary Oct9

Meeting to celebrate the centennial of R.A. Fisher's famous 1918 paper on the theory of quantitative trait inheritance:

100 years of quantitative genetics theory and its applications: celebrating the centenary of Fisher 1918

The meeting will take place on Tuesday October 9, 2018, at the Royal College of Surgeons, Edinburgh (<https://www.rcsed.ac.uk/>). There will be 8 invited speakers, with the Fisher Memorial Lecture at 5pm, followed by a reception.

In addition, 4 early career speakers and up to 30 posters will be selected from submitted abstracts by the organising committee.

Registration is through a website provided by the Royal Statistical Society (https://events.rss.org.uk/rss/frontend/reg/thome.csp?pageID=71232&ef_sel_menu=-1389&eventID=230).

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CHARLESWORTH
<Brian.Charlesworth@ed.ac.uk>

Brian

ExeterU GenotypeToFitness Nov22-23

Dear all,

On behalf of the Genetics Society of the UK we are pleased to extend a very warm invitation to the 2018 autumn meeting - Genotype to Phenotype to Fitness. The meeting will be held on 22-23 November 2018 at Reed Hall, Exeter University, UK.

Registration and abstract submission is now OPEN at <https://my.genetics.org.uk/item.php?eventid=1014>

The meeting will bring together researchers working with diverse genetic techniques across a multitude of systems, but who are nonetheless connected by a shared passion for understanding adaptive evolution. The meeting will have four themed open sessions over the two days, each session featuring 2-3 of our invited speakers

together with contributed talks and posters selected from abstracts submitted. The four themed sessions are titled Genotype to Phenotype, Constraint and Conflict, Genes in Environments and Micro to Macro. We encourage everyone to interpret these themes broadly - they are intended to help identify common ground for discussion, not to limit scientific scope! In addition to the open sessions there will be an Early Career Researcher symposium offering opportunities for early career researchers to present in an especially supportive environment.

Confirmed Speakers: Matthew Webster (Uppsala), Nina Wedell (Exeter), Patrik Nosil (Sheffield), Susan Johnston (Edinburgh), Edze Westra (Exeter), Chris Jiggins (Cambridge), Anne Charmantier (Montpellier), Miltos Tsiantis (Max Planck, Cologne), Katrina McGuigan (Queensland), Walter Salzburger (Basel)

Abstract deadline: 31st August 2018

For further information: <http://www.genetics.org.uk/-events/genotype-to-phenotype-to-fitness/> Best wishes,

Alastair Wilson, Ben Longdon, Kay Boulton, Frank Hailer, Helena

Autumn Meeting Organising Committee

“Wilson, Alastair” <A.Wilson@exeter.ac.uk>

Marseilles EvolBiol Sep25-28 Deadline

Dear All , the dead line for the : 22nd evolutionary biology meeting at Marseilles

(September 25-28 2018) is June 30. See aeb.fr and follow the evolutionary biology meeting link.

best regards Pierre

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

MLBS Virginia SEPEEG EvolutionaryGenetics Oct5-7

Please join us for the 44th annual SEPEEG conference at Mountain Lake Biological Station (MLBS). The con-

ference will be held Oct. 5th-7th, 2018. The scientific fields represented at the meeting are diverse, and span evolution, ecology, genetics, and behavior. SEPEEG is a single-session meeting that provides a comfortable, engaging environment for formal and informal interactions between attendees. The meeting generally attracts at least 120 participants, who are at all career stages and from diverse institutions throughout the southeastern United States.

Please visit <http://mlbs.virginia.edu/SEPEEG-2018> for more information.

Registration Cost: Registration cost covers room, food, and conference expenses. General Registration Rate: \$135 Student Members of the American Society of Naturalists: \$90 Conference Attendees staying off site: \$105 (food is included in this cost)

Joshua Puzey <jrpuzey@gmail.com>

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Joshua Puzey <jrpuzey@gmail.com>

Oslo EcolEvolutionGenomics Aug30

Dear Colleagues,

The Centre for Ecological and Evolutionary Synthesis (CEES) at the Department of Biosciences, University of Oslo, is pleased to announce the 2018 Oslo Symposium on Ecology, Evolution and Genomics.

Symposium website: <http://www.mn.uio.no/cees/english/research/news/events/research/others/2018/oslo-symposium-on-ecology-evolution-and-genomics/>
The co-organisers are CEES Chair Nils Chr. Stenseth and CEES Researcher Jeffrey Hutchings (Dalhousie University, Canada).

Symposium Theme: Bridging the Fundamentals of Ecology, Evolution, and Genomics: Challenges and Solutions.

Location and Details: 30 August 2018 (9:00 am - 5:00 pm) at the Gamle festsal, Domus Academica, Karl Johans gate 47 in central Oslo. This year's Oslo Symposium on Ecology, Evolution and Genomics will feature six invited plenary talks followed by a poster session for postgraduate students (MSc, PhD), postdoctoral researchers, and interested attendees.

Keynote speaker: Spencer Barrett (University of Toronto, Toronto, CANADA).

Plenary speakers: Per Ahlberg (Uppsala University, Uppsala, SWEDEN), Kirsten Bomblies (John Innes Centre, Norwich, UK), Felicity Jones (Friedrich Miescher Laboratory, Max Plank Institute, Tübingen, GERMANY), Judith Mank (University College London, UK; University of British Columbia, CANADA), Rebekah Oomen (Dalhousie University, Halifax, CANADA; CEES, University of Oslo, NORWAY).

Format and objectives: The plenaries will allow time for contemplative, but provocative, presentations and discussions. In preparing their talks, the invited speakers have been asked to think broadly about fundamental questions in ecology and evolution for which genomics has played an integral role. Speakers also have been asked to look ahead to identify questions that might soon be answerable, to identify challenges that might affect such research progress, and to offer solutions and ideas as to how the scientific community might best proceed. The plenary talks will be followed by a poster session by interested graduate students, postdocs, and

established researchers.

Registration: There is no registration fee for attending the Oslo Symposium. However, because of seating-capacity restrictions, attendees do need to register their names and affiliations. Link to registration form: <https://skjema.uio.no/oslo-symposium-on-eco-evo-geno> Further information: Please contact Jeffrey Hutchings (jhutch@dal.ca) or Nils Chr. Stenseth (n.c.stenseth@ibv.uio.no).

Tore Wallem <tore.wallem@ibv.uio.no>

ParkCityUtah EvolutionaryMedicine Aug1-4

CME now approved! The University of Utah School of Medicine has designated this meeting for up to 29.75 hours of AMA PRA Category I Credit.

The meeting also includes a special wilderness medicine preconference August 1st. <https://isemph.org/-annualmeeting#id.OOrfXfn> The 4th Annual International Society for the Evolution, Medicine & Public Health (ISEMPH) brings together evolutionary biologists, anthropologists, public health researchers and medical professionals to discuss the latest advances in using evolutionary biology to improve human health.

The meeting is Aug 1-4 in Park City, a recreation paradise just above Salt Lake City. Register now before fees go up. <https://isemph.org/annualmeeting>

The program is here <http://isemph.org> <https://evmedreview.com/isemph-meeting-program/> PLENARY SPEAKERS

EVOLUTION OF DISGUST AS A PARASITE AVOIDANCE BEHAVIOUR Val Curtis London School of Hygiene & Tropical Medicine

LEARNING AND PERTURBING THE EVOLUTIONARY MECHANISMS DRIVING THERAPEUTIC RESISTANCE IN CANCER AND PATHOGENS Jacob Scott Cleveland Clinic

BUILDING A COSTLY BRAIN: IMPLICATIONS FOR THE EVOLUTION OF HUMAN CHILDHOOD AND THE DEVELOPMENTAL ORIGINS OF METABOLIC DISEASE Chris Kuzawa Northwestern University

RESISTANCE EVOLUTION AND ITS MANAGEMENT IN A MULTI-DRUG HOSPITAL PATHOGEN Andrew Read Pennsylvania State University

ADOLESCENT REPRODUCTIVE DEBUT: LIFE HISTORY TRADEOFFS IN A CLINICAL CONTEXT
Katie Hinde Arizona State University

SPECIAL CME PRE-CONFERENCE: EVOLUTION AND WILDERNESS MEDICINE'S ADAPTATION TO EXTREME ENVIRONMENTS
Joe Alcock, Chair Faculty: Cynthia Beall, Rick Henriksen, Melissa Ilardo, Michael Lauria, Scott McIntosh, Diane Rimple, Blair Wolf

SYMPOSIUM I: EVOLUTION AND HEALTH BEHAVIOUR
Chair: Gillian Pepper
Presentations: Athena Aktipis, Bruce Ellis, Mike Gurven, Dandara Ramos

SYMPOSIUM II: COMPARATIVE ONCOLOGY
Co-Chairs: Athena Aktipis & Amy Boddy
Presentations: Lisa, Abegglen, Athena Aktipis, Amy Boddy, Valerie Harris

SYMPOSIUM III: NOVEL SOLUTIONS TO CHEMOTHERAPEUTIC RESISTANCE
Chairs: Michael Hochberg
Presentations: Sam Brown, Ben Chan, Michael Hochberg, Nina Wade

SYMPOSIUM IV: EVOLUTION AND MEDICINE IN LIGHT OF THE MICROBIOME
Chair: Seth Bordenstein
Presentations: Katherine Amato, Seth Bordenstein, Jennifer Stearns

SYMPOSIUM V: ADAPTATION AND CRITICAL CARE
Chair: Joe Alcock
Presentations: Scott Aberegg, Janelle Ayres, and John Marshall

Randolph Nesse <nesse@asu.edu>

Puerto Rico Evolutionary Anthro Nov1-4 Call Abstracts

APPROACHING DEADLINE - CALL FOR ABSTRACTS ALAB2018 (<http://www.pr-science.org>) XV CONGRESS of the Latin American Association of Biological Anthropology (ALAB2018) 1-4 NOVEMBER 2018, MAYAGUEZ, PUERTO-RICO

Abstract submission is still open for the 15th Congress of the Latin American Association for Biological Anthropology, that will take place in Mayagüez, Puerto Rico from November 1- 4, 2018.

The deadline for abstract submission is Friday, June 22nd, 2018. The ALAB is a corporation that brings together scholars interested in the fields of Physical Anthropology and Human Biology. Its members can be

located in Latin American countries or elsewhere if their investigations relate to Latin America.

The ALAB congresses are held every two years since 1990, offering Latin American researchers and to those interested in anthropological studies on Latin America a periodic opportunity for the discussion of scientific experiences and issues linked to the development of the discipline in a local, regional and continental context. The overall objective of the Congress is to bring together scholars in our field in a healthy environment for the contact, discussion of problems and new ideas, and the development of collaborative networks of researchers and students.

While preparing your abstract, please consider that:

Word count of an abstract is limited to 300 words, excluding the title, author names and affiliations.

You will need to specify in which symposium, if any, you want your abstract to be included. If you believe your submission does not fit in any of the available symposia, please specify "Other". New symposia could be built from the abstracts submitted. In addition, there will be space in the schedule for free communications.

Please specify if you wish your presentation to be oral or by poster. We will try to fulfill the wishes of everyone, but please be aware that we might be able to offer you only your second option.

Abstract acceptances will be published after July 27, 2018. Please visit our website at <http://www.pr-science.org/> for more information.

We are looking forward to hearing from you ALAB Organizing Committee Mayaguez, Puerto Rico

Taras K Oleksyk and Juan Carlos Martinez Cruzado
University of Puerto Rico at Mayaguez Mayaguez, PR
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Taras K Oleksyk <taras.oleksyk@upr.edu>

Salzburg Evolution Jul4-8

EVOLUTION - Genetic Novelty/Genomic Variations by RNA-Networks and Viruses

Salzburg, 4-8 July 2018, St. Virgil Conference Center

www.RNA-Networks.at Guenther Witzany

(organizer)

"Witzany Günther Mag. Dr."

<Guenther.Witzany@stadt-salzburg.at>

Sherbrooke RECOMB Oct9-12 DeadlineExtension

Hi,

Due to several requests, the deadline for paper submission for RECOMB Comparative Genomics 2018 has been moved to June 25th 2018.

See <https://recombcg2018.usherbrooke.ca/> for details about the conference.

Thank you!

Mathieu Blanchette - co-PC chair, RECOMB-CG 2018
Aida Ouangraoua - co-PC chair, RECOMB-CG 2018

Mathieu Blanchette <blanchem@cs.mcgill.ca>

Sherbrooke RECOMB Oct9-12 FinalCall

RECOMB-CG 2018, FINAL CALL FOR PAPERS

16th RECOMB Satellite Conference on Comparative Genomics, RECOMB-CG 2018

Magog-Orford (Sherbrooke), Quebec, Canada - October 9-12, 2018

<https://recombcg2018.usherbrooke.ca> SCOPE

The annual RECOMB Comparative Genomics Satellite Conference (RECOMB-CG) brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and the analysis of novel experimental results. The program will include keynote talks, contributed talks, and a poster session.

The 16th RECOMB-CG conference will be held at the Manoir des Sables, in beautiful Magog-Orford, near Sherbrooke, Québec, Canada on October 9-12 2018. With this Call for Papers we invite high-quality original full papers on topics related to the conference theme. The conference will also have a poster session. A detailed call for posters will be published later on the conference

web page.

TOPICS

Papers are solicited on, but not limited to, the following topics: - genome evolution - population genomics - genome rearrangements - genome variation, diversity and dynamics - phylogenomics - comparative tools for genome assembly - comparison of functional networks - gene identification and/or annotation - cancer evolutionary genomics - comparative epigenomics - paleogenomics - epidemiology

IMPORTANT DATES

- Paper Submission Deadline: June 18, 2018 - Author Notification: July 20, 2018 - Final Version Due: August 3, 2018 - Conference: October 9-12, 2018

DETAILS ON SUBMITTING MANUSCRIPTS

Submitted papers must have not been published or be currently under consideration for publication in any other journal or conference with formal proceedings. Each accepted paper has to be presented by one of the authors at the conference.

Accepted papers will be published in the conference proceedings, a volume in the Lecture Notes in Bioinformatics (LNBI) series. In addition, authors of selected papers will be invited, but not required, to submit a significantly extended version of their papers to Algorithms for Molecular Biology. Extended papers submitted will be handled by the Program Committee co-chairs. Authors who choose to publish their extended manuscripts will have to pay the journal's publication fees.

Authors are encouraged to submit their manuscripts in PDF format according to the LNBI series guidelines:

<http://www.springer.com/us/computer-science/lncs/-conference-proceedings-guidelines> Submitted papers must be within 15 pages (in the LNBI format), with optionally a clearly marked appendix containing supplementary material made available to the reviewers.

All submissions must be made online, through the EasyChair submission system, at the following address:

<https://easychair.org/conferences/?conf=recombcg2018>

Authors need to register on that web site before submitting. A standard PDF file must be received by midnight on June 18, 2018 (any time zone) in order for a submission to be considered. Re-submission of already submitted papers will be possible until midnight June 18, 2018 (any time zone).

CONFIRMED KEYNOTE SPEAKERS

Belinda Chang (Department of Ecology and Evolutionary Biology, University of Toronto, Canada) Dannie Du-

rand (Department of Biological Sciences, Carnegie Mellon University, USA) Daniel Durocher (The Lunenfeld-Tanenbaum Research Institute, Mount Sinai Hospital, University of Toronto, Canada) Christian Landry (Institute for Integrative Systems Biology, Laval University, Canada) Gwenaël Piganeau (Banyuls Oceanographic Observatory and National Centre for Scientific Research, France) Xavier Roucou (Department of Biochemistry, University of Sherbrooke, Canada)

PROGRAM COMMITTEE

Max Alekseyev (George Washington University) Lars Arvestad (Stockholm University) Sèverine Bérard (U. Montpellier) Mathieu Blanchette (McGill University), co-chair Anne Bergeron (U. du Québec à Montréal) Marília Braga (Bielefeld University) Alessandra Carbone (CNRS, Université Pierre et Marie Curie) Cedric Chauve (Simon Fraser University) Leonid Chindelevitch (Simon Fraser University) Miklós Császár (University of Montreal) Daniel Doerr (Bielefeld University) Ingo Ebersberger (Goethe University Frankfurt) Nadia El-Mabrouk (University of Montréal) Oliver Eulenstein (Iowa State University) Guillaume Fertin (University of Nantes) Pawel Gorecki (University of Warsaw) Michael Hallett (Concordia University) Katharina Jahn (ETH Zurich) Asif Javed (Genome Institute of Singapore) Manuel Lafond (University of Ottawa) Jens Lagergren (Stockholm University) Kevin Liu (Michigan State University) Joao Meidanis (UNICAMP)

— / —

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>

UGoettingen EvolutionOfSensation Sep27-28

Dear colleagues,

We want to kindly remind you to register for our 6th meeting #Sensation @GOEEvolution 2018 taking place in Göttingen from September 27th to 28th 2018 (<http://goevol.uni-goettingen.de/index.php?id=meeting20180>).

Registration is still possible until July 15th 2018 following this link:

<http://goevol.uni-goettingen.de/index.php?id=addgroup0> Costs to register are 10 euro for students,

20 euro for Postdocs and PIs.

For more details see email below or visit our website at <http://goevol.uni-goettingen.de/index.php?id=meeting20180> . Looking forward to meeting you!

Best regards,

The GOEvol Team <https://goevol.uni-goettingen.de/>
Twitter: @GOEvolution

On behalf of the GOEvol organizing team,

Max S. Farnworth

Georg-August-University of Göttingen

Johann-Friedrich-Blumenbach Institute of Zoology and Anthropology

Department of Evolutionary Developmental Genetics

Göttingen Center for Molecular Biosciences (GZMB)

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http://www.researchgate.net/profile/Max_Farnworth

Twitter: @StephesMax

m789farnworth@t-online.de

UHuddersfield UK ProgrammingEvolBiol Sep2-6

A new sponsor + deadline extended!

Dear all

We are pleased to announce that our conference is now officially supported by the Society of Genetics! On this occasion we are extending the deadline for registration - please send your abstracts in by the end of this week - midnight July 1st!

For information about the conference and registration, please go to our website <http://pebconference.info/>. Looking forward to seeing you in Lake District, The organisers - Marisa, Marina and Jarek

On 13 June 2018 at 06:53:47, evoldir@evol.biology.mcmaster.ca (evoldir@evol.biology.mcmaster.ca) wrote:

Dear all,

this is a reminder that the deadline for registration on the upcoming Programming for Evolutionary Biology Conference is approaching - the date is on the 20th of June! See our announcement below and on <http://pebconference.info/> and apply!

Looking forward to meeting you at the conference,

The organisers - Marisa, Marina and Jarek

We are pleased to announce the fourth Programming for Evolutionary Biology Conference, which will take place in Buttermere, Lake District, UK, on September 2-6 (Sunday to Thursday). The conference is organised by postgraduate students and staff at the Department of Biological and Geographical Sciences, University of Huddersfield, UK.

Details are available at <http://pebconference.info/>.

The Programming for Evolutionary Biology conference brings together scientists broadly interested in applying bioinformatic tools to answer evolutionary and ecological questions. Unlike other conferences featuring mostly talks and poster sessions, PEB aims to serve as a platform for discussing common programming pitfalls encountered during research and features workshops to further develop participants' bioinformatic skills. The conference is small (<50 participants), has an informal atmosphere and is predominantly aimed at postgraduate students and early-career researchers.

For the duration of the conference, we are taking over the entire youth hostel in Buttermere, Lake District, Cumbria (<https://www.yha.org.uk/hostel/buttermere>), a relatively remote village in one of the most beautiful valleys in the District (<https://www.nationaltrust.org.uk/-buttermere-valley>). We will be providing transport to and from Buttermere for the participants.

The programme includes up to 18 short (15 min) talks and presentations before lunch and up to 6 computational workshops and tutorials in the afternoon. We will have pleasure of welcoming two fantastic keynote speakers: Dr Nicola Nadeau from the University of Sheffield and Dr Rui Martiniano from the Wellcome Trust Sanger Institute, University of Cambridge. Confirmed workshops include: using GIS in R, run by Dr Anna Krystalli from the University of Sheffield, cloud computing, run by Martin Callaghan from the University of Leeds and parameter selection in Stacks for the analysis of RAD-seq data, run by Marisa Martin Cerezo from the University of Huddersfield; with more workshops coming soon (feedback and suggestions are welcome during the registration process!).

The cost of the conference is 275 including 4 nights' accommodation and full board. To register, please fill in the registration form, along with an abstract and short cover letter regarding your participation in the conference:

<https://goo.gl/forms/a1gH9fqzmFYnjS492>

Registration deadline is at midnight on Wednesday, 20th of June.

Please spread the news and we are looking forward to meeting you at the conference!

The organisers - Marisa, Marina and Jarek <http://pebconference.info/>

Jarek <bryk@evolbio.mpg.de>

UMinnesota MidwestPopGen Aug24-25

APPROACHING DEADLINE - CALL FOR ABSTRACTS MIDWEST POPGEN <https://mwpg2018.wordpress.com/> The fifth annual midwest popgun meeting! Aug 24 & 25 2018 Cargill Building St. Paul campus. of the University of Minnesota

Abstract submission is still open for the 5th midwest popgun meeting. Abstracts for talks are due on Friday

June 22nd but will be considered though monday June 25. [conference registration is open until aug3]

The conference is free and includes a bbq on friday, and a trip to the Minnesota State fair (you buy your own ticket) on sat. We are sponsored by Speciation Ales the only evolution themed brewery in the country!

This is an opportunity for graduate students, postdocs and young profs to share their work and to meet like minded scientists from around the midwest. Cant wait to see you all!

Follow the link at <https://mwpg2018.wordpress.com/> to register

Note: This meeting follows a free symposium on machine learning for genomics and phenomics at the same location! check them both out

Yaniv Brandvain Assistant Professor University of Minnesota - Twin Cities ybrandva at umn dot edu

Yaniv Brandvain <ybrandva@umn.edu>

UToronto EvolPlantReproduction Aug10-11

The Department of Ecology and Evolutionary Biology at the University of Toronto cordially invites you to BarrettFest on August 10-11 in Toronto, Canada. The weekend will feature a symposium entitled 'Evolution of Plant Reproductive Systems: From Muddy Boots to Genomics', which includes a diverse international list of leaders in the field that will be speaking about the latest theoretical and empirical work on the evolution of plant reproduction. The weekend will also provide an opportunity to celebrate Spencer Barrett's 70th birthday and 40 year career as a Professor at U of T. There is no cost to attend the symposium, but please register at <https://barrettfest.eeb.utoronto.ca>. Banquet tickets are available at <https://barrettfest.eeb.utoronto.ca>. We look forward to welcoming you to Toronto, Canada.

Organizers,

Stephen Wright Marc Johnson Daniel Schoen

marc.johnson@utoronto.ca

GradStudentPositions

Cambridge Genomics	10	LundU OatGenomics	16
Edinburgh EvolutionaryGenomics	11	METU Ankara ArchaeogenomicsPopGen	17
FSchillerU NicheSpecialization	12	Newcastle UK MarineBioinformatics	18
Germany SocialInsectAgeing	13	Princeton WeekendPreview EEB expenses paid	19
Gottingen AnnelidPhylogenomics	13	SouthernIllinoisU EvolutionFrogs	19
iDiv Leipzig PalmGenomics	14	StockholmU PlantSystematics	20
ImperialCollegeLondon PopGenMachineLearning ..	15	TexasTechU BighornSheepMicrobiomes	21
LouisianaTechU MicrobialEvolution	16	UArkansas NeuroEvoDevo	21

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UOsnabrueck 6 CellularEvolution	25	UZurich PlantMycorrhizalInteractions	29
UOxford PredictingAntimicrobialSpread	26		

Cambridge Genomics

Supervisors: Chris Jiggins, Richard Durbin Industrial partner: Miha Pipan (Entomics)

A PhD studentship is available to start from October 2018 on the genome and domestication of *Hermetia illucens*, commonly known as the black soldier fly (BSF), funded by the UK National Productivity Investment Fund through the Biotechnology and Biological Sciences Research Council.

By feeding on organic waste biomass, such as food, agricultural and manure wastes, BSF larvae are capable of converting waste biomass into a sustainable and renewable source of sought-after nutrients. BSF larvae are rich in lipids and proteins, and BSF larvae-derived meals are effective feedstuffs for a range of commonly farmed livestock species ranging from poultry to farmed fish. This project will study the genome of the BSF and apply population genetic and machine learning methods for analysis of the signatures of domestication in industrial strains.

We have already obtained a preliminary assembly of the BSF genome using a single Chromium 10X library with a total length of 1.1Gb and scaffold N50 of 1.05Mb. The sequenced individual was from a trio family for which further siblings are available. We have also established a stock derived entirely from the original founder pair that can be used for future genetic analysis. The studentship will improve the genome assembly, using long-read sequence for a single additional sibling individual and for the parents. This will permit a trio-based assembly approach whereby offspring reads are separated into haplotypes before assembly using parental kmers, from which we anticipate obtaining multi-megabase scale assemblies for both parental haplotypes. The genome will be annotated using publicly available transcriptome data, using the BRAKER pipeline, which we have used recently for annotation of butterfly genomes. An extensive RNAseq data set has already been published in which larvae were exposed to a variety of diets, providing

a resource for annotation of larva-expressed genes.

To study the process of domestication we will obtain Illumina WGS resequencing data for a population sample of the industrial strain of BSF, and for at least one outgroup population/species. The student will map these data to the reference genome, call genotypes and use both composite likelihood and machine learning approaches in order to scan the genome for regions that have been subject to recent selection. Genome regions that have been under adaptive selection during the process of domestication will be potential targets for future genetic manipulation of the BSF for further optimisation of its efficiency. In addition, comparison to other dipteran genome sequences will identify longer time frame patterns of conservation and evolutionary divergence.

URGENT DEADLINE 30 June 2018 Contacts: c.jiggins@zoo.cam.ac.uk, rd109@gen.cam.ac.uk The scheme is advertised here on FindaPhD.com <<https://www.findaphd.com/search/PhDDetails.aspx?CAID=3968&LID=290>>

Professor of Evolutionary Biology (2014) Department of Zoology University of Cambridge Tel: (+44)(0)1223 769021 Mob: (+44)(0) 7549-524-481 <http://www.heliconius.org/> http://heliconius.zoo.cam.ac.uk/@mel_rosina

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

The Ecology and Evolution of *Heliconius* Butterflies Available through all good bookshops, or direct from Oxford University Press

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

Edinburgh Evolutionary Genomics

Project title: Causes and consequences of mutational variation in the mammalian genome

Supervisors: Peter Keightley and Konrad Lohse, Institute of Evolutionary Biology, University of Edinburgh, UK

Project Description

Spontaneous mutations are the ultimate source of genetic variation and are therefore of central importance in evolutionary biology. Understanding the nature of variation arising from spontaneous mutation is important for diverse questions, including the genetic basis of complex trait variation, the causes of inbreeding depression and the maintenance of nucleotide variation in the genome. We are recruiting a PhD student to join our team addressing such fundamental evolution, and is open to applicants from the EU. A key component of the project is an ambitious, spontaneous mutation accumulation (MA) experiment in mice, the first highly replicated MA experiment in a mammalian species. With our collaborators at the Max Planck Institute for Evolutionary Biology (Ploen, Germany) we are maintaining a large cohort of MA lines, bred by full-sib mating, for many generations in the near-absence of selection. Different lines will accumulate different spontaneous mutations and therefore diverge molecularly and phenotypically. The PhD project is expected to be within some or all of the areas described below. The project is flexible, however, and can be tailored to the interest of the successful applicant.

Applicants are strongly encouraged to contact the principal supervisor ahead of application to discuss the project.

A. The nature of variation from new mutation.

(a) Theoretically, inbred lines should harbour little genetic variation, but there are several factors which could lead to inbred lines harbouring more variation than expected.— We will test this by quantifying nucleotide variation in our inbred MA line progenitors by deep genome sequencing and bioinformatic analysis. This step is a necessary for the following two studies.

(b) Variation in the mutation rate within a species have been little studied, but is fundamental for understanding the maintenance of genetic variation. We will address

this question by large-scale deep sequencing and bioinformatic analysis of house mouse MA lines of different strains and potentially families of wild house mice.

(c) The relationship between nucleotide and phenotypic variation arising from mutation are largely unknown. Divergence between MA lines for complex traits quantifies the new mutational variation. We will relate the accumulation of phenotypic differences, in traits such as growth rate, reproductive fitness and gene expression, to differences in the accumulation of mutations in different genomic site classes among lines.

B. Understanding variation in diversity across the genome.

Genetic diversity in natural populations varies across the genome, but the causes of this variation are poorly understood. It is clear that variation in diversity is caused by interactions between mutation, natural selection, recombination and genetic drift. We will explore avenues of research that might help tease apart these factors. (a) Are patterns of diversity across the genome consistent between different species with different effective population sizes? It will be especially relevant to determine how diversity relates to the rate of recombination and the local density of functional genomic elements. (b) Are there signals in genomic polymorphism data, for example in the joint frequency distribution of linked sites that can differentiate between different forms of selection? We will also explore whether new computer simulation approaches can be used to efficiently model the joint effects of mutation, recombination, selection and genetic drift across the genome.

Further Information

The studentship is funded by a 5 year ERC grant, which includes a substantial budget for genome sequencing, consumables and travel to conferences.

Training is an integral part of the studentship, including attendance of bioinformatics courses and courses in population and quantitative genetics and statistics run as part of the Institute of Evolutionary Biology's MSc in Quantitative Genetics and Genome Analysis.

Prospective applicants are encouraged to contact Peter Keightley <peter.keightley@ed.ac.uk> to discuss the project in the first instance. Formal applications can be made via <https://www.ed.ac.uk/biology/prospective-students/pgr/how-to-apply> by 21 July 2018.

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

“peter.keightley@ed.ac.uk” <peter.keightley@ed.ac.uk>

FSchillerU NicheSpecialization

PhD position in Meta-analysis of Individual Niche Specialization

A PhD position in meta-analysis of individual niche specialization is available at the Institute of Ecology and Evolution at Friedrich Schiller University Jena, Germany. The position is funded by the German Research Foundation (DFG) within the recently granted collaborative research center (SFB/TRR 212) entitled: /A Novel Synthesis of Individualization across Behavior, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC³)/.

***The project:** The project /The behavioural ecology of individualized niches in light of meta-analyses/ will use quantitative methods to synthesize the current knowledge on individual niche specialization. Meta-analyses offer the formal framework, a framework that is growing in popularity and importance in all fields of quantitative research. Meta-analyses allow a formal assessment of the generalizability of research findings and an exploration of context dependencies. The project requires and trains conceptual thinking, quantitative analysis and thorough overview of topical issues in behavioural and evolutionary ecology. The project will collaborate intensely with various empirical projects within the SFB. It promises strong training in statistical analyses, deep conceptual understanding and advances in several of subfields of ecology and evolution concerned with individualization. It promises to result in several summarizing and therefore potentially very influential scientific publications. The skillset acquired during this project will be highly valuable inside and outside academia.

***The collaborative research center:** The position will be embedded within a larger collaborative research center (SFB) comprising 18 principle investigators, 8 postdocs and 16 PhD students based at Bielefeld University, the University of Münster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualization across behavior, ecology and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programs. For more information, visit the SFB website (www.uni-bielefeld.de/biologie/crc212).

Main responsibilities

of results on individualized niche ecology from the published literature,

of published effects using modern meta-analytic methodology,

with other research groups in the collaborative research center,

scientific publications for international peer-reviewed journals.

Applicant's profile

We seek a bright and highly motivated candidate with Master's degree in a relevant field, like evolutionary or behavioral ecology or statistics,

knowledge in basic statistics, including experience with statistical software such as R,

in both biological and statistical questions,

to read deeply into the scientific literature on specific topics,

oral and written communication skills in English,

experience with scientific writing will be advantageous.

Remuneration

The position is available starting as soon as possible and will be fixed-term till end of 2021. Salary will be paid according to Remuneration level 13 (65%) of the Wage Agreement for Public Service in the Federal States (TV-L). Severely handicapped people are given preference for equal qualifications, aptitude and professional qualifications.

Application procedure

The ***deadline for application is 17th June 2018***, late applications will be considered until the position is filled. To apply, please provide (i) a letter of motivation, including a statement of your research interests, skills and experience relevant to the position, (ii) a CV including publication list, (iii) names and contact details of two referees willing to write confidential letters of recommendation. All materials should be sent, preferentially as a single pdf file by email, to the address below. For further information on the projects and the department, please contact Holger Schielzeth (see email below) and/or visit the website of the Population Ecology Group Jena (www.popecol.uni-jena.de).

Prof. Dr. Holger Schielzeth, Friedrich Schiller University Jena, Institute of Ecology und Evolution, Population Ecology Group, Dornburger Str. 159, 07743 Jena, Germany, E-Mail: holger.schielzeth@uni-jena.de

Holger Schielzeth <holger.schielzeth@uni-jena.de>

Germany SocialInsectAgeing

We invite applications for 7 PhD positions within the framework of the new Research Unit *Sociality and the reversal of the fecundity/longevity trade-off* (FOR 2281) funded by the German Research Foundation (DFG) www.so-long.org Why do organisms age? The genetic underpinnings of ageing seem to be highly conserved from nematode worms to humans. Across animals, ageing is characterized by a trade-off between fecundity and longevity, with an increase in fecundity commonly associated with accelerated senescence and a drop in lifespan. A major exception to this pattern is found within the social insects. Some social insect queens are record holders with respect to longevity whereas their sterile workers are short-lived. The aim of the Research Unit (www.so-long.org) is to explore, in a highly integrative and interdisciplinary fashion, the ultimate and proximate reasons for the apparent reversal in the fecundity/longevity trade-off associated with sociality by using all major clades of social insects, with *Drosophila melanogaster* as model non-social organism. Projects will apply a broad range of approaches from experimental manipulation, field-based studies and molecular genetic studies (e.g. qPCR, RT-PCR, NGS) to theoretical evolutionary modelling and bioinformatic analyses. Beyond the project work, PhD candidates will attend and learn in workshops, can organize summer schools, have the opportunity to participate in lab rotations and to attend international conferences.

PhD positions will be available on the following topics: Comparative analysis of molecular mechanisms of ageing in flies and social insects (Dr. Claudia Fricke, University of Münster; claudia.fricke@uni-muenster.de)

Defying senescence - The causes of death and the costs of living of ant queens (PD Dr. Jan Oettler / Prof Dr. Jürgen Heinze, University of Regensburg; jan.oettler@biologie.uni-regensburg.de; juergen.heinze@biologie.uni-regensburg.de)

A comparative approach to the fecundity/longevity trade-off across two origins of eusociality in the bees (Prof. Dr. Robert Paxton, University of Halle / Dr. Karen Meusemann, University of Freiburg; robert.paxton@zoologie.uni-halle.de; karen.meusemann@biologie.uni-freiburg.de)

Functional basis of the fecundity - longevity reversal in the ant *Temnothorax rugatulus* (Prof. Dr. Susanne

Foitzik, University of Mainz / Dr. Barbara Feldmeyer, Senckenberg BiK-F Frankfurt; foitzik@uni-mainz.de, barbara.feldmeyer@senckenberg.de)

Uncovering the functional basis of the reversal of the fecundity/longevity trade-off in a termite (Prof. Dr. Judith Korb, University of Freiburg; judith.korb@biologie.uni-freiburg.de)

Reversal of the fecundity / longevity trade-off across social transitions in ants (Dr. Volker Nehring, University of Freiburg / Prof. Dr. Susanne Foitzik, University of Mainz, / Dr. Romain Libbrecht, University of Mainz; volker.nehring@biologie.uni-freiburg.de, foitzik@uni-mainz.de, rllibrec@uni-mainz.de)

Why and how does sociality change the fecundity / longevity trade-off in termites? (Prof. Dr. Judith Korb, University of Freiburg / Prof. Dr. Ido Pen, University of Groningen; judith.korb@biologie.uni-freiburg.de, i.r.pen@rug.nl)

All applicants should have a strong background in evolutionary biology and, depending on the project, also skills in bioinformatics (e.g. scripting) or field work. For further details of specific projects, email the relevant contact person listed above. Within your application, please state your preferred project, in ranked order from 1 (most preferred) to 3. The research consortium will jointly select candidates for the positions. Skype/phone interviews are scheduled for the last week of July and 1st week of August. Start of Position is anticipated to be 1. Oct 2018 with a kick-off meeting from the 3.- 5. Sept 2018

Interested candidates should send their applications (incl. CV, a letter of motivation, and contact details of two academic references) as single file pdf by 8. July 2018 to: Judith.Korb@biologie.uni-freiburg.de

For further information please contact: Prof. Dr. Judith Korb Zoology : Evolutionary Biology & Ecology University of Freiburg Hauptstrasse 1 D-79104 Freiburg Germany Judith.Korb@biologie.uni-freiburg.de www.so-long.org Deadline for applications: 8. July 2018

Göttingen AnnelidPhylogenomics

The Johann-Friedrich-Blumenbach Institute of Zoology and Anthropology at the Georg-August-Universität Göttingen is looking to fill the position of a Doctoral/Ph.D. Student for research on Phylogenomics of Nereididae (Annelida) using a target enrichment strategy.

The position is funded by the German Science Foundation (DFG) for a period of three years, with a salary according to the German salary scale TV-L E13 (65%), and should be filled by October 2018.

The nereidid annelid *Platynereis dumerilii* is the best-known lophotrochozoan model system. Surprisingly, a detailed phylogenetic analysis of nereidids is lacking so far. The main objective of this project is to reconstruct a well-supported phylogeny for nereidids by using data from hybrid target enrichment with subsequent Illumina sequencing. Baits for target enrichment will be based on a set of transcriptomes from selected nereidid species generated within this project. This phylogenetic framework will be used to the current classification of nereidids and finally provide a stable placement of the model annelid *Platynereis dumerilii*. Based on this phylogeny, ancestral state reconstruction will be used to infer the evolution of reproductive modes, life-style and habitat preference of nereidid worms.

Applicants need to hold a diploma or MSc degree in biology or a related field and to have solid experience with molecular methodology, particularly with respect to molecular systematics. Experience in generating and/or analysing next generations sequencing data is desirable. Knowledge about annelids or other lophotrochozoans would be helpful, but is not necessary. Working language is German and English.

Doctoral students are supposed to take part in seminars and supervising students. This position is designed to foster young researchers and scientists and give the successful applicant the opportunity to pursue a doctoral degree.

The University of Göttingen is an equal opportunities employer and places particular emphasis on fostering career opportunities for women.

Qualified women are therefore strongly encouraged to apply in fields in which they are underrepresented. The university has committed itself to being a family-friendly institution and supports their employees in balancing work and family life. The mission of the University is to employ a greater number of severely disabled persons. Applications from severely disabled persons with equivalent qualifications will be given preference.

With submission of your application, you accept the processing of your applicant data in terms of data-protection law. Further information on the legal basis and data usage is provided in the 'Guideline General Data Protection Regulation (GDPR)' (German version only).

Applications containing the common documents should be sent by July 1, 2018 in electronic form or by ordinary mail to Prof. Dr. Christoph Bleidorn, Johann-

Friedrich-Blumenbach-Institut für Zoologie und Anthropologie, Animal Evolution and Biodiversity, Georg-August-Universität Göttingen, Untere Karspule 2, 37073 Göttingen, Germany, cbleido@gwdg.de.

Please note: With submission of your application, you accept the processing of your applicant data in terms of data-protection law. Further information on the legal basis and data usage is provided in the Hinweisblatt zur Datenschutzgrundverordnung (DSGVO) – Prof. Dr. Christoph Bleidorn Georg-August-Universität Göttingen Johann-Friedrich-Blumenbach Institute for Zoology & Anthropology Animal Evolution and Biodiversity Untere Karspule 2 37073 Göttingen Germany

<http://www.researchgate.net/profile/Christoph.Bleidorn> Member of the German Centre for Integrative Biodiversity Research (iDiv) <http://www.idiv.de/idiv-global/?lang=en> Systematics & Biodiversity <http://www.tandfonline.com/toc/tsab20/current> Follow me on twitter! <https://twitter.com/C.Blei> Christoph Bleidorn <christoph.bleidorn@gmail.com>

iDiv Leipzig PalmGenomics

The German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig is one of four National Research Centres funded by the German Research Foundation (DFG). Its central mission is to promote theory-driven synthesis and data-driven theory in this emerging field. The concept of iDiv encompasses the detection of biodiversity, understanding its emergence, exploring its consequences for ecosystem functions and services, and developing strategies to safeguard biodiversity under global change. It is located in the city of Leipzig and it's a central institution of the Leipzig University, jointly hosted by the Martin-Luther-University Halle-Wittenberg, the Friedrich Schiller University Jena and the Helmholtz Centre for Environmental Research (UFZ). Furthermore, it gains support by the Max Planck Society, the Leibniz Association and the Free State of Saxony. More Information about iDiv: www.idiv.de. The Evolution & Adaptation research group focuses on the interchange between (macro-) ecology and evolution, to understand the global distribution of genetic, taxonomic and functional diversity. We investigate micro-evolutionary processes to understand how these play out over macro-evolutionary time scales. Understanding these patterns and the processes underlying them is

important for predicting how adaptable biodiversity is to current and future global change.

Integrated in iDiv, the Leipzig University, offers the following position in our new Evolution and Adaption Junior Research Group as soon as possible:

Doctoral Researcher “Genomic signatures of palms with megafaunal fruits on Madagascar” (initially limited until 30 September, 2020 (iDiv funding period), 65 % of a full-time employment) Salary: Entgeltgruppe 13 TV-L

Background:

Madagascar harbours exceptional biodiversity, but this tropical hotspot also faces increasing threat from human activities and climate change. Plants with large, ‘megafaunal’ fruits are common across the flora of Madagascar, especially within the palm (Arecaceae) family. However, Pleistocene extinctions of large-bodied ‘megafaunal’ fruit-eating and seed-dispersing animals (such as giant lemurs) may have hindered the dispersal of taxa with megafaunal fruits. In this project we aim to investigate the micro- and macroevolutionary consequences of dispersal limitation for megafaunal-fruited palms on Madagascar, using a comparative framework. Specifically, we aim to (i) identify genomic signatures of dispersal limitation in megafaunal-fruited palm populations, (ii) reconstruct demographic history and identify historical genetic bottlenecks in these species, and (iii) evaluate whether these species may be adapting to dispersal by smaller-bodied frugivores, by evolving smaller fruits with smaller seeds. This project integrates the fields of plant evolution, phylogeography, and plant-frugivore interaction ecology. It will be in collaboration with researchers from Kew Botanical Gardens, UK (Dr. Bill Baker), Aarhus University, Denmark (Dr. Wolf Eiserhardt), the University of Amsterdam, the Netherlands (Dr. Daniel Kissling) and Botanic Garden of the Ruhr-University Bochum, Germany (Dr. Wolfgang Stuppy), among others.

Job description: * - collecting genetic samples from palm populations on Madagascar, and measuring their functional traits * - identifying Malagasy frugivore communities and their functional traits * - using novel genomic techniques (e.g. RAD sequencing) to infer connectivity, demographic history and phylogeographical patterns * - writing and publishing of scientific papers in peer-reviewed journals * - presentation of results at international conferences * - participation in iDiv’s PhD training program yDiv

Requirements:

Applicants should hold a Master’s or equivalent degree in a related field of research (e.g. ecology, (molecular) biology, genetics, phylogenetics, phylogeography). The

successful candidate should be innovative, able to work on his or her own initiative, and willing to spend several months in the field (Madagascar). Therefore prior experience with tropical fieldwork and basic living conditions is advantageous. Furthermore, the successful candidate should have prior experience using molecular techniques, preferably with bioinformatics for large genetic/genomic datasets. An interest in acquiring additional necessary skills (e.g. programming) for handling and statistically analyzing large datasets is essential. Candidates should be team-oriented and have strong organizational skills, in order to manage this collaborative research project within an international consortium. Excellent English communication skills (speaking and writing) are required. We seek candidates with an independent mind and the ambition to publish in internationally leading journals.

Applications are accepted until 30th June 2018.

Applications should include:

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ImperialCollegeLondon PopGenMachineLearning

The advert for the next QMEE PhD studentships at Imperial College London is now live at:

<https://www.findaphd.com/search/-PhDDetails.aspx?CAID=3289&LID=112> With a closing date of 25th July. Starting date will be October 2018.

We have a project proposal on deep learning and genomics, detailed here: <https://mhasoba.pythonanywhere.com/qmee.cdt/default/-view-proposals/view/proposals/36?signature=-668d3d78372f7770d43d9d94aee2cbc05f45c5cc> in collaboration with Professor Xia Hong from University of Reading (Computer Science).

Eligibility: Standard RCUK eligibility applies, see details at <https://www.imperial.ac.uk/qmee-cdt/how-to-apply/>. Briefly, you need to be either British or EU national resident in the UK for the past 3 years. Priority

will be given to candidates that received a quantitative training during their UG or Master.

Please contact me if you are eligible and interested in the position.

Kind Regards

Matteo Fumagalli m.fumagalli@imperial.ac.uk

Matteo Fumagalli Lecturer in Quantitative Evolution Department of Life Sciences Imperial College London Silwood Park Campus Munro Building, N1.6 Ascot, Berkshire SL5 7PY, UK Tel: +44 (0)20 7594 3793 m.fumagalli@imperial.ac.uk <https://www.imperial.ac.uk/people/m.fumagalli> "Fumagalli, Matteo" <m.fumagalli@imperial.ac.uk>

LouisianaTechU MicrobialEvolution

The Maness Organismal Biology Lab in The School of Biological Sciences at Louisiana Tech University is accepting applications for a Master's/PhD student interested in environmental microbiology/microbial ecology. The student will develop a research project investigating microbes with the ability to degrade environmental toxins or pollutants. Applicants should have an interest in environmental science, genetics, enzyme kinetics, and/or geographical information science as well as undergraduate STEM education. Student support is ~\$27,000/yr from a graduate assistantship in the School of Biological Sciences and an NSF grant. Duties for the assistantship will be to assist with teaching the lab component of one of the School of Biological Sciences courses. The position will begin in the Fall 2018-19 academic term.

Applicants should be motivated, creative, organized, and have strong communication skills. Coursework in Genetics or Geographic Information Science is recommended, but not required. Students of diverse backgrounds are encouraged to apply. Successful candidates will have an undergraduate degree in Biology, Environmental Science, or related field. Students must meet admission requirements for the M.S. in Biology Program/PhD in Molecular Sciences and Nanotechnology at Tech and be accepted into that program to be eligible for the assistantship.

To apply send: (1) a statement of research interests and goals, (2) unofficial transcripts, (3) CV, and (4) list of three references with contact info to Terri Maness: tmaness@latech.edu. Application deadline is 5pm CST June 15, 2018.

– Terri J. Maness Assistant Professor, School of Biological Sciences Herbert McElveen Endowed Professor of Applied and Natural Sciences Environmental Science Program Coordinator PO Box 3179 Louisiana Tech University Ruston, LA 71272 email: tmaness@latech.edu Office: (318)-257-2724 Website: <http://manesslablatech.weebly.com/> < <http://www2.latech.edu/~tmaness/> >

Terri Maness <tmaness@latech.edu>

LundU OatGenomics

Bioinformatician

We are seeking a motivated and experienced bioinformatician to join the ScanOats Industrial Research Center to perform work in the field of oat genomics. We have recently sequenced and assembled the hexaploid oat genome and now the in-depth analysis can begin. An enthusiastic outlook to scientifically tackling this 12.5Gbp hexaploid genome is absolutely necessary. Your role will involve developing computational approaches that integrate next generation sequence data to address the goals of ScanOats. Our areas of research on oat seed quality include: 1) lipids and lipases, 2) total fibers, 3) antioxidants, 4) proteins, and 5) Fusarium resistance. You will interact with researchers from different backgrounds including biochemistry, plant breeding, biotechnology and bioinformatics, and also with researchers within the other work packages of ScanOats as well as the ScanOats industrial partners Lantmannen, Oatly and Swedish Oat Fiber.

For more information <https://lu.mynetworkglobal.com/en/what:job/jobID:211909/> PhD student We are seeking a motivated individual with a genuine interest in laying the foundation for their academic career in crop genomics to join the ScanOats Industrial Research Centre. You will begin your PhD in the field of oat genomics by developing computational approaches that integrate NGS data to identify and characterize the genetics associated with oat lipids, lipases, antioxidants, and other factors involved in rancidity during oat storage. You will interact with researchers from different backgrounds including biochemistry, plant breeding, biotechnology and bioinformatics.

The work will be conducted in collaboration with researchers within the other subprojects of Scanoats as well as with the ScanOats industrial partners Lantmannen, Oatly and Swedish Oat Fiber.

Read more at <https://lu.varbi.com/en/what:job/-jobID:211714/> Lund University was founded in 1666 and is repeatedly ranked among the world's top 100 universities. The University has 40 000 students and 7 400 staff based in Lund, Helsingborg and Malmo. We are united in our efforts to understand, explain and improve our world and the human condition. LTH forms the Faculty of Engineering at Lund University, with approximately 9 000 students. The research carried out at LTH is of a high international standard and we are continuously developing our teaching methods and adapting our courses to current needs.

ScanOats is a newly established industrial research centre in collaboration between the academy and the industry. We conduct basic and applied research on oats and oat-based products. Oat is an important crop both for the Swedish agriculture and for the food chain.

ScanOats is unique in the sense that we cover the entire chain from basic research, genome sequencing, cultivar development, field testing, mild processing and fractionation, and clinical health trials.

Dennis Eriksson <dennis.eriksson@tbiokem.lth.se>

METU Ankara ArchaeogenomicsPopGen

Postdoc and PhD positions in archaeogenomics, population genetics, bioarchaeology, and archaeological modeling

Applications are invited for multiple Ph.D. and postdoc positions in an ERC-funded interdisciplinary research project on the Neolithic Transition in Southwest Asia.

We seek applicants with backgrounds in molecular biology, population genetics, anthropology, archaeology, and computer science.

The work will be conducted at METU, Ankara, in collaboration with Hacettepe University, and major Neolithic excavations in the region, including Aatalhöyük and Aatalhöyük.

THE PROJECT:

The successful applicants will join the 5-year research project **NEOGENE: Archaeogenomic analysis of genetic and cultural interactions in Neolithic Anatolian societies**, supported by a European Research Council Consolidator Grant.

Using state-of-the-art ancient genomics and modeling approaches, NEOGENE aims to shed fresh light on a most dramatic transition period in prehistory: the emergence of sedentism and farming 10,000 years ago in Anatolia. The project involves constructing genetic kinship networks in Neolithic villages, mapping inter-regional patterns of gene flow, describing the evolution and dispersal of domestic sheep, and joint modeling of material culture exchange and demic processes that drove the Neolithic Transition across West Eurasia.

TASKS AND REQUIREMENTS:

The successful candidates will be working in one of the following fields:

§Ancient DNA: Researchers with PhD or MSc degrees in biology or a related field, to conduct wet lab experiments, including experimental protocol development for DNA extraction, library preparation and capture.

§Population genomics: Researchers with PhD or MSc degrees in population genetics, statistical genetics, or a related field, to work in genomic data analysis and population genetic modelling, including method development for demographic inference, kinship and selection estimation.

§Human bioarchaeology: Researchers with an MSc/MA degree in anthropology, or a related field, with experience in human skeletal biology, to study bioarchaeological aspects related to Neolithization.

§Archaeology < span style="font-size:11pt;font-family:Arial;color:black">: Researchers with PhD or MSc/MA degrees in archaeology, to work in archaeological data mining, digital archaeology, and statistical analysis.

§Computer science: Researchers with PhD or MSc degrees in computer science or an informatics-related field, to work in archaeological modelling, evolutionary algorithms and simulation.

EMPLOYMENT AND STUDY CONDITIONS:

For postdocs, the positions are planned for 2 years, with possible extension.

For Ph.D. students, the positions will be for 4 years, and the students will complete the METU and/or Hacettepe University Graduate Programs. Note that METU programs are in English.

NEOGENE's diverse and vibrant research environment is composed of the research groups run by Mehmet Somel (evolutionary genetics and computational biology, at METU Biological Sciences: <http://compevo.bio.metu.edu.tr/>), Füsün -zer (ancient DNA at METU Biological Sciences,

adna.bio.metu.edu.tr/en), Yılmaz Selim Erdal (human bioarchaeology, at Hacettepe Anthropology: <http://hacettepe.academia.edu/Y%C4%B1lmazSelimErdal>), Cigdem Atakuman (Neolithic archaeology and material culture studies at METU Settlement Archaeology: <http://sa.metu.edu.tr/assoc-prof-dr-cigdem-atakuman>), Elif Sürer (serious games and simulation, at METU Informatics Institute: <http://blog.metu.edu.tr/elifs>). We also closely collaborate with multiple archaeology teams working in the region.

METU is Turkey's top public research university, with the largest share of national science funding among the country's universities. The METU student population stands at 27,000, and we host about 2,000 international students and staff.

The successful candidates will receive salary commensurate with experience. They will further enjoy access to on-campus housing. The METU campus includes a >3,000 hectare forest area and a lake, with access to a wide selection of recreational sports.

APPLICATION:

For further information on NEOGENE, please contact Mehmet Somel (neogene@metu.edu.tr).

Postdoc and PhD candidates should send (1) a CV, (2) a statement of interest that mentions the part of the project the candidate plans to work in (max. 2 pages), (3) contact information for three referees, (4) an academic transcript (for PhD student applications only), via email to neogene@metu.edu.tr.

The emails should be titled according to the type of application and

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Newcastle UK MarineBioinformatics

A competitive PhD studentship in marine bioinformatics/molecular biology is available at Newcastle University, UK <https://www.ncl.ac.uk/> rated as one of the top 150 universities in the world. This 3-year fellowship provides a full tuition fee waiver, a competitive living stipend, and a considerable research allowance.

Title: Revealing Adaptive Divergence of Aquatic Rubiscos (RADAR)

Abstract: Photosynthesis is the most important biological process on a planetary scale, and most of the known life depends on it. Photosynthesis harvests energy from the sun to combine carbon dioxide and water, and provide oxygen and the building blocks of life. Surprisingly for such an important process, photosynthesis is not very efficient. Less than 5% of energy from the sun is transformed into chemical energy of sugars by a typical crop plant like wheat or potato. Imagine how crop yields could be improved and how much land could be saved for wildlife if we would find a way to increase efficiency of photosynthesis! The good news is there are several potential ways to address this problem. Photosynthesis is a complex, multi-step process which gives rise to multiple opportunities to address the efficiency of the process. It is possible that multiple solutions could be combined in a single crop to produce more food and/or biofuel using less land and water. One of the bottle-necks in photosynthesis is the performance of an enzyme called Rubisco which is responsible for the fixation of carbon dioxide into sugars. Almost all organic carbon on Earth is fixed by Rubisco. Bacteria, algae and plants have different forms of Rubisco, and the most efficient ones are found in marine organisms. Rubiscos from plants represent 'the tip of an iceberg' yet they attracted most of the research effort. We propose to look at 'the understudied submerged part of an iceberg', Rubiscos from aquatic archaea, bacteria and algae, which are both the most abundant and structurally diverse. Aims: find and characterize new forms of Rubiscos and their chaperones from the aquatic environments for fundamental research and applications in synthetic biology. Methods: 1. Bioinformatics' tools will be used for bioprospecting of in-house obtained eDNA samples and publicly available NGS data collected from the aquatic environments. 2. Codon-optimized genes encoding Rubisco and its chaperones will be expressed in a range of hosts. 3. New forms of Rubisco and its chaperones will be characterised using biochemical and structural analysis.

This project is funded and open for citizens of UK and EU only.

The position will start in 2018 as soon as the suitable candidate will be found.

For further information if you are interested in applying, contact Dr Maxim Kapralov <http://www.ncl.ac.uk/nes/staff/profile/maximkapralov.html> by email maxim.kapralov@newcastle.ac.uk

In your email include your CV with contact information for two references including your most recent/current supervisor.

â euro Â Maxim.Kapralov@newcastle.ac.uk

Princeton Weekend Preview EEB expenses paid

Princeton EEB Scholars Preview Weekend

The Department of Ecology and Evolutionary Biology at Princeton University is offering a special preview weekend 'V *the EEB Scholars Program* 'V this upcoming October 4th-7th for students considering graduate school. The goal of this weekend is to invite competitive prospective graduate applicants to campus in order to showcase the department, demystify the graduate application process, and highlight participants' research experience. We especially encourage students from underrepresented minority groups and those inhabiting other axes of underrepresentation in STEM to apply.

Please see < <https://eeb.princeton.edu/graduate/eeb-scholars-program> > for more information and to apply. The application deadline is July 15, 2018. The *EEB Scholars Program* is open to all prospective graduate students, including rising juniors and seniors, as well as international applicants. We particularly encourage students from developing nations to apply. Travel, food, and lodging expenses will be covered by Princeton EEB.

Please direct any questions to EEBScholars@princeton.edu.

– Amanda Savagian PhD Candidate & EEB Scholars Coordinator Ecology & Evolutionary Biology Princeton University savagian@princeton.edu

SouthernIllinoisU EvolutionFrogs

Evolution of South American Poison frogs (genera *Ameerega* and *Ranitomeya*) Zoology Department, Southern Illinois University Carbondale, Carbondale, IL.

A doctorate position is available to study the evolution of S. American poison dart frogs. Neotropical poison frogs are a species-rich family (Dendrobatidae) that exhibit a diversity of mating systems, parental care strategies and phenotypes. The Brown lab is looking for a student to develop a research program studying ANY core aspect

of the lab's research. The ideal student will be prepared to conduct field-based research, have some experience in molecular ecology/population genetics, genomic and/or geospatial analyses. The selected candidate MUST be highly interested in phylogenetics, population genetics, or genomics. This position includes several trips to South America and fully funded lab work.

As follows are a few key projects that could be your graduate research:

*Speciation, species boundaries and hybridization in the *Ameerega bassleri* complex: insights from natural history, acoustic and morphological data, geospatial data, sub-genomic and paleoclimatology. This group is a highly diverse group of three species with dramatic phenotypic variation across its range. It also has experienced several historical hybridization events among the taxa that have muddled and complicated their evolutionary histories. This research will be aimed to understand factor driving and maintaining speciation in natural situations.

**Phylogeography and spatial biodiversity patterns of the poison frog genus *Ranitomeya*: insights from sub-genomic data, geospatial analysis and phylogenetics. The thumbnail poison frogs are some of the most amazing species on earth— half the taxa are involved in Mullerian mimicry, they exhibit intensive parental, and they often display incredible phenotypic variation among populations... This group in an endless fountain of evolutionary questions.

***The genetic consequences of future climate change: spatially explicit predictions of within-species genetic diversity using climatic, demographic, and genetic data. This research will expand upon a lab methodology that accounts for climatic, geographic, and biological complexity. This framework is promising for understanding evolutionary consequences of climate change and guiding conservation planning.

For more information on the Brown Lab please visit the lab website at: <http://www.jasonleebrown.org> and the Zoology Department at SIUC <http://www.zoology.siu.edu>. Students will find all the brains of a nationally ranked research university and all the heart of a small college at SIUC.

Carbondale is located in southern Illinois and provides a close link to many forested areas and lakes. The regional landscapes varies from bottomlands to uplands with rolling hills, bluffs, and rugged topography. This makes it perfect home for outdoor lovers (when they are not in the rainforest of S. America).

Interested students are encouraged to contact Dr. Brown (jason.brown@siu.edu) ASAP. Please include a brief de-

scription of your research interests related the Brown Lab, a CV, and names of two references (with contact info). Competitive funding options are available. US and Canadian students ONLY. Application will be considered as they are received. Applicants will no longer be considered after July 15th 2018. Start date of position is August 2018 (preferred) or January 2019.

Jason Brown <jason.brown@siu.edu>

StockholmU PlantSystematics

PhD position in Plant Systematics at Stockholm University

Closing date: 10 August 2018.

We have an opening for a highly motivated postgraduate fellow to work on the research project “Genome evolution in parasitic plants” in the group of Dr. Gitte Petersen at Stockholm University.

The complete ad with information on how to apply is available on the Stockholm University webpage: <https://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjob=6027&rmlang=UK> Project description The Department of Ecology, Environment and Plant Sciences invites applications for a four-year PhD position part of the project Genome evolution in parasitic plants. Several groups of angiosperms are parasites, which makes them more or less dependent on a host for nutrient supply. This project aims at understanding the evolution and consequences of host-parasite interactions at the genomic level. The current PhD project will primarily focus on evolution of organelle genomes in parasitic plants. Special emphasis will be given to Mistletoes and related genera, in which substantial and unexpected alterations of the mitochondrial genome are already documented. Comparative studies of completely assembled organelle genomes will be supplemented with targeted sequencing and analysis of selected genes.

Qualification requirements In order to meet the general entry requirements, the applicant must have completed a second-cycle degree, completed courses equivalent to at least 240 higher education credits, of which 60 credits must be in the second cycle, or have otherwise acquired equivalent knowledge in Sweden or elsewhere. In order to meet the specific entry requirements, the general syllabus for doctoral studies in the field of Plant Systematics stipulates that applicants must have completed at least 60 higher education credits in the second cy-

cle, of which 15 credits must be from a course in Plant Systematics, and 30 credits from a project in Plant Systematics. Applicants may also have otherwise acquired equivalent knowledge in Sweden or elsewhere. The qualification requirements must be met by the deadline for applications.

Selection The criteria used in the selection for admittance to research training in Plant Systematics are knowledge of theory and applications in the research field, ability to communicate orally and in writing, knowledge of English, creativity, initiative, independence and collaboration ability. Hands-on experience with Next Generation Sequencing and bioinformatics tools will be considered as special merits, as well as good knowledge of phylogenetics. Admission Regulations for Doctoral Studies at Stockholm University are available at: www.su.se/rules. Terms of employment Only a person who will be or has already been admitted to a third-cycle programme may be appointed to a doctoral studentship. The term of the initial contract may not exceed one year. The employment may be extended for a maximum of two years at a time. However, the total period of employment may not exceed the equivalent of four years of full-time study. Doctoral students should primarily devote themselves to their own education, but may engage in teaching, research, and administration corresponding to a maximum of 20 % of a full-time position. Please note that admission decisions cannot be appealed. Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

Contact For more information, please contact project leader Gitte Petersen, telephone: +46 8 16 43 97, gitte.petersen@su.se. Further information about the position can be obtained from the Subject Representative, Professor Catarina Rydin, telephone: +46 8 16 12 15, catarina.rydin@su.se.

Application Apply for the position at Stockholm University’s recruitment system by clicking the “Apply” button. It is the responsibility of the applicant to ensure that the application is complete in accordance with the instructions in the job advertisement, and that it is submitted before the deadline.

gittep@snm.ku.dk

TexasTechU BighornSheepMicrobiomes

The Phillips Laboratory (Department of Biological Sciences, Texas Tech University) is accepting applications from highly motivated individuals interested in pursuing a graduate degree in Biology, with a research project focusing on the dynamics of microbiomes in wild populations of bighorn sheep. The successful applicant will be an individual that is excited about the opportunity to integrate bioinformatics, biostatistics, ecology, and evolutionary biology to understand and publish results about complex biological systems. No prior experience in scripting (mainly bash and R) is required, but only applicants that are serious about the opportunity to develop advanced scripting capabilities and strong foundations in biostatistics and ecological principles need apply. This position is available at the master's or PhD level, but only individuals currently holding a master's degree or with experience in microbiome research will be considered to enter at the PhD level. The position will be supported by a Research Assistantship funded by the Texas Bighorn Society and the Wild Sheep Foundation. The position also provides teaching experience in the form of Teaching Assistantships. Collaboration with researchers in Tech's Department of Natural Resource Management will be a part of this position, and research findings may inform disease risk across portions of bighorn sheep range in Texas. This position will provide career development through a diverse and technical training experience.

Applicants should send their CV and a Statement of Interest to Caleb Phillips (caleb.phillips@ttu.edu, subject line = bighorn microbiome).

Caleb D. Phillips, Ph.D. Curator of Genetic Resources, Natural Science Research Laboratory Assistant Professor, Biological Sciences Texas Tech University, Lubbock Texas Office: 806-834-8181 caleb.phillips@ttu.edu

"Phillips, Caleb" <Caleb.Phillips@ttu.edu>

UArkansas NeuroEvoDevo

The Nakanishi lab at the University of Arkansas seeks applicants interested in pursuing a MS or PhD in evolutionary developmental biology of animals. Current research efforts of the lab are focused on reconstructing deeply conserved mechanisms of how nervous systems develop and function by using cnidarians 'V sea anemones and jellyfish in particular. Student's research projects may involve gene expression analyses (e.g. in situ hybridization and immunohistochemistry), reverse genetics (e.g. CRISPR-Cas9), embryology (e.g. descriptive morphology, cell-lineage tracing and tissue transplantation), genomics (e.g. RNA-seq and ChIP-seq), and advanced microscopy (confocal and electron microscopy, and live-cell imaging). Research and teaching assistantships are available.

Start dates are flexible. Requirements: Bachelor's degree in biology or related field. The ideal candidate will have a strong interest in evolutionary biology, and experiences in molecular biology, developmental biology, neurobiology, genomics/bioinformatics and/or microscopy techniques. Knowledge of invertebrate zoology is a plus but not required.

Application: please submit by email 1) a description of your research interests, 2) a CV, 3) unofficial copies of academic transcripts, and 4) contact information for 2 references to: nnakanis@uark.edu.

Nagayasu Nakanishi, Ph.D Assistant Professor Department of Biological Sciences University of Arkansas Fayetteville, AR 72701 479-575-2031 (office) 479-575-7393 (lab) nnakanis@uark.edu <https://wordpressua.uark.edu/nakanishi-lab/> nnakanis@uark.edu

UFreiburg 7 EvolutionaryTradeOffs

We invite applications for 7 PhD positions within the framework of the new Research Unit 'Sociality and the reversal of the Fecundity/longevity trade-off' (FOR 2281) funded by the German Research Foundation (DFG) www.so-long.org Why do organisms age? The

genetic underpinnings of ageing seem to be highly conserved from nematode worms to humans. Across animals, ageing is characterized by a trade-off between fecundity and longevity, with an increase in fecundity commonly associated with accelerated senescence and a drop in lifespan. A major exception to this pattern is found within the social insects. Some social insect queens are record holders with respect to longevity whereas their sterile workers are short-lived. The aim of the Research Unit (www.so-long.org) is to explore, in a highly integrative and interdisciplinary fashion, the ultimate and proximate reasons for the apparent reversal in the fecundity/longevity trade-off associated with sociality by using all major clades of social insects, with *Drosophila melanogaster* as model non-social organism. Projects will apply a broad range of approaches from experimental manipulation, field-based studies and molecular genetic studies (e.g. qt RT PCR, NGS) to theoretical evolutionary modelling and bioinformatic analyses. Beyond the project work, PhD candidates will attend and learn in workshops, can organize summer schools, have the opportunity to participate in lab rotations and to attend international conferences.

PhD positions will be available on the following topics: Comparative analysis of molecular mechanisms of ageing in flies and social insects (Dr. Claudia Fricke, University of Münster; claudia.fricke@uni-muenster.de) Defying senescence - The causes of death and the costs of living of ant queens (PD Dr. Jan Oettler / Prof Dr. Jürgen Heinze, University of Regensburg; jan.oettler@biologie.uni-regensburg.de; juergen.heinze@biologie.uni-regensburg.de) A comparative approach to the fecundity/longevity trade-off across two origins of eusociality in the bees (Prof. Dr. Robert Paxton, University of Halle / Dr. Karen Meusemann, University of Freiburg; robert.paxton@zoologie.uni-halle.de; karen.meusemann@biologie.uni-freiburg.de) Functional basis of the fecundity - longevity reversal in the ant *Temnothorax rugatulus* (Prof. Dr. Susanne Foitzik, University of Mainz / Dr. Barbara Feldmeyer, Senckenberg BiK-F Frankfurt; foitzik@uni-mainz.de; barbara.feldmeyer@senckenberg.de) Uncovering the functional basis of the reversal of the fecundity/longevity trade-off in a termite (Prof. Dr. Judith Korb, University of Freiburg; judith.korb@biologie.uni-freiburg.de) Reversal of the fecundity / longevity trade-off across social transitions in ants (Dr. Volker Nehring, University of Freiburg / Prof. Dr. Susanne Foitzik, University of Mainz, / Dr. Romain Libbrecht, University of Mainz; volker.nehring@biologie.uni-freiburg.de; foitzik@uni-mainz.de; rllibrec@uni-mainz.de) Why and how does sociality change the fecundity / longevity trade-off in termites? (Prof. Dr. Judith Korb, Uni-

versity of Freiburg / Prof. Dr. Ido Pen, University of Groningen; judith.korb@biologie.uni-freiburg.de, i.r.pen@rug.nl)

All applicants should have a strong background in evolutionary biology and, depending on the project, also skills in bioinformatics (e.g. scripting) or field work. For further details of specific projects, email the relevant contact person listed above. Within your application, please state your preferred project, in ranked order from 1 (most preferred) to 3. The research consortium will jointly select candidates for the positions. Skype/phone interviews are scheduled for the last week of July and 1st week of August. Start of Position is anticipated to be 1. Oct 2018 with a kick-off meeting from the 3.- 5. Sept 2018

Interested candidates should send their applications (incl. CV, a letter of motivation, and contact details of two academic references) as single file pdf by 8. July 2018 to: Judith.Korb@biologie.uni-freiburg.de

For further information please contact: Prof. Dr. Judith Korb Zoology : Evolutionary Biology & Ecology University of Freiburg Hauptstrasse 1 D-79104 Freiburg Germany Judith.Korb@biologie.uni-freiburg.de www.so-long.org Deadline for applications: 8. July 2018

Karen Alice Meusemann
<karen.meusemann@biologie.uni-freiburg.de>

UMontreal EvolutionSexDetermination

PhD POSITION : EVOLUTIONARY BIOLOGY/BIOINFORMATICS

The position :

The Breton lab (University of Montreal) is looking for an ambitious and highly motivated PhD student interested in understanding the genetic and epigenetic mechanisms of sex determination in the marine mussel *Mytilus edulis*.

PROJECT : The blue mussel *Mytilus edulis* is the most important cultured mollusc and therefore a major economic driver in the Gulf of St. Lawrence (Fisheries and Oceans Canada), and one of the most important in the world. Once successful in southern North Carolina, *M. edulis* has undergone a worrying decline in recent years in the Atlantic Provinces and the United States. Different hypotheses have been proposed to explain the

reasons for this decline: overexploitation, ocean acidification, pollution, diseases, increased predators and global warming. Notably, global warming has been used as a hypothesis in several other studies to explain the decline of blue mussel populations, a result that could be attributable, among other things, to a drastic change in the sex ratio (i.e. the ratio of males and females), which could jeopardize the viability of certain populations. Indeed, marine mussels and oysters are known to have a sex ratio regulated by the environment (temperature and/or food). However, unlike oysters, very few studies have focused on sex determination mechanisms in marine mussels. A major reason for studying sexual determinism in mussels relates to their economic and nutritional importance. It is widely accepted that the success of livestock operations is largely related to the characteristics of the breeding populations (natural or captive), and in particular the need to control sex ratios, reproduction periods, fecundity and fertility.

This FRQNT-funded project aims to better understand the genetic and epigenetic mechanisms of sex determination in *Mytilus edulis*. Therefore, the successful applicant should have experience or a strong interest in bioinformatics, evolutionary biology and molecular biology.

Funding (15K/yr) is available to support the successful candidate for three years in addition to a limited travel budget. Expected start date is September 2018 or January 2019. The Universite de Montreal is a French language institution where graduate work may be undertaken in English or French.

Interested students should contact s.breton@umontreal.ca and attach a CV, academic transcript, contact details of two academic referees, and a brief description of their research interests.

The position will remain open until a suitable candidate is found.

Please note that only those selected for an interview (Skype or telephone) will be contacted. Preference will be given to Canadian citizens and permanent residents.

sophie breton <breton.sophie@gmail.com>

UNewSouthWales DevelopmentalPlasticity

PhD Scholarship in Developmental Plasticity

Project: Developmental temperatures as drivers of phenotypic change.

Supervisors: Lisa Schwanz, Shinichi Nakagawa, and Rob Brooks

Evolution & Ecology Research Centre, School of Biological, Earth and Environmental Sciences

University of New South Wales, Sydney, Australia.

Environmental temperatures have a profound impact on developing animals. The Schwanz Lab and collaborators have recently quantified the impact of developmental temperatures on reptile traits, and are continuing to examine how this plasticity impacts animal populations under changing climates. This project will examine plasticity in response to developmental temperatures, plasticity's role in creating phenotypic variation, and the influence on population response to environmental change. Potential projects include: 1) quantifying temperature-based developmental plasticity across animal taxa; 2) quantifying and comparing other sources of developmental plasticity (e.g. maternal diet and oviposition behavior); 3) analyzing reaction norms of plasticity. Addressing these issues will determine the relative importance of climate and temperature for organismal traits, and how they shape animal ecology and evolution. The studies to be undertaken are flexible and will depend on the student's interests.

The research will employ quantitative syntheses of published literature, with potential expansion to focused empirical experiments in reptiles or invertebrates. The ideal candidate for this project will have a Bachelor's or Master's degree in Biology, with an emphasis in animal ecology and evolution, and a strong interest in phenotypic plasticity. Essential skills and experience include: experience with an independent research project; strong writing skills; strong statistical skills and competence in R programming. Experience working with large datasets would be valuable.

A scholarship is available through UNSW's highly-competitive Scientia program (AU\$40,000/yr stipend for 4 years + tuition covered + AU\$10,000/yr career development funds). <https://www.2025.unsw.edu.au/>

apply/ Interested students should lodge an Expression of Interest at: <https://www.2025.unsw.edu.au/apply/-scientia-phd-scholarships/developmental-temperatures-drivers-phenotypic-change>

The deadline for EOIs is 20 July 2018, with applications due 3 September 2018 for early 2019 enrolment.

Lisa Schwanz <l.schwanz@unsw.edu.au>

UNewSouthWales EvolutionaryDynamicsVegetation

PhD Scholarship for Evolutionary Dynamics of Vegetation

INSTITUTION: Evolution & Ecology Research Centre, School of Biological, Earth and Environmental Sciences University of New South Wales, Sydney, Australia

PROJECT: the Short and Long-term Effects of Climate Change on Vegetation

SUPERVISORS: Dr Daniel Falster, A/Prof Will Cornwell, and Dr Matin De Kauwe

ABOUT: Climatic change is set to reconfigure ecological systems, as key drivers of vegetation composition and function - such as rainfall and temperature - shift away from their historical norms. Vegetation will respond over a range of timescales, from short-term acclimation, to medium-term adjustments in the abundance of current species, to long-term evolutionary responses, including adaptation and/ or selective replacement of species. In this project, the student will compare the pace and impact of these different responses, using process-based models; and then outline scenarios of alternative future states.

The student will receive a stipend of \$40K AUD per year for four years, as well as up to \$10k each year for career development. The project is based in the School of Biological, Earth & Environmental Sciences, at the University of New South Wales, Sydney Australia; supervised by Dr Daniel Falster, A/Prof Will Cornwell, and Dr Matin De Kauwe. Both international and domestic applications are strongly encouraged. Strong interest and background in quantitative techniques and eco-evolutionary dynamics is essential.

WHEN: Interested students must lodge an Expression of Interest by 20 July 2018, with full applications due 3 September 2018 for enrolment in early 2019.

MORE: For further information see <http://danielfalster.com/blog/2018/06/-01/PhD/> "daniel.falster@unsw.edu.au" <daniel.falster@unsw.edu.au>

UNewSouthWales PhenotypicPlasticity

PhD Scholarship in Phenotypic Plasticity

Project: The role of the social environment in triggering gene expression differences associated with developmental plasticity.

Supervisors: Michael Kasumovic, Russell Bonduriansky, and Terry Ord

Evolution & Ecology Research Centre, School of Biological, Earth and Environmental Sciences

University of New South Wales, Sydney, Australia.

We know that the social environment can have massive effects on the strength and direction of selection that adults experience. More recently, however, research has shown that the adult social environment can also affect the developmental trajectory, physiological underpinnings, and gene expression that juveniles undergo; this can have important effects on adult phenotypes. This project will explore the various ways the social environment affect juvenile development and adult behaviour, and the role that gene expression plays in moderating both. Students can take the project in any direction they wish.

The research will employ quantitative syntheses of published literature, with potential expansion to focused empirical experiments in crickets, spiders, or any suitable organism for the study. The ideal candidate for this project will have a Bachelor's or Master's degree in Biology, with an emphasis in animal behaviour and evolution, and a strong interest in phenotypic plasticity. Essential skills and experience include: experience with an independent research project; strong writing skills; strong statistical skills and competence in R programming. Experience working with molecular techniques and statistical analyses surrounding genomic data would be valuable (but not necessary if the candidate is willing to learn).

A scholarship is available through UNSW's highly-competitive Scientia program (AU\$40,000/yr stipend for 4 years + tuition covered + AU\$10,000/yr career

development funds. <https://www.2025.unsw.edu.au/apply/> Interested students should lodge an Expression of Interest at: <https://www.2025.unsw.edu.au/apply/scientia-phd-scholarships/how-extreme-climatic-variation-affects-gene-expression-and-phenotypic> But should contact Michael (m.kasumovic@unsw.edu.au) for help with the application.

The deadline for EOIs is 20 July 2018, with applications due 3

September 2018 for early 2019 enrolment.

Michael Kasumovic <m.kasumovic@unsw.edu.au>

UOsnabrueck 6 Cellular Evolution

The Research Training Group “EvoCell: Cellular Mechanisms of Evolutionary Innovation” at the University of Osnabrueck invites applications for 6 Positions for PhD Candidates

(salary grade E 13 TV-L, 65 %)

starting October 1st, 2018 for a duration of three years.

The international research training group “EvoCell: Cellular mechanisms of evolutionary innovation” aims at bridging the current gap between evolution and cell biology that is highly relevant to many fields. An interdisciplinary approach with complementary expertise in organismic, cell, theoretical and computational biology will take advantage of different model systems ranging from membrane vesicles (P1) over bacteria (P2, P3) and yeast cells (P4) to multicellular animal and plant eukaryotic systems (P5, P6). The participating groups provide a collaborative research environment including access to the state-of-the-art research equipment of the Center for Cellular Nanoanalytics Osnabruck (CellNanOS) and an association with the SFB 944 - Physiology and dynamics of cellular microcompartments. Successful candidates will participate in a structured training program offering scientific courses, training in transferable and outreach skills and participation in research symposia.

Description of Responsibilities:

- Cooperation in the research activities of the Research Training Group
- The position offers the possibility to pursue a doctorate degree
- Teaching duties

Required Qualifications:

- An excellent master degree/diploma in biology or related fields including modelling

Desirable qualifications:

-A strong interest for research at the intersection between evolution and cell biology

- Good English language skills (the training group language is English)

Projects offered:

P1 Evolution of complexity of cell membrane (A. Mulki-djanian/Physics)

P2 The evolution of multicellular clusters in bacteria: causes and consequences (C. Kost/ Biology)

P3 Modelling the interplay between metabolic evolution on a cell-level and community dynamics in microbial systems (K. Frank/ Environmental Systems Research)

P4 Evolution of TORC1 signaling in the control of serine homeostasis (F. Frohlich/ Biology)

P5 Evolution of regulatory networks controlling sexual reproduction in land plants (S. Zachgo/ Biology)

P6 The evolution of cytoskeletal regulation and neuronal complexity (R. Brandt/ Biology)

For more information on the projects, visit:

<https://www.biologie-cms.uni-osnabrueck.de/fileadmin/Medien/Allgemein/pdf/->

[Evocell_Information_for_applicants.pdf](#)

or the

homepages of the participating groups.

Osnabruck University has been certified as a family-friendly university committed to helping working/studying parents and careers balance their family and work life.

The university aspires to ensure equal opportunities for men and women and strives to work towards a gender balance in schools or departments where new appointments are made.

If equally qualified candidates apply, preference will be given to those with special needs.

Applications should include a curriculum vitae, list of publications, certificates of academic qualifications, and addresses of two referees together with a short statement describing your research interest and motivation to join the research training group.

Deadline for application is June 16th, 2018.

Application documents should be sent via email as one single PDF to:

bewerbung@biologie.uni-osnabrueck.de.

Further information about the graduate school or the application procedure is available from the speaker Prof. Dr. C. Kost: christian.kost@uni-osnabrueck.de

Christian Kost <christiankost@gmail.com>

UOxford PredictingAntimicrobialSpread

Note early deadline: Wednesday 11 July

An opportunity has arisen for a D.Phil. (Ph.D.) place on the BBSRC-funded Oxford Interdisciplinary Bioscience Doctoral Training Partnership in the area of Artificial Intelligence, specifically 'Predicting the spread of antimicrobial resistance from genomics using machine learning'.

If successful in a competitive application process, the candidate will join a cohort of students enrolled in the DTP's one-year interdisciplinary training programme, before commencing the research project and joining Danny Wilson's research group at the Big Data Institute. See www.danielwilson.me.uk This project addresses the BBSRC priority area 'Combating antimicrobial resistance' by using ML to predict the spread of antimicrobial resistance in human, animal and environmental bacteria exemplified by *Escherichia coli*. Understanding how quickly antimicrobial resistance (AMR) will spread helps plan effective prevention, improved biosecurity, and strategic investment into new measures. We will develop ML tools for large genomic datasets to predict the future spread of AMR in humans, animals and the environment. The project will create new methods based on award-winning probabilistic ML tools pioneered in my group (BASTA, SCOTTI) by training models using genomic and epidemiological data informative about past spread of AMR. We will apply the tools collaboratively to genomic studies of *E. coli* in Kenya, the UK and across Europe from humans, animals and the environment, Enterobacteriaceae in North-West England, and *Campylobacter* in Wales. Genomics has proven effective for asking 'what went wrong' in the context of outbreak investigation and AMR spread; here we will address the greater challenge of repurposing such information using ML for forward prediction of future spread of AMR. Scrutiny will be intense because future predictions can and will be tested, raising the bar for the biological realism required while producing computationally efficient tools.

Attributes of suitable applicants: Understanding of genomics. Interest in infectious disease. Some numeracy, e.g. mathematics A-level, desirable. Experience of coding would help.

Funding notes: BBSRC eligibility criteria for studentship funding applies (<https://www.ukri.org/files/legacy/news/training-grants-january-2018-pdf/>). Successful students will receive a stipend of no less than the standard RCUK stipend rate, currently set at 14,777 per year.

How to apply: send Dr Wilson a CV and brief covering letter/email (no more than 1 page) explaining why you are interested and suitable by the ***Wednesday 11 July*** initial deadline. (He will invite the best applicant/s to submit with him a formal application in time for the Friday 13 July second-stage deadline).

Daniel Wilson <daniel.wilson@bdi.ox.ac.uk>

UPadua ComparativeGenomics

PhD project: Comparative and evolutionary genomics of marine animals and arthropods of veterinary interest

Dear evoldir members a PhD project in Veterinary Sciences, described below, will be available, on an entrance competition basis, at the Department of Biomedicine and Food Science (University of Padua, Italy). Irrespective to the official label associated to this project (Veterinary Sciences), the focus of this study is strongly oriented toward the evolution of mitochondrial genomes in selected groups of Animals.

Project title:

Comparative and evolutionary genomic of animals, with particular reference to marine species and taxa of veterinary interest:

Comparative and evolutionary genomics of marine animals and arthropods of veterinary interest

Short description: The project will be developed through a bioinformatic approach applied to genomic data generated using the Illumina technology. Genomic sequences (18 gigabases/taxon) are available for more than one hundred species of Crustacea, Teleost Fishes and Hymenoptera. Comparative and evolutionary studies will be performed on the mitochondrial genomes of a selected group of taxa. The nuclear genes will be also analysed to identify slow and fast evolving markers useful for species identification. The study will be extended to

the genomic sequences, already identified with BLAST, that belong to viruses, bacteria and protists, infecting these animals. The bioinformatics analyses will be performed using a cluster of servers already available in the laboratory of the proponent of the project.

See the following link for further details <http://www.dottorato.veterinaria.unipd.it/node/2152>: The supervisor of the project will be prof. Enrico Negrisolò

Negrisolò on Google scholar <https://scholar.google.it/citations?user=3DZUN4qcUAAAAAJ&hl=-3Dit>

Negrisolò on Research Gate https://www.researchgate.net/profile/Enrico_Negrisolò

To apply see <http://www.unipd.it/en/research/-doctoral-degrees-phd-programmes/phd-programmes-calls-and-admissions> The deadline is 26 June 2018 1.P.M. local time.

Enrico Negrisolò

“enrico.negrisolò@cribi.unipd.it”

<enrico.negrisolò@cribi.unipd.it>

UPadua Italy GuppySexualSelection

PhD scholarship for a project on sexual selection in guppies (*Poecilia reticulata*)

Supervisor Andrea Pilastro, University of Padova, Italy

Proposed project

Aim of this project is to explore how social environment shapes the evolutionary dynamics associated with pre- and post-copulatory sexual selection in the guppy (*Poecilia reticulata*). The project will be part of a collaboration with J. Evans (University of Western Australia), A. Wilson (University of Exeter, UK) and F. Garcia-Gonzalez (Doñana Biological Station, Spain). The candidate will have to possibility to spend part of the three-years project at one, or more of these institutions. Potential candidates are encouraged to contact me (andrea.pilastro@unipd.it).

Application deadline: 26th June 2018, Starting: Oct 1st, 2018

For more information: University of Padova <http://www.unipd.it/en/> Department of Biology <https://www.biologia.unipd.it/en/> PhD School in Biosciences <https://dottorato.biologia.unipd.it/> -

Andrea Pilastro Dept. of Biology, University of Padova via Ugo Bassi 58/B - 35131 Padova, Italy

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UPadua

PhilosophyEvolutionaryBiology

University of Padua

BIOSCIENCES PhD program - 2018

<https://dottorato.biologia.unipd.it> CALL FOR ADMISSION TO THE PhD COURSES 2018

The call has been published.

Deadline: 13:00 (CEST) on June 26th 2018.

Curriculum: Evolution, Ecology and Conservation

Title: Philosophy of Evolutionary Biology: Extended Synthesis and Human Evolution (tutor: Telmo Pievani)

The general frame of the position is philosophy of science applied to evolutionary biology. The issues will be related to the theoretical proposals, the implications and the debates surrounding the so-called “Extended Evolutionary Synthesis” and its models (i.e. niche construction, multiple sources of variation, plasticity, exaptation, bio-cultural evolution, macroevolutionary patterns). The research will focus on contemporary debates in philosophy of evolutionary biology, dissecting ideas like progress, human nature, human races, anagenetic vs cladogenetic phylogenies, mosaic evolution, niche construction in human evolution, etc. The position is indicated for philosophers of science or biologists and anthropologists with a solid training in philosophy of science and a general competence in evolutionary biology.

For further info on this project please contact prof. T. Pievani (dietelmo.pievani@unipd.it).

Best regards

Telmo Pievani

Telmo Pievani

University of Padua - Department of Biology

Rector’s Delegate for Institutional Communication

Full Professor - Philosophy of Biological Sciences

Via U. Bassi, n. 58/B

35131 Padova - Italy

tel. (0039)-049-8276193

email: dietelmo.pievani@unipd.it

www.telmpievani.com

Telmo Pievani

<telmo.pievani@gmail.com>

Murienne (philippe.gaubert@univ-tlse3.fr and jerome.murienne@univ-tlse3.fr). Application deadline is 1st July 2018. Starting date is 1st November 2018.

Philippe Gaubert <philippe.gaubert@univ-tlse3.fr>

UPaulSabatier France PangolinConservation

Subject: Graduate position: Universite Paul Sabatier, Toulouse, France

A 3-yr doctorate position is available at the Laboratoire Evolution et Diversite Biologique (EDB; <http://www.edb.ups-tlse.fr/>) to develop genomic-based tools for tracing the pangolin trade. Pangolins are scaly Afro-Asian mammals that suffer from an unprecedented rise in the amplitude of their illegal trafficking, involving both intra- and inter-continental networks. The successful candidate will use genomic approaches to assess the phylogeographic patterns of the eight species of pangolins, from which turnkey genomic tools will be implemented to track the pangolin trade through its different scales.

The ideal candidate should be motivated by lab work, and highly interested in phylogenomics and the development of diagnostic tools for conservation genetics. Experience in genomic and / or degraded DNA analyses would be a plus.

The position and lab work are fully supported by an ANR - Agence Nationale de la Recherche research grant (<http://www.agence-nationale-recherche.fr/Project-ANR-17-CE02-0001>).

The successful candidate will be co-supervised at EDB by Philippe Gaubert (<http://www.edb.ups-tlse.fr/-Gaubert-Philippe>) and Jerome Murienne (<http://www.edb.ups-tlse.fr/Murienne-Jerome>), in a highly motivating multi-disciplinary and -linguistic environment. EDB is located within the campus of the Universite Paul Sabatier (UPS), one of the top research establishments in France. Toulouse is France's second largest university town, with 120,000 students, and benefits from an enjoyable situation at the foot of the Pyrenees, between the Mediterranean and the Atlantic coasts.

Applicants should send their CV (2 pages max.) and a Statement of Interest including academic referents to Philippe Gaubert and Jerome

UToulouse HorseEvolGenomics

PhD fellow in Ancient DNA and Horse Evolutionary Genomics

University of Toulouse, Prof Ludovic Orlando

Applications are invited for a three-year PhD fellowship in the field of Ancient DNA and Horse Evolutionary Genomics. The research program will be developed within the framework of the PEGASUS ERC (<http://orlandoludovic.wixsite.com/pegasus-erc>), led by Professor Ludovic Orlando. It will be carried out in the new research Centre called AGES (Archeology, Genomics, Evolution and Societies) that he recently developed in France (<http://amis.cnrs.fr/?Archeology-Genomics-Evolution-and-Societies-AGES>) at the University of Toulouse (<http://www.univ-tlse3.fr/home/home-page-en-379161.kjsp?RH=ACCUEIL>). Research at AGES is aimed at tracking the impact of the many ecological, societal and cultural transitions present in our recent evolutionary past using a true multi-disciplinary approach, merging together classical archaeological and historical approaches with the latest advances in molecular and statistical genomics. Animal domestication, especially that of the horse, represents one of such historical turning points.

Project The project will focus on analyzing an extensive dataset of (ancient) horse genomes and epigenomes recently produced in the group to identify the prehistorical and historical modifications underlying the origins of the modern horse. It follows up on our recent publications demonstrating that modern domestic horses descend from a domestication wave that replaced in the 3rd millennium BCE the horse stock that was previously domesticated in the Eneolithic period (Librado et al. Science 2017; Gaunitz et al. Science 2018). Identifying the exact geographical and temporal locus of this mysterious second domestication centre represents one of the core objectives of the project. In addition to cover the key transitional period represented by the 3rd mill. BCE, our current dataset includes a series of archaeological contexts within the last 4,000 years where key equestrian technologies and novel utilizations of the horse have emerged. It also largely extends our current

knowledge of the worldwide diversity present in modern horses. The principal supervisor is Professor Dr Ludovic Orlando (<http://amis.cnrs.fr/?Orlando-Ludovic>).

We are seeking a highly motivated, hard-working and productive student who is interested and capable of interacting and contributing to a research team consisting of archaeologists, molecular biologists, bioinformaticians, and evolutionary biologists. The ideal candidate will have a background in statistical genomics and/or population genomics and will show proficiency with Bash and other programming languages such as R, Perl and/or Python. S/he will be an experienced user of state-of-the-art packages aimed at the analysis of genome-scale sequence data for several hundreds of individual genomes (eg. Samtools, GATK, Picard, PLINK, ANGSD, Admixtools, etc). S/he will show great abilities to work in an international environment and will be familiar with the molecular methods underlying genome sequencing. International experience and first-hand experience in the analysis of ancient DNA and/or High-Throughput DNA Sequencing data will be considered positively.

Job description The PhD student will be expected to:
 * Manage and carry through his/her research project
 * Take PhD courses * Write scientific articles as well as the PhD thesis * Participate in scientific meetings
 * Contribute to other research activities in the group * Disseminate research

Opportunities for teaching might open in case of interest but will not be compulsory.

Key assessment criteria

- A master's degree related to the subject area of the project, at the time of the employment. * The grade point average achieved * Professional qualifications relevant to the PhD program * Previous publications * Relevant work experience * Other professional activities * Language skills (the applicant must be fluent in English, which is the language at AGES)

Application Procedure

The application will be sent electronically to Ludovic Orlando (ludovic.orlando@univ-tlse3.fr) and must include:
 * Curriculum vitae (with publication record, if any) * Diplomas and transcripts of records (BSc and MSc) * Motivation letter * Contact details from two references
 * Documentation of English language qualifications, cf. general rules and guidelines, p. 5

The University wishes our staff to reflect the diversity of society and thus welcomes applications from all qualified candidates regardless of personal background. Proficiency in communicating in English is compulsory.

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UZurich PlantMycorrhizalInteractions

PHD POSITION IN PLANT-MYCORRHIZAL INTERACTIONS

We are seeking a PhD student with a background (MSc degree) in ecology, evolutionary biology, or a closely related discipline. The successful applicant will be based at the Department of Evolutionary Biology and Environmental Studies of the University of Zurich, Switzerland.

The mutualism between plants and arbuscular mycorrhizal fungi (AMF) is widespread and has persisted for over 400 million years. The stability of this mutualism depends on a 'fair trade' between plants and fungi, and on mechanisms that protect this system from exploitation by 'cheaters'. Indeed, plants and AMF are able to discriminate symbiotic partners through a range of mechanisms and invest selectively into different partners, depending on the relative quality of their service.

The successful applicant will analyze the trade of carbon and nutrients among plants and AMF in a series of experiments, using methods that include isotope labeling and molecular tools. The overall objective of the project is to characterize the strategies of both partners in the light of game-theoretical and network-based predictions. A particularly important question will be how strategies of plants and fungi scale from pairwise interactions to systems with multiple species involved.

We are looking for a highly motivated, enthusiastic, and independent PhD candidate who has a strong interest in ecological and evolutionary questions. An accurate and clean laboratory working style is absolutely essential. Experience with standard molecular biological techniques is beneficial. A high standard of written and spoken English is essential.

The successful applicant will be supported and supervised by Pascal Niklaus and Jordi Bascompte (University of Zurich), Ansgar Kahmen (University of Basel), and Marcel van der Heijden (Agroscope Reckenholz).

http://www.ieu.uzh.ch/en/staff/member/-niklaus_pascal.html http://www.ieu.uzh.ch/en/staff/member/bascompte_jordi.html http://www.ieu.uzh.ch/en/staff/member/vanderheijden_marcel.html

botanik.unibas.ch/forschungsgruppen-der-botanik
<http://www.agroscope.admin.ch> The PhD candidate will benefit from training offered within the PhD program in ecology (<http://www.ieu.uzh.ch/en/teaching/-phd/graduate.html>) and the Zurich-Basel Plant Science Center (<http://www.plantsciences.uzh.ch/en.html>), through which this project is funded.

Important parts of the experimental setup have been prepared so that the successful candidate can capitalize immediately on previous work. The position is opened immediately, and the successful applicant should there-

fore start no later than September 1, 2018. Salaries will follow University of Zurich regulations.

The University of Zurich is the largest University of Switzerland and offers outstanding work conditions, a high quality of life in Zurich, and an excellent support environment.

To apply, please send a single pdf containing motivation letter, complete CV, and the names of two references to pascal.niklaus@ieu.uzh.ch, with subject PSC-PLANT-AMF.

“Pascal A. Niklaus” <Pascal.Niklaus@ieu.uzh.ch>

Jobs

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AnnArbor Michigan FishMuseumCollectionsManager

Posting Title: Research Museum Collection Manager -
Fish Division

Posting salary range: \$48,000 - \$56,000

The Department of Ecology and Evolutionary Biology (EEB) is seeking a Collection Manager for the Museum of Zoology (UMMZ) Fish Division (<https://lsa.umich.edu/ummz/fishes.html>), located at the new state of the art Research Museums Center (RMC) in Ann Arbor, Michigan. The UMMZ develops and maintains zoological collections explicitly for use in research and education, benefiting science, society, and the university

at large. The scientific role of the UMMZ is to train students and engage in systematic biology and biodiversity studies. These broad and overlapping fields entail the discovery and study of the diversity of organisms, their evolutionary relationships, and the processes that originate biodiversity. EEB has an outstanding, diverse and collaborative group of researchers in evolutionary biology, biodiversity science, and ichthyology.

The UMMZ Fish Collection is worldwide in its geographic scope and one of the largest of its type, including more than 200,000 lots and 3.3 million specimens representing 98% of fish orders. The collection is particularly strong in Neotropical, North American, African and Southeast Asian freshwater holdings. Historical collections often date back to the early 20th Century and include irreplaceable samples from North and Central America, Asia and Madagascar.

We seek candidates with a strong commitment to a vision of the Fish Collection as a key resource for research and education within the University and to the ichthyological community nationally and internationally. The position offers exciting opportunities for mentoring, and career development, including limited research within the context of the Fish Division curatorial priorities.

Responsibilities: 1. Growth, Maintenance and Digitization (GMD) of the fish collections, including fluid, cleared-and-stained and skeleton specimens, tissue samples, and ancillary collections such as paper archives, field notes, geographic and environmental data, and digital assets such as photography, X-rays, and micro CT scans. Activities may include organizing and participating in field expeditions (including international collecting), coordinating and contributing directly to digitization efforts, as well as writing collection-based grants to support the fish collection. 2. Working with faculty curators to develop and implement policies, standards, and procedures. This involves, as necessary, developing standard operating procedures for acquisition, accessioning, databasing, archival and use of new or emerging genomic, digital resources and other ancillary collections. Reviewing, updating, and enhancing the fish collections management plan. 3. Accessioning and cataloguing of new specimens, tissues and ancillary collections into the collection and the electronic database. This activity includes coordinating curatorial priorities with faculty curators and the daily management of staff workers, work-study students, graduate curatorial assistants and other personnel. 4. Support of and coordination with faculty curators, student researchers and visiting collaborating researchers to plan and develop research projects utilizing the research collections and/or enhance collection resources. 5. Being involved in grant writing to secure grant funding for research projects

that enhance collection resources. 6. Maintenance and growth of the fish genomic resources in the Liquid Nitrogen Facility. This activity involves the accessioning of new samples, database cross-referencing to voucher specimens, as well as development and maintenance of database records on genomic resources in the Fish Division. 7. Coordinate and process inter-departmental and inter-institutional loans and exchanges. Activities include the packing and unpacking of loans (specimens and tissues) and securing state, federal and international permit requirements when appropriate, as well as the electronic exchange of digitized information. Facilitating the establishment of Memoranda of Understanding or Material Transfer Agreements among institutions for loans, exchange and import/export of collection-related materials nationally and internationally. 8. Routine maintenance and updating of the data portal through which our holdings are made accessible to researchers across the world. This activity is performed in ongoing coordination with faculty curators and requires regular attention to both our electronic, searchable database and a server that connects us to the international community. 9. Training and supervision of staff volunteers, work-study students, graduate curatorial assistants, and when needed, visiting

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Charlotte North Carolina Tech Bioinformatics

Genomics Software Developer

Job Description

The David H. Murdock Research Institute is currently seeking a Genomics Software Developer. Qualified candidates will have both applied software development and integration skills and a theoretical understanding of their application. The incumbent must have a strong technical background in computer science or bioinformatics; knowledge of biology is desired. The primary role will be to identify, develop, integrate, and implement programs to provide research support for various projects within the genomics sequencing laboratory. The incumbent will be an active computer science contributor to computational projects as a bioinformatics team

member. The incumbent must be comfortable with working in a dynamic, fast changing environment, and able to communicate complex informatics principles, methods, analyses, and results to end users from diverse backgrounds.

Additionally, the chosen candidate will be self-motivated, able to communicate equally well with both computer and biological scientists and enhance the performance of an interdisciplinary team. The incumbent will apply his or her education, training and experience to work independently on numerous goals, including implementation of automated analytical tools necessary for the collection and analysis of data generated by the DHMRI's high throughput genomics efforts.

The Bioinformatics Group within the DHMRI supports all laboratories within our facility including: Genomics, Analytical Sciences, *In Vitro*Sciences, and NMR. Candidates with computer science or bioinformatics experience in these areas are of specific interest.

Qualifications

Minimum Requirements

§BS with 2-3 years' experience or MS in Computer Science, Bioinformatics, or related discipline

§Strong Statistics: SAS / R / MATLAB

§OS: Unix/Linux, Windows

§Programming: Java/C++/C# .Net. Scripting: Perl, Shell, Python

§API/Integration Development

Preferred Experience

§Experience in handling large data sets (structured and unstructured) such as sequencing, proteomics and imaging data

§Prior work in Biology / Chemistry / Genomics.

§Analytical pipeline development.

§In-depth understanding, analysis and processing of data from various post-genomic technologies and their application (Statistical analysis and integration of genotyping, gene expression, chromosomal copy number and structural computational biology datasets).

§Experience using relational databases and database query language. Experience programming in a database query language. Familiarity with relational databases, SQL language, Unix and programming tools preferred.

§Expertise in methods and technologies utilized for integrative analysis of biosciences and clinical data, such as ontologies, semantic web technologies and data exchange standards.

§This position requires strong communication skills and the ability to communicate across domains with biologists, chemists and systems biology teams.

§Wide understanding of commercially available bioinformatics/clinical genomics tools and databases.

§Excellent communication and collaborative skills working as a part of multidisciplinary teams.

§Excellent written and oral communication skills.

§Detail-oriented and organized, with strong initiative and sense of ownership when driving projects to completion.

Equal Employment Opportunity

We are proud to be an EEO/AA employer M/F/D/V.

Rebekah Rogers <rebekah.rogers@gmail.com>

ClarkU ParttimeTeaching MolSystematics

Department of Biology Clark University Worcester MA 01610

Part-Time Instructor â euro Â

The Department of Biology is seeking a part-time instructor for the fall 2018 semester to teach the following undergraduate level course:

Molecular and Evolutionary Systematics (BIOL 254).

This is a lecture-only course that runs Monday and Friday, 10:25-11:40pm.

Preference is for applicants with a Ph.D. but we will consider those nearing completion of the degree. Previous teaching experience is preferred. We expect to offer \$5,000 for course coverage.

Part-time faculty expectations include the following; excellent attendance record, regularly scheduled office hours, adherence to undergraduate program requirements.

The fall semester begins August 27, 2018 and ends December 21, 2018.

Interested applicants should electronically submit a resume and cover letter (or questions) concerning this position directly to the Chair of the Biology Department, Justin Thackeray (jthackeray@clarku.edu).

“AA/EOE Minorities and women are strongly encouraged

to apply”

Justin Thackeray <JThackeray@clarku.edu>

FieldMuseum Chicago Director

Director and Full Curator, Integrative Research Center
Chicago, IL, USA

The Field Museum seeks a dynamic leader and researcher with museum experience to serve as Director of its Integrative Research Center and Full Curator. The Field Museum is one of the world’s leading natural history museums with globally important research in Natural History, including Anthropology, Botany, Geology, and Zoology. The Museum’s Integrative Research Center (IRC) is comprised of the curatorial staff, and the Museum’s interdisciplinary laboratory facilities including the Pritzker Laboratory for Molecular Systematics and Evolution, an Elemental Analysis Facility, a Scanning Electron Microscopy Lab, and Fossil Preparation Facilities and associated staff. The Director of the Integrative Research Center will report to the Vice President of Science and Education

The new director will (1) demonstrate a strong commitment to the Museum’s mission of research, scholarship, training, and provide sound leadership, management, and fiscal direction to support and develop diverse programs within the IRC; (2) work collaboratively with the IRC section heads and other IRC staff to promote research in each of the museum’s science foci; (3) advance interdisciplinary investigations and training both within and outside the museum; (4) work with the IRC Committee of the Board of Trustees to carry out the museum’s collections-based research mission, (5) work in collaboration with the Vice President, Science and Education, and the IRC section heads to help secure grants and cultivate the donor community, and (6) collaborate with broader museum leadership and leverage IRC expertise to support other mission-based areas of the museum, including collections, environmental and cultural heritage conservation, educational outreach, and exhibitions.

The Integrative Research Center is comprised of 21 curators, and approximately 40 full and part-time administrative, research, and support staff. We maintain academic ties including cross-appointments with the University of Chicago, University of Illinois at Chicago, Northwestern University, and other universities. Numerous graduate and postdoctoral students are supervised

by or work with curators, and visiting national and international researchers and collaborators are often in residence in the IRC for various periods.

The ideal candidate will possess:

- an innovative vision for research at a free-standing natural history museum that serves multiple constituencies
- an active collections-based research program
- a doctoral degree in a discipline related to collections-based natural or cultural history
- a significant record of scholarship and research sufficient to be tenured at The Field Museum
- management experience, preferably in a museum setting
- a significant record of extramural funding success and experience with donor development
- a strong record of collaboration with diverse institutional constituencies.

For inquiries and additional information, contact the chair of the search committee, Thorsten Lumbsch (tlumbsch@fieldmuseum.org).

Review of applications will begin on August 29, 2018. To apply, please provide a cover letter stating interests and qualifications, a full curriculum vitae, contact information for three references, and five representative scholarly publications to the search committee chair at IRCDirectorSearch@fieldmuseum.org.

All application materials must come through IRCDirectorSearch@fieldmuseum.org, applications received through the online application site or through any other email will not be reviewed.

https://www.fieldmuseum.org/about/-careers?hireology_job_id=207329 – Matthew P. Nelsen
The Field Museum Integrative Research Center (Insects)
1400 S. Lake Shore Drive Chicago, Illinois 60605, USA

mpnelsen@gmail.com <https://www.fieldmuseum.org/about/staff/profile/2556> <https://sites.google.com/site/mpnelsen/> Matthew Nelsen
<mnelsen@fieldmuseum.org>

FloridaAtlanticU LabTech CavefishEvolution

The Kowalko laboratory is seeking a Lab Technician to perform research in molecular biology and behavior in a laboratory that studies the evolution of a small freshwater fish, the blind Mexican cavefish. Primary responsibilities include breeding and maintaining cavefish and zebrafish, performing general molecular biology

techniques (cloning, transgenesis, genome editing, etc.), performing behavioral analyses, collecting and analyzing data, contributing to publications, equipment and facilities maintenance and management, and ordering. The Lab Technician will perform these tasks under the supervision of the principal investigator.

Minimum Qualifications:

A Bachelor's degree in molecular biology, genetics, or a related field from an accredited institution is required.

Salary:

30,000 + benefits

Please apply at <https://fau.edu/jobs/> Johanna Kowalko, Ph.D. Adjunct Assistant Professor and Assistant Scientist Department of Genetics, Development and Cell Biology Iowa State University 640 Science Hall II Ames, Iowa 50011 (515) 294-2360

Johanna Kowalko <jkowalko@gmail.com>

iDiv LeipzigU Tech PlantEvolution

The German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig is one of four National Research Centres funded by the German Research Foundation (DFG). Its central mission is to promote theory-driven synthesis and data-driven theory in this emerging field. The concept of iDiv encompasses the detection of biodiversity, understanding its emergence, exploring its consequences for ecosystem functions and services, and developing strategies to safeguard biodiversity under global change. It is located in the city of Leipzig and it's a central institution of the Leipzig University, jointly hosted by the Martin-Luther-University Halle-Wittenberg, the Friedrich Schiller University Jena and the Helmholtz Centre for Environmental Research (UFZ). Furthermore, it gains support by the Max Planck Society, the Leibniz Association and the Free State of Saxony. More Information about iDiv: www.idiv.de. The Evolution & Adaptation research group focuses on the interchange between (macro-) ecology and evolution, to understand the global distribution of genetic, taxonomic and functional diversity. We therefore generate genetic (genomic) data (e.g. from plants from Madagascar), and build databases of biodiversity data (such as functional traits) to investigate the link between genes and phenotype. Understanding these links is important for predicting how adaptable biodiversity is to current and future global change.

Integrated in iDiv, the Leipzig University, offers the following position in our new Evolution and Adaptation Research Group as soon as possible:

Leipzig, 18 June 2018

Biological-Technical Assistant

(initially limited until 30. September 2020) Salary: Entgeltgruppe 6 TV-L * - Combining (botanical) data sources (such as monographs and floras) to build databases for biodiversity data (using Access or SQL) * - Measuring functional plant traits from herbaria or fresh sample material * - General laboratory organization (incl. setting up a new laboratory) and laboratory maintenance * - Planning and conducting molecular and cell biology experiments * - Analysis of generated data and preparation of suitable presentations Requirements:

* - successful professional qualification as Biological-Technical Assistant or an equivalent degree * - hands-on experience in molecular and cell biology techniques (DNA/RNA isolation, PCR, real-time PCR, cloning) would be preferable * - experience in building databases would be preferable * - very good computer skills (MS Windows, MS Office etc.) * - good spoken and written English skills * - strong team-player, but can also work independently * - very good work organization and reliability * - experienced to work in interdisciplinary and international teams Applications with the usual documents are preferred in English and are accepted with reference file number 134/2018 until July 9, 2018 via our application portal under apply.idiv.de. We prefer applications via our application portal, hard copy applications can be sent to: Deutsches Zentrum für integrative Biodiversitätsforschung (iDiv) Halle-Jena-Leipzig Personalabteilung Deutscher Platz 5e, 04103 Leipzig Questions concerning our application process can be sent to: hr@idiv.de. Applying via email is questionable under data protection law. The sender assumes full responsibility. Severely disabled persons are encouraged to apply and will be given preference in the case of equal suitability. By sending us your application documents you consent to the processing of the data contained within for the purpose of the selection process for the advertised position. You can revoke your consent at any time. The processing takes place exclusively for this selection process and is carried out on the basis of Article 6 of the GDPR (General Data Protection Regulation). This

includes passing on data to the members of the selection committee, the HR office, the Commissioner for Equal Opportunities, the Representative Body for Severely Disabled Employees and the Staff Council as part of their organizational or legal responsibilities. Your data will be stored for a maximum of 6 months following

completion of the selection process and subsequently deleted.

In accordance with the GDPR you have the right to receive information from the recipient of the application about your personal data, the right to correction, deletion or restriction of processing, as well as a right to object to processing.

If you have any questions, please contact the Leipzig University data protection officer (Mr Thomas Braatz, Augustusplatz 10, 04109 Leipzig, tel.: 03419730081).

Dr. Renske E. Onstein Head of research group “Evolution and Adaptation” German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig Deutscher Platz 5e 04103 Leipzig Germany

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LouisianaU 2 MarineEvolution

LUMCON is currently advertising for two new faculty positions in Coastal and/or Marine Sciences that should be of interest to evolutionary biologists

CLUSTER HIRE FOR COASTAL OR MARINE SCIENCE FACULTY POSITIONS AT LUMCON

The Louisiana Universities Marine Consortium for Research and Education (LUMCON; <https://lumcon.edu>) seeks to hire two new Assistant Professors in the second phase of multi-year faculty expansion. We invite well-qualified coastal or marine scientists, regardless of discipline, to apply. We are interested in scientists that address a wide range of fundamental problems in ocean and coastal sciences, as well as interdisciplinary research questions, using observations, modelling, theory and/or field and laboratory experiments. Candidates should have notable research achievements, demonstration of funded research, or potential for funded research, and a strong commitment to education and outreach. Preference will be given to candidates who can clearly demonstrate a research program that maximizes the locality and research assets of the DeFelice Marine Center and complements and extends the strengths of LUMCON and the consortium.

The LUMCON DeFelice Marine Center, located at the upper end of Terrebonne Bay in the Mississippi River deltaic plain between the Atchafalaya and Mississippi rivers, is in close proximity to numerous habitats including extensive marshes, estuaries, rivers large and small, and the open Gulf of Mexico. The Center facilities include a seawater system, multiple wet labs, a race-track flume, state-of-the art environmental chambers, extensive aquaculture and experimental tank facilities, a marsh mesocosm facility, and a fleet of research vessels. Our research vessel fleet and proximity to the coast facilitate the use of a broad mix of traditional and innovative instruments and observational techniques to make measurements in many settings from open-ocean to coastal regions. In addition, LUMCON represents a consortium of universities and colleges across the State of Louisiana.

The position carries a 9-month salary. The initial appointment is for three years; following a review, the contract may be renewed for three more years. A six-year review similar to tenure is conducted for promotion to Associate Professor, but LUMCON is not a tenure-granting institution.

Submit electronic copies of 1) a letter of interest; 2) curriculum vita; 3) research statement; 4) education and outreach statement; 5) a statement of how your research program would use the location of LUMCON’s Defelice Marine Center and its assets, develop collaborations with faculty at both the Marine Center and at consortium member universities, and collaboratively utilize the resources of the consortium member universities; and 6) the name, affiliation, address, phone and email address of three references to hr@lumcon.edu with the subject LUMCON FACULTY CLUSTER HIRE. Specific questions about the positions can be directed to Dr. Craig R. McClain, Executive Director, cmclain@lumcon.edu (985-851-2801).

Review of applicants will begin September 15, 2018 and continue until the positions are filled.

LUMCON is an AA/EO employer.

– Brian J. Roberts Associate Director of Science Associate Professor and REU Program Director Louisiana Universities Marine Consortium (LUMCON) 8124 Highway 56 Chauvin, LA 70344 Phone: (985)851-2821 FAX: (985)851-2874 broberts@lumcon.edu

Brian Roberts <broberts@lumcon.edu>

ManchesterU AnimalAdaptations

Lecturer in Animal Physiology and Behaviour at Manchester Metropolitan University

Applications are welcome from candidates with experience in animal physiology with strong links to animal behaviour or animal welfare. This post is based in the Division of Biology and Conservation Ecology, within the School of Science and the Environment and will complement and build upon our existing animal physiology and behaviour research profile. We have a strong interest in animal sensing and motion, social systems, animal communication and environmental adaptations. We would be especially interested in receiving applications from candidates with research and teaching experience in comparative physiology, including neurophysiology and endocrinology.

Please click here for further details: <https://www.jobs.ac.uk/job/BKU489/lecturer-animal-physiology-and-behaviour/>

Dr Robyn A. Grant Senior Lecturer in Comparative Physiology & Behaviour

Conservation, Evolution and Behaviour Research Group Neuroscience Research group Division of Biology and Conservation Ecology Manchester Metropolitan University Chester Street Manchester M1 5GD +44 (0)161 2476210 <http://www.sste.mmu.ac.uk/staff/staffbiog/default.asp?StaffID=965> “Before acting on this email or opening any attachments you should read the Manchester Metropolitan University email disclaimer available on its website <http://www.mmu.ac.uk/emaildisclaimer>”

Robyn Grant <Robyn.Grant@mmu.ac.uk>

MaxPlanckInst Seewiesen 3FieldAssist AvianEvolution

The Department of Behavioural Ecology and Evolutionary Genetics at the Max Planck Institute for Ornithology in Seewiesen, Bayern, Germany (see http://www.orn.mpg.de/2622/Department_Kempenaers), is

seeking three to four field assistants to work from 1st November 2018 to 30th April 2019. These assistants will work as part of a long-term study on the reproductive biology of a blue tit (*Cyanistes caeruleus*) population in a protected forest site in Southern Germany.

Work will include: - catching birds at feeders and nest-boxes using traps and/or mist nets - measuring and banding birds - maintenance of electronic nest-box and feeder hardware and equipment - setting up experimental equipment - data collection, entry, and management

Successful candidates must have experience in catching and handling birds, including extensive experience in mist netting. Applicants should also be highly motivated and well organised, with capabilities of working both in a group and independently. Field work hours can be long and tiring, thus applicants must be prepared to work in all types of weather conditions, at any time (including weekends and holidays), with typically only one day off per week.

The working language at the Institute is English, so good knowledge of the language is required. A full, clean driver's licence is essential, with driving experience of at least one year. Experience in driving vehicles with manual transmission is also a necessity. Applicants from outside the EU must ensure they are eligible to remain in Europe for the duration of their contract.

Successful candidates should be vaccinated against Tick Borne Encephalitis (TBE or FSME) before commencing the field work. In addition, applicants should be aware that Lyme disease spread by ticks is common in the area, and should inform themselves about the disease in advance.

The Max Planck Institute for Ornithology employs a dynamic, dedicated, and international group of researchers who are focused on exploring the fields of evolution, ecology, genetics, and neurobiology.

In an effort to employ more people with disabilities, the Max-Planck-Society specifically encourages people with disabilities to apply for the position. To increase the employment of women in areas where they are under-represented, the Max-Planck-Society also encourages women to apply for this position.

Review of applications and calls for interviews will begin in August 2018. If you are interested in applying for one of the field assistant positions as described above, please apply (including your CV) via email to kbeck@orn.mpg.de

Kristina Beck

Department of Behavioural Ecology and Evolutionary Genetics

Max-Planck-Institute for Ornithology
 Eberhard-Gwinner-Straie, House 7
 82319 Seewiesen
 Germany
 “Beck, Kristina” <kbeck@orn.mpg.de>

MichiganStateU ChairFishWildlife

Professor and Chairperson, Department of Fisheries and Wildlife

College of Agriculture and Natural Resources, Michigan State University

The Department of Fisheries and Wildlife at Michigan State University invites applications and nominations for the position of Professor and Chairperson. We seek a leader who will strategically focus the intellectual resources of our faculty, students and staff to address natural resource issues confronting society. The Department’s size, diversity, and commitment to the land-grant philosophy represent a substantial opportunity for a leader with the vision and desire to grow our impacts across the Great Lakes region, the nation, and the globe. The Chairperson will provide leadership of the Department in all teaching, research, extension, and outreach programs; maintain and enhance a creative, productive, and inclusive environment for faculty, staff, and students; oversee transparent Department processes and administrative decisions; and serve as the principal representative of the Department, regularly interacting with senior leadership of the College, MSU Extension, MSU AgBioResearch, and partner agencies and stakeholders with whom the Department has cooperative agreements.

Candidates must have been awarded a doctorate in a field related to any of the Department’s academic programs; qualify for the rank of full professor; have experience in personnel, program, and budget administration; demonstrate outstanding leadership and interpersonal skills; and exhibit commitment to fostering diversity and inclusion across a range of academic and professional activities. Competitive candidates should possess a demonstrated record of scholarship, teaching, and leadership; and be able to nurture the Department’s existing and extensive collaborations within natural and social sciences and across natural resource sectors and to leverage these collaborations to garner additional funds and

resources for Departmental programs. We seek candidates with experience overseeing academic department budgets and administering a large, multidisciplinary, and diverse faculty with a variety of appointments and assignments across the college and university. A strong record of team building is highly desired.

The Department of Fisheries and Wildlife is a vibrant community of scholars made up of 43 core faculty, 100 graduate and 240 undergraduate students, 31 research associates, and 6 full-time staff. Our Mission is to build local, national, and international capacities to conserve ecosystems that support fish, wildlife, and society through integrated programs in research, education and engagement. Collectively, we are tackling challenges and developing solutions in areas including, but not limited to: managing for sustainable harvest of fisheries and wildlife populations, developing sound governance structures and effective policies, assessing the ecological status of animal populations and their ecosystems at broad geographic scales, and understanding and responding to drivers of global change.

Candidates seeking the challenge and opportunity to lead an outstanding department should submit their application to the MSU Careers website (Posting #504297). For more information on the position, please contact search committee co-chairs Dr. Michael Wagner (mwagner@msu.edu) or Dr. Richard Kobe (kobe@msu.edu). Review of applications will begin August 1, 2018 and continue until the position is filled. The expected start date is August 2019 or sooner. Michigan State University is an equal opportunity/affirmative action employer and proactively upholds the Americans with Disabilities Act (ADA). Additionally, MSU is proactive in exploring employment opportunities for dual career families, both inside and outside the University, and respects all family forms.

Patricia A. Soranno, Professor and Founding-Editor-in-Chief

Limnology & Oceanography Letters

Department of Fisheries and Wildlife

Natural Resources Building, 480 Wilson Road, Rm 334D

Michigan State University, East Lansing, MI 48824

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Phone: (231)714-9591 | Twitter: @PASmsu2 | soranno@msu.edu

“Soranno, Patricia” <soranno@anr.msu.edu>

NHM Los Angeles County Tar Pits

Job Announcement Curator, Rancho La Brea

The Natural History Museum of Los Angeles County (NHMLA) is seeking a Curator for its renowned late Pleistocene Rancho La Brea collections housed at the La Brea Tar Pits & Museum. The successful candidate will conduct collection-based research in evolutionary biology and paleoecology broadly defined to include systematics, biogeography, global change, and/or biodiversity science, particularly as it relates to Rancho La Brea's vast collection of microfossils. The NHMLA, the largest natural history museum in the western United States, has recently finished a dramatic transformation including new ground-breaking exhibitions and a 3.1-acre wildlife garden, and it anticipates completing a similar transformation at the La Brea Tar Pits & Museum during the next decade. The successful candidate will play an instrumental role in the development and implementation of this exciting vision.

The La Brea Tar Pits & Museum constitutes one of the world's richest Ice Age fossil sites and has to date yielded an estimated 5 million specimens representing more than 600 species of animals and plants of Late Pleistocene and Holocene age. These collections afford a huge potential for a broad array of research and public programs and are continuously growing through ongoing excavations. The successful candidate will be responsible for: developing a dynamic, productive, and scientifically significant program of research to build a growing scientific and public profile; overseeing the development and curation of important collections; maintaining and strengthening the NHM's presence in key professional and governmental networks; and establishing active internal NHM collaborations, especially with the Education, Exhibits, Marketing and Communications, and Advancement Departments.

The successful candidate will have a Ph.D., a strong track record of published research, and experience in generating funding to support research. Experience in collections management would be an advantage, as would an interest in creative ways of engaging the public in research (e.g., community science). The Curator will be expected to develop an active and publicly engaging research program, develop working relationships with local universities, mentor students and postdoctoral fellows, and maintain research through obtaining competi-

tive grants and/or funding from other external sources. The candidate must have the vision and capability to build a research program that can be integrated within the NHMLA's ongoing efforts to document and interpret biotic responses to environmental change. The Curator will manage the collection's growth and undertake research in ways that increase both its scientific and public appeal.

The ability to communicate effectively and engage with a wide variety of audiences, including the public and the NHMLA's various stakeholders, is paramount. The successful candidate will be expected to oversee staff and supervise the NHMLA's Rancho La Brea programs. The Curator will actively participate in a broad range of museum activities, such as exhibits, education, outreach, training of educators, public communications including (but not limited to) media interactions, and fundraising. More specifically, the successful candidate will be expected to play a key role in the ongoing transformation of the La Brea Tar Pits & Museum. The Curator will also be responsible for building productive ties with local universities, professional associations, educators, and other relevant organizations within the scientific and general community.

The Natural History Museum of Los Angeles County is seeking applicants who have demonstrated experience and commitment working with a diverse community. This is a full-time position with a salary and title commensurate with experience.

The application deadline is September 1st, 2018. The starting date is July 1st, 2019. Applicants should send a cover letter, vision statement, curriculum vitae, and the full contact information of at least three professional references as a single PDF document to thayden@nhm.org, La Brea Tar Pits & Museum Curatorial Search, Research & Collections, Natural History Museum of Los Angeles County, 900 Exposition Blvd., Los Angeles, CA 90007, USA.

The Natural History Museum of Los Angeles County is an Equal Opportunity Employer. Please, No Phone Calls, No Fax.—

Jann Vendetti, Ph.D. Twila Bratcher Endowed Chair in Malacological Research Natural History Museum of Los Angeles County 900 Exposition Blvd. Los Angeles, CA 90007— <http://sacoglossa.myspecies.info/> <http://research.nhm.org/malacology/jannvendetti@yahoo.com>

Jann Vendetti <jannvendetti@yahoo.com> Jann Vendetti <jannvendetti@yahoo.com>

NIAB Cambridge UK QuantitativeGenetics

Senior Research Scientist (Quantitative Genetics), NIAB, Cambridge, UK A position is available for an enthusiastic and talented genetic data analyst to work on crop genetics research projects at NIAB (National Institute of Agricultural Botany), Cambridge, UK. NIAB is the UK's fastest growing crop science organisation, with rapidly expanding research capabilities in plant genetics, agronomy, farming systems and data science, the largest national field trials capability, and strong research links with industry, government and academia. The NIAB Genetics and Breeding team carries out leading-edge crop genetics research, with direct translation to plant breeding programmes in the UK and elsewhere. Ongoing projects generate large genetic data sets for gene discovery (e.g. QTL mapping, especially in multi-founder ("MAGIC") populations, GWAS), screening of genetic resources, crop genomics, and genomic selection. The successful applicant will play a leading role in the curation, analysis and interpretation of these data, including data QC, model fitting, statistical analysis and development of novel analysis pipelines, as well as dissemination and publication of results. Initially, the successful applicant will largely work on genetic mapping and QTL mapping projects involving NIAB's wheat MAGIC populations. The successful candidate will also have the opportunity to provide wider data analysis support across NIAB, including in the design of experiments. Opportunities will be available to develop and grow research interests within the overall NIAB genetics and breeding research portfolio. This is a permanent post and we are seeking a researcher with a background in quantitative genetics or statistics and an interest in agriculture and plant breeding.

The successful applicant should have a PhD in quantitative genetics, plant genetics, or a related subject area, and be experienced in genetic data analysis, particularly genetic mapping and QTL mapping, as well as the use of statistical software, preferably R. A good understanding of experimental design is also critical. Some basic bioinformatics experience and/or programming skills (e.g. Python) are desirable, together with a good scientific publication and presentation record. Some knowledge of plant breeding and crop science would also be beneficial. A proven ability to work independently and as part of a team are both essential, as are good communication

skills. The post will require travel within the UK and internationally.

Starting salary is in the range of pounds 30,084 to pounds 34,316 pa depending on qualifications, skills and experience. Further details and an application form are available at: <http://www.niab.com/vacancies/-index/> or from the HR Office, NIAB, Huntingdon Road, Cambridge CB3 0LE, Tel No. 01223 342282, Email: jobs@niab.com, quoting Ref No. SV/A999.

Closing date for applications: 4 July 2018

Dr Keith Gardner | Genetics and Breeding NIAB | Huntingdon Road | Cambridge | CB3OLE Tel (direct) +44 (0)1223 342484 | Tel (office) +44 (0)1223 342200

Keith Gardner <Keith.Gardner@niab.com>

NortheasternU Tech EcologicalGenomics

A position for a technician is available in the laboratory of Dr. Kathleen Lotterhos at Northeastern University. The successful candidate will be responsible for diverse responsibilities, including lab management, preparing libraries for next generation sequencing, writing and managing code for lab projects (ranging from simulating genomic data to bioinformatics and analysis), and field work.

Candidates are required to have a Bachelors or Masters degree with the following skills: 1) Knowledge of Python or R, and Bash 2) Experience analyzing next-generation sequencing data 3) Experience preparing samples for Illumina sequencing 4) Excellent organizational and documentation skills 5) Able to work both independently and as part of a collaborative team

The following expertise is desirable but not necessary:

1) IT experience including server maintenance

Candidates with a diversity of skills, experiences, and backgrounds are encouraged to apply!!

You can apply directly here: <https://neu.peopleadmin.com/postings/55036> and feel free to contact me for more information.

Kathleen E Lotterhos Assistant Professor Department of Marine and Environmental Sciences Northeastern University Marine Science Center, Room 113 430 Nahant Rd Nahant, MA 01908 Phone: 781.581.7370 ext 304

Katie Lotterhos <k.lotterhos@northeastern.edu>

TexasAMU CorpusChristi EvolutionaryMarineBiol

Job Title Assistant Professor, Marine Biology Agency Texas A&M University - Corpus Christi Department S&E - Life Sciences Proposed Minimum Salary Commensurate Job Location Corpus Christi, Texas Job Type Faculty

Job Description The Department of Life Sciences at Texas A&M University-Corpus Christi invites applications for a tenure-track Assistant Professor of Marine Biology. Appointment may start as early as spring 2019. Applicants whose research focus is complementary to strengths already present in the department (<https://sci.tamucc.edu/member.php?who=all&program=lsci>) are especially encouraged to apply. Applications are particularly encouraged from individuals with active, federally-funded research programs and strong external collaborations who can take advantage of our modern research laboratories and equipment, including those associated with our molecular, microscopy and analytical facilities.

The successful candidate will be expected to develop a vigorous, externally-funded research program, supervise graduate and undergraduate researchers, teach undergraduate and graduate courses, and pursue scholarly research in support of the Biology Master's and Marine Biology Master's and PhD Programs. The typical teaching assignment for doctoral faculty in the Department of Life Sciences is 3 courses per academic year.

Research lab space will be located in a new state-of-the-art three-story building, Tidal Hall, which will be completed in autumn 2018 to support 6 new instructional labs and 34 research labs. The Department of Life Sciences has 23 tenured or tenure-track faculty, 6 professional assistant faculty and over 1,200 science majors. It offers BS degrees in Biology and Biomedical Science, MS degrees in Biology, Marine Biology and Fisheries & Mariculture, and a PhD in Marine Biology.

Required Qualifications: Ph.D. degree in marine biology or a closely related discipline. Preferred Qualifications: Postdoctoral experience TO APPLY: http://hr.tamucc.edu/Job_Opportunities/index.html To be considered for the position, all required documentation must be uploaded.

A completed application will include: 1. Cover letter including qualifications; 2. Curriculum vitae; 3. Statement describing research interests; 4. Statement describing teaching & mentoring philosophies; and 5. The names and contact information of 3 references.

Deadline for applications is September 15, 2018.

For more information, please contact: Dr. Mike Wetz Search Chair, Department of Life Sciences, Email: michael.wetz@tamucc.edu Phone: (361)-825-2132

All positions are security-sensitive. Applicants are subject to a criminal history investigation, and employment is contingent upon the institution's verification of credentials and/or other information required by the institution's procedures, including the completion of the criminal history check. Equal Opportunity/Affirmative Action/Veterans/Disability Employer committed to diversity.

Chris.Bird@tamucc.edu

UCalifornia Berkeley LabTech PupfishCichlidspeciation

The Martin Fish Speciation Lab seeks an enthusiastic and detail-oriented laboratory manager for research on the rapid evolution and ecological diversification of new fish species. Primary responsibilities will involve caring for laboratory pupfish and cichlid colonies, molecular genetics, behavioral data collection, and specimen curation within the Museum of Vertebrate Zoology. Tasks include daily feeding and maintenance of the fish colonies, construction of new flow-through aquatic facilities, DNA extractions and genomic library preparation, curation and dissection of preserved fish specimens, and training undergraduate researchers. Interest in ichthyology, evolution, genomics, and ecology is highly desirable.

Pupfishes present a rare opportunity to investigate the recent origins of spectacular adaptive radiation and the evolution of novel niches (e.g. scale-eating) localized to a single Bahamian island despite thousands of similar Caribbean environments. Our lab also investigates Cameroon crater lake cichlids, one of the most celebrated examples of sympatric speciation in nature, and the role of gene flow in their diversification.

Education and Experience Required:

We are seeking applicants with strong attention to detail who are thorough, well-organized, and able to work

collaboratively with other researchers. Preferred qualifications include a Bachelor's degree in Biology (or related field) and some molecular training or experience with animal care. However, no previous research experience is necessary; on-the-job training will be provided for all tasks. The successful applicant will enjoy caring for animals in an unstressful and flexible work environment. Those with a passion for aquarium fishkeeping and possible interest in applying to graduate school are strongly encouraged to apply. For more information on our research, please check out our website <<http://labs.bio.unc.edu/martin/>>.

Salary:

This is an hourly position and pay is dependent on previous experience. For recent graduates, this will be approximately \$15 per hour. Work schedule is flexible and includes some weekend fish care responsibilities, but approximately 40 hours per week. Part-time, overtime, and permanent salary position requests can also be discussed.

Start Date:

Early January 2019 if possible. Later start dates are also possible 'V please inquire. This position is for one year with the potential for renewal up to four years.

To apply, please email Chris Martin (chmartin@unc.edu) by August 1st with your resume/CV and describe why you are interested in this position, career goals, and any past research or animal care experience. Please note that the lab is moving from UNC to UC Berkeley starting in January 2019.

Christopher Martin

Assistant Curator of Ichthyology, Museum of Vertebrate Zoology

Assistant Professor, Department of Integrative Biology
University of California, Berkeley

<http://labs.bio.unc.edu/martin/> @fishspeciation

Christopher Martin <chmartin@unc.edu>

UCollege Dublin
ComparativeEpigenetics

Lecturer / Assistant Professor in Comparative Animal Epigenetics

University College Dublin, Ireland

University College Dublin is seeking to appoint a permanent Lecturer / Assistant Professor in Comparative Animal Epigenetics, to the School of Biology & Environmental Science. We are looking for a candidate with research interests in the area of comparative epigenetics, with specialisation in animal evolutionary and/or ecological epigenetics, who will contribute to the 'Genetics and Evolutionary Biology' research theme of the School. The candidate should study environmentally driven epigenetic variation (preferably in natural populations) and the heritability and evolutionary impact of these epigenetic effects, within and across species.

The candidate is expected to lead an original and innovative scientific research programme as well as contribute to the teaching of zoology, genetics and comparative biology. The candidate should complement and engage with current academic staff and research programmes within the School and wider UCD community.

Candidates should have a PhD in an appropriate discipline and will be expected to provide teaching of various aspects of biology primarily in the Zoology and Genetics undergraduate degree programmes. The candidate will also contribute to graduate programmes delivered by the School. Applications should include a 5-year relevant research plan detailing possible funding opportunities (both Irish and international), and a teaching portfolio.

95 Lecturer/Assistant Professor (above the bar) Salary Scale: euro52,325 - euro82,267 per annum

Closing Date: 17:00hrs (local Irish Time) on 31 July 2018.

Applications must be submitted by the closing date and time specified. Any applications which are still in progress at the closing time of 17:00hrs (Local Irish Time) on the specified closing date will be cancelled automatically by the system. UCD do not accept late applications.

Prior to application, further information (including application procedure) should be obtained from the UCD Job Vacancies website: <https://www.ucd.ie/workatucd/>, with the job ref 010383.

For more information please contact: Prof. Jeremy Simpson (jeremy.simpson@ucd.ie, Head of School) / Prof. Emma Teeling (emma.teeling@ucd.ie).

Emma Teeling <emma.teeling@ucd.ie>

UOklahoma GenomicsLabManger

Title of Position: Laboratory Manager - Research Assistant
Start Date: Fall 2018

Position requires a Masters or higher degree (PhD preferred) in a biological science related field, with at least five years of experience in genomics. Strong organization skills and the ability to manage a genomics wet-lab is a must. Duties include managing a multi-PI research group that is active in the use of genomic technologies, including genome reconstruction, ancient biomolecules and microbiome research (see LMAMR.ORG).

Earliest start date: August 1st, 2018. Salary: 60-65K plus fringe.

The Laboratory Manager is responsible for overseeing to the day-to-day functioning of the laboratory spaces, implementing safety protocols, maintaining active records of projects, leading laboratory meetings, as well as a point person for laboratory training of graduate and undergraduate students, visiting scholars, and post-docs. The Laboratory Manager may serve as the point person for PI led projects to which they have been assigned, with publication attribution proportionate to the level of contribution. Other duties relevant to laboratory management may be assigned, such as trouble shooting protocols, lab calendar management, and coordination with staff, students, and faculty. Strong communication skills are a must.

Complete the application at <https://jobs.ou.edu/> Job Number 182011 with Cover Letter and complete CV (with references)

For additional questions, contact

Dr. Cecil M. Lewis, Jr. Email: cmlewis@ou.edu With subject line: ATTN - Lab Manager Search

“Lewis, Cecil M. Jr.” <cmlewis@ou.edu>

UppsalaU PlantEvolGenomics

Tenure-track position as Assistant Professor in Plant Evolutionary Genomics at Uppsala University

Department of Ecology and Genetics, division in Plant Ecology and Evolution, Evolutionary Biology Centre.

The position includes research, teaching at graduate and undergraduate level, outreach activities and some administration. The holder is expected to establish research of highest international standards within the subject area, and to contribute to the development of research and teaching of the department.

The ranking of eligible applicants will be based primarily on research and teaching expertise, of which particular weight will be given to research expertise.

Research in Plant Evolutionary Genomics involves molecular analyses to understand evolutionary and ecological processes underlying the generation and maintenance of biological diversity among plants. The subject area includes functional studies of variation at the molecular level as well as analysis and interpretation of large-scale omics-data to understand biological function, evolution of diversity, and adaptation of plants to the abiotic and biotic environment.

The position is for four years and tenure-track: An associate senior lecturer (the Swedish term for Assistant Professor) has the right to apply for promotion to senior lecturer. If the associate senior lecturer is deemed suitable and fulfills the criteria for promotion established by the Faculty Board he/she shall be promoted and employed as senior lecturer (permanent position). At a subsequent step, an application for promotion to full professor can be made.

According to the Swedish Higher Education Ordinance those qualified for appointment as associate senior lecturer are persons who have obtained a doctoral degree or achieved the equivalent competence. Priority is given to those who obtained their degree no more than seven years prior to the end of the application period.

The Evolutionary Biology Centre (EBC) of Uppsala University offers a vibrant research environment. It bridges a broad range of disciplines in the biological sciences, and is an internationally very strong environment within the field of evolutionary biology. Information about EBC and the Department of Ecology and Genetics can be found at <http://www.abc.uu.se/?languageId=3D1/> and <http://www.ieg.uu.se/?languageId=3D1> The position is part of the SciLifeLab Fellow program and comes with a core funding of three million SEK per year for four years, which includes substantial funds to cover running costs. SciLifeLab (www.scilifelab.se) is a national centre for large-scale hypothesis driven research within molecular bioscience.

More detailed information about the position and information about how to apply can be found at

<http://www.uu.se/en/about-uu/join-us/details/-?positionId=3D217586> Closing date for application is September 17, 2018

For further information about the position, please contact Professor Jon Agren jon.agren@ebc.uu.se or Professor Ulf Lagercrantz Ulf.Lagercrantz@ebc.uu.se

Jon Ågren Plant Ecology and Evolution Department of Ecology and Genetics Evolutionary Biology Centre Uppsala University Norbyvägen 18 D SE-753 36 Uppsala Sweden

När du har kontakt med oss på Uppsala universitet med e-post innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här: <http://www.uu.se/om-uu/dataskydd-personuppgifter/> E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: <http://www.uu.se/om-uu/dataskydd-personuppgifter/> "jon.agren@ebc.uu.se" <jon.agren@ebc.uu.se>

UQueensland EvolutionaryBiol

Call for Expressions of Interest: Mid-Career Research Fellowships in Biological Sciences at the University of Queensland The School of Biological Sciences at The University of Queensland is seeking expressions of interest from applicants interested in applying for the Australian Research Council Future Fellowship scheme. These government fellowships offer 4-years of salary and research funds to outstanding Australian and non-Australian mid-career researchers (details on the scheme can be found at: <http://www.arc.gov.au/future-fellowships>). UQ's School of Biological Sciences is seeking to support a small number of outstanding candidates in the anticipated 2018 round of this scheme. We will consider any applicants whose research complements our School's existing research strengths but are particularly interested in candidates with strong quantitative skills. For selected candidates, we will be offering negotiated setup packages to help successful fellows establish their own research group as well as negotiated extensions of employment as teaching and research academics in the School following the completion of awarded fellowships.

The School of Biological Sciences (<http://www.biology.uq.edu.au/>) at The University of Queensland is internationally recognised, and is one of

the largest and most productive Biology departments in Australia, with a thriving graduate student and postdoctoral community. The School has strengths in ecology, evolution, genetics, and conservation biology.

Research within the School is diverse, including both empirical and theoretical approaches in taxa ranging across microbes, animals and plants, in a range of marine, freshwater and terrestrial ecosystems. The School offers a highly collaborative environment, including a variety of non-academic and industry partnerships, and collaborations across institutions nationally and internationally.

If interested please submit a CV and a brief expression of interest (no more than 1 page) outlining how your research programme will complement research within the School, and meets the Future Fellowship scheme objectives of being innovative, internationally competitive research, building collaborations across industry or research, and generating economic, environmental, social and/or cultural benefits for Australia.

Please direct questions and submit expressions of interest to Dr Katrina McGuigan by 30 June 2018: k.mcguigan1@uq.edu.au

Katrina McGuigan <k.mcguigan1@uq.edu.au>

UtahStateU ForestEvolution

Assistant Professor of Silviculture and Applied Forest Ecology

Utah State University, Logan, Utah

The Department of Wildland Resources at Utah State University is seeking applications for a full-time 9-month tenure-track Assistant Professor position in silviculture and applied forest ecology. We are seeking a scholar dedicated to the use and development of silvicultural approaches to meet a range of functional goals in forested landscapes. The position consists of 50% research, 40% teaching, and 10% service, to start August 1, 2019. Application review will begin September 10, 2018.

The appointed faculty member will develop an externally-funded research program that achieves an international reputation for research and graduate training in applied forest ecology and resource management. Research foci may include, but are not restricted to (i) how silvicultural approaches can increase resilience and adaptive capacity of forested ecosystems, given changes

in climate patterns, insect activity, fire regimes, and other impacts; (ii) how forest structure, composition, and spatial/temporal patterns of treatments can be manipulated to achieve specific sets of ecological and social/economic goals; (iii) how large datasets can be used to understand and predict forest ecosystem or structural responses to multiple interacting stressors. An important aspect of this position is the ability to work across disciplinary and institutional boundaries, and to collaborate with federal and state agencies. Effective communication with a variety of stakeholders is essential, consistent with the Land Grant mission of Utah State University. We are seeking candidates who can prosper within a collaborative environment.

To learn more about the position, including minimum and preferred qualifications, and to apply, go to <https://usu.hiretouch.com/job-details?jobid=3540>. For additional questions, contact the search committee chair (Dr. Karen Mock, karen.mock <at>usu.edu).

Utah State University is Utah's Land Grant institution. USU is in Logan, which offers the amenities of a college town within the Cache Valley metropolitan zone of ~115,000 people and enjoys a low cost of living. Cache Valley is positioned between the Wellsville and Bear River mountain ranges at the eastern edge of the Great Basin. Logan offers a superb array of outdoor activities minutes from campus (climbing, cycling, hiking, skiing, fishing), and is within a day's drive of ten national parks. As an affirmative action/equal opportunity employer, USU is dedicated to recruiting strong candidates from a diverse applicant pool, including women, minorities, veterans, and persons with disabilities. USU is sensitive to the needs of dual-career applicants and offers competitive salaries with outstanding medical, retirement, and professional benefits.

Karen Mock <karen.mock@usu.edu>

UWyoming CoreFacilityScientists

Core facility scientists for nucleic acid and biogeochemistry analyses:

The Microbial Ecology Collaborative at the University of Wyoming seeks two suitably qualified research scientists, with expertise in standard laboratory methods in nucleic acid analysis, liquid handling (e.g., robotics for large-scale DNA extractions and library preps), and biogeochemistry analyses (e.g. fundamental, high throughput chemical, physical, and biological assessment of soil,

water, waste, plant, and animal materials). Duties (to be divided between the positions) will include operation, maintenance, and repair of liquid-handling robots, an ion chromatograph, TOC, CN elemental analyzers, ICP-MS, microplate reader, and other laboratory equipment. Additionally, the scientists will develop and perform laboratory protocols with QA/QC, support analytical and preparative instruments, analyze data and keep records, and support and train clients. Participation in the instruction and training of students and research scientists is expected.

This search is part of a new 5-year, \$20 million NSF EPSCoR RII Track-1 grant to the University. In this project we will study microbial life and its ecological consequences; additional details can be found at <http://www.uwyo.edu/epscor/microbial-ecology>. These are full-time (12-month) appointments as Academic Professional Research Scientists and will collaborate with the team of chemists and life scientists in the UW Stable Isotope Facility. Salary is competitive and health insurance and retirement benefits are included. Applicants should submit their curriculum vitae, a letter of interest, and names and contact information for three references through an online application. Review of applications will continue until suitable applicants are identified.

The University of Wyoming invites diverse applicants to consider our employment opportunities. We are also especially interested in candidates who have experience working with diverse populations and/or diverse initiatives.

The University of Wyoming is located in Laramie, a town of 30,000 in the heart of the Rocky Mountain West. The state of Wyoming continues to invest in its university, helping to make it a leader in academics, research and outreach. The university has state-of-the-art facilities in many areas and the community provides the advantages of a major university.

Located in a high mountain valley near the Colorado border, Laramie offers both outstanding recreational opportunities and close proximity to Colorado's Front Range, a bustling group of metropolitan cities including Denver, Boulder, and Fort Collins. This beautiful mountain landscape offers outdoor enjoyment in all seasons, with over 300 days of sunshine annually. For more information about the region, please visit <http://visitlaramie.org/>. For additional information and to apply please see: https://jobs.uwyo.edu/psp/EREC/UWEXTERNAL/-HRMS/c/HRS_HRAM.HRS_CE.GBL?Page=-HRS_CE_JOB_DTL&Action=A&SiteId=-6&JobOpeningId=9700&PostingSeq=1 "Catherine E. Wagner" <Catherine.Wagner@uwyo.edu>

Whitman College EvoEco Teaching Lab Coordinator

Biology Department Whitman College Walla Walla WA USA

Seeking a coordinator to prep for undergraduate teaching labs in ecology and evolutionary biology.

Posting Number: 0600484 Job: Biology Lab and Safety Coordinator Department: Division III Supervisor's Name: Biology Department Chair Position Type: Staff FLSA: Exempt

Position Purpose:

PURPOSE 1) Help with the preparation, set-up, clean up, and equipment up-keep for a specific set of biology Ecology and Evolution courses. Oversee student employment dedicated to those courses.

PURPOSE 2) Member of the Biology Department administrative team. Duties include seeing to the administrative needs of the teaching greenhouse and department museum collections and assisting the Science Outreach Coordinator with program development.

PURPOSE 3) Safety Coordinator for the Biology Department including, training student employees in proper safety procedures and maintaining department safety compliance.

Principal Accountabilities: Purpose 1 1. Setting up for ecology/evolution labs 2. Ordering supplies/reagents for these labs; keeping records of such orders and associated budgets 3. Storage and record keeping for supplies. 4. Managing field trip organization, such as scheduling and delivery of vans, occasional driving when needed, menu preparation and food acquisition, equipment maintenance and packing, collection of receipts, etc. 5. Be available to assist during labs, including driving on field trips and helping as needed in the classroom. This includes maintaining familiarity with equipment and software used in laboratories and being able to assist students and faculty when using this equipment. 6. Supervising student employees for the above duties. 7. Maintaining live organisms needed for classes in this area, including (but not limited to) protists, fungi, invertebrates, and plants.

Purpose 2 1. Managing student employees in the greenhouse and department museum collections, including ordering, paperwork, and general upkeep. 2. Handling

details associated with guest lectures, to include scheduling, posters/brochures, food acquisition and delivery, ushers, etc. 3. Assisting with educational events for elementary through high school students. 4. Maintaining live organisms for displays and outreach and supervising students to accomplish these tasks.

Purpose 3 1. Safety Coordinator for the Biology Dept. Maintain a student employee training program, and other compliance requirements for the department.

Minimum Qualifications: B.A. or B.S. degree in the life sciences with emphasis or experience in evolutionary or ecological biology. Must have an interest in whole organism biology, ideally across a breadth of organisms. Familiarity with spreadsheets necessary. Previous academic laboratory or field experience is desired. Must have excellent communication and organizational skills and the ability to work with different faculty, staff and students.

Preferred Qualifications: Individuals must be able to explain and/or demonstrate that they possess the knowledge, skills, and abilities to safely perform the essential functions of the job, with or without reasonable accommodation.

1. **People Skills.** Much of the time is spent interacting with students, faculty and staff. Must be able to multi-task and have a positive attitude, and maintain open lines of communication. 2. **Self-directed.** Some direction and training will be given, however, most work will be self-initiated. 3. Must have or be willing to acquire working familiarity with chemicals and equipment routinely used in biology laboratories. Must know or be willing to learn basic safety procedures for working with and disposing of such chemicals. 4. Must have or be willing to acquire working knowledge of laboratory equipment such as autoclaves, centrifuges, field equipment, & chemical hoods, and understand the safety issues of such items. 5. Must be physically able to load/unload reagents and equipment items from shelves/cabinets/other storage areas; transport such to various labs around the building. Equipment may include that which requires assistance: large or heavy items such as camping equipment, field boxes, and microscopes. 6. Must have valid driver's license and complete Whitman College's van driving certification.

Work Hours Full-time position

Special Instructions to Applicants: Whitman College is building a diverse academic community and welcomes nominations of and applications from women, members of historically underrepresented minority groups, persons with disabilities, and others who would bring additional dimensions to the College's learning environ-

ment. Whitman is responsive to the needs of dual career couples. Whitman College is an Equal Employment Opportunity employer.

Tim Parker Chair, Department of Biology Whitman College Walla Walla, WA 99362 USA +1.509.526.4777 parkerth@whitman.edu

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Finding NullAlleles Question

Hi all, Is there any software for the detection of null alleles on SSR data? It would be more preferable to be on line I run Microchecker on my PC but I dont know if it works properly.

kind regards

Vassilis Papatotiropoulos

Vassilis Papatotiropoulos <vpapasot@gmail.com>

HSmithPrize MolEcol Nominations

Nominations for the Harry Smith Prize in Molecular Ecology

The editorial board of the journal Molecular Ecology has established a new prize to recognize the best paper published in Molecular Ecology in the previous year by graduate students or early career scholars with no more than five years of postdoctoral or fellowship experience. The prize comes with a cash award of US\$1000 and an announcement in the journal. The winner will also be asked to join a junior editorial board for the journal to offer advice on changing research needs and potentially serve as a guest editor. As with the Molecular Ecology Prize, the winner of this annual prize will be selected by an independent award committee.

The prize is named after Professor Harry Smith FRS,

who founded the journal and served as both its Chief and Managing Editor during the journal's critical early years. He continued as the journal's Managing Editor until 2008, and he went out of his way to encourage early career scholars. In addition to his editorial work, Harry was one of the world's foremost researchers in photomorphogenesis, where he determined how plants respond to shading, leading to concepts such as "neighbour detection" and "shade avoidance," which are fundamental to understanding plant responses to crowding and competition. More broadly his research provided an early example of how molecular data could inform ecology, and in 2008 he was awarded the Molecular Ecology Prize that recognized both his scientific and editorial contributions to the field.

Please send your nomination with a short supporting statement (no more than 250 words; longer submissions will not be accepted) directly to Rose Andrew (randre20@une.edu.au) by Tuesday 31 July 2018.

With thanks on behalf of the Harry Smith Prize Selection Committee

"Rieseberg, Loren" <lriesebe@mail.ubc.ca>

LearningEvolution ParmenidesFoundation

The Parmenides Center for the Study of Thinking seeks young applicants (Masters/PhD) to participate in its Learning in Evolution, Evolution in Learning project. Applicants must have a strong background in mathematical modelling. Basic programming skills are also needed. Knowledge in at least three of the following fields is mandatory: machine learning cognitive psychology, neuroscience and evolutionary biology. Stipends for a maximum of 3 years are in the range of 1000-1500 EUR.

Applications with CV, publication list and a motivation letter should be sent to Professor Eors Szathmary

szathmary.eors@gmail.com

by the end of June.

Thank you!

Carsten

– Parmenides Stiftung Kirchplatz 1 82049 Pullach
Tel +49.89.4520935.0 Skype: Parmenides.Foundation
carsten.freitaeger@parmenides-foundation.org

Carsten Freitäger <carsten.freitaeger@parmenides-foundation.org>

Panama VolResAssist ForestEvolution

Other: Panama. VolResAssist. Tropical Forest Ecology. Smithsonian Tropical Research Institute, Panama-Bangor University, UK

We are looking for a highly motivated volunteer research assistant to support us in unravelling the mechanisms driving secondary succession of tropical forests.

Research Hyper-diverse mature tropical rainforests have been largely degraded due to human expansion. Recovering forests present 70% of the global forest cover. These secondary forests can restore some of the original forests' benefits, yet they recover slowly and differ to mature forests in tree species composition. Understanding the mechanisms driving tropical forest dynamics following disturbance is imperative to promote the recovery of ecosystem functionality and mitigate land-use impacts. Species-specific interactions between trees and their natural enemies that have evolved for thousands of years might be the key. Our current project will assess the impact of soil fungi in secondary succession of tropical forests. The project will involve field work and a large greenhouse study in Gamboa, Panama. This collaborative project between Bangor University (UK), Bayreuth University (Germany) and the Smithsonian Tropical Research Institute (USA, Panama) will offer an ideal opportunity to gain research experience in the tropics!

Job Description The intern will assist in a variety of tasks, involving field work (e.g. seed collection), intense manual labour (e.g. soil sieving) and greenhouse work. Working hours will vary strongly between days, but working weeks will never exceed 45 hours. Applicants must be in good physical condition to be able to meet the demands of working sometimes long hours under challenging tropical field work conditions, i.e. high humidity and heat. Ability to drive a 4x4 transmission truck is desirable but not required. We expect the intern to have a strong interest in ecology and to be willing to follow protocols to ensure the quality of data. We are more than happy to help in developing and discussing ideas for own research projects. We will contribute 500 USD to the flight costs. Due to a limited research budget, we cannot offer accommodation, but will help in

finding a place to live in Gamboa (rooms in shared flats are available from 200-250 USD per month, including all bills). Start date is between May and August 2018, with earlier availability being preferred. A minimum stay of 3 months is required. For applicants being able to join the project in mid-May, the minimum duration can be negotiated.

Location Gamboa is a small town next to the Panama Canal. With its vibrant scientific community, it presents a stimulating background to develop and exchange research ideas and explore a broad variety of ecological research in the Tropics. Gamboa is an ideal base to discover Panama and Central America: on your daily stroll through the town you can watch huge ships passing by on the canal or discover the forest that starts directly behind the greenhouses with its fascinating wild-life (toucans, gigantic butterflies, agoutis, etc.). Panama City can be reached in 45 min via an adventurous bus ride.

Applicants should send a cover letter, CV and the names and e-mail addresses of at least two professional or academic references to Anita Weissflog (anita.weissflog@bangor.ac.uk). Shortlisted applicants will be invited for a Skype chat.

This position will be filled as soon as possible.

I am looking forward to hearing from you! Cheers,

Anita

anita.weissflog@bangor.ac.uk

Software DAMBE update

Dear Colleagues,

In the last few months I have been testing the distance-imputing functions for PhyPA (phylogenetics by pairwise alignment), by reading a set of unaligned sequences, computing distances, randomly remove a subset of distances so that they are “missing” and then impute the distances. I have accidentally released a DAMBE version with such testing functions for PhyPA. A new version has been uploaded. Please download to replace your current version. I apologize for this. PhyPA generates trees comparable to maximum likelihood method in quality (better for highly diverged sequences). If you have a PhyPA tree that is not as good, you most likely are using a test version of PhyPA (where good computable distances were replaced by imputed distances).

(The reason for implementing distance imputation motivated by my effort to elucidate viral phylogeny in which viruses A may share no homologous sequences with virus B, so D_{AB} cannot be computed, but a third virus C may have one sequence segment homologous to A and another sequence homologous to B, so that D_{AC} and D_{BC} can be computed. The sequence homology is often so remote that no meaningful multiple sequence alignment can be obtained. Through distance imputation and PhyPA, a viral tree can then be produced.)

(PhyPA is a function in DAMBE that build phylogenetic trees from pairwise alignment. It is accessed in DAMBE by clicking “Phylogenetics|Distance Methods|Phylogenetics by Pairwise Alignment”. DAMBE is freely available at <http://dambe.bio.uottawa.ca/DAMBE/dambe.aspx>)

Xia X. 2016. PhyPA: phylogenetic method with pairwise sequence alignment outperforms likelihood methods in phylogenetics involving highly diverged sequences. *Molecular Phylogenetics and Evolution* 102:331-343
Xia, X. 2018. DAMBE7: New and improved tools for data analysis in molecular biology and evolution. *Molecular Biology and Evolution* 35:1550-1552.

Best Xuhua <http://dambe.bio.uottawa.ca> <http://science.uottawa.ca/biology/people/xia-xuhua>
“Xuhua.Xia@uottawa.ca” <Xuhua.Xia@uottawa.ca>

Software PGT update

Dear Colleagues,

I have added a new function to PGT software (raised geophylogeny to reduce branches crossing each other). Here is the link to a sample output:

http://dambe.bio.uottawa.ca/PGT/PGT_raised.PNG
which you may compare with the previous flat geophylogenies here:

http://dambe.bio.uottawa.ca/PGT/-PGT_flat_regular.PNG http://dambe.bio.uottawa.ca/-PGT/PGT_flat_terrain.PNG Producing such geophylogenies is extremely easy (just a few clicks in fact).

PGT is the easiest to use and generate the highest resolution geophylogenies. It is freely available for the Windows/Mac/Linux platforms at:

<http://dambe.bio.uottawa.ca/PGT/PGT.aspx>

Best Xuhua <http://dambe.bio.uottawa.ca> <http://science.uottawa.ca/biology/people/xia-xuhua>

science.uottawa.ca/biology/people/xia-xuhua Xuhua Xia <Xuhua.Xia@uottawa.ca>

WalshLynch QuantTraits

Mike Lynch and I are pleased to announce that our book “Evolution and Selection of Quantitative Traits” can now be pre-ordered from

Amazon

<https://www.amazon.com/Evolution-Selection-Quantitative-Traits-Bruce/dp/0198830874> or Oxford University Press

<https://global.oup.com/academic/product/evolution-and-selection-of-quantitative-traits-9780198830870>
~1500 pages at \$150 (10 cents a page)

The full table of contents, as well as the subject and author indexes can be found in the “files” section of the book’s facebook page: “Quantitative Genetics Book”

<https://www.facebook.com/groups/-1879483065683161/> Chapters

1. Changes In Quantitative Traits Over Time
2. Neutral Evolution In One- And Two-Locus Systems
3. The Genetic Effective Size Of A Population
4. The Nonadaptive Forces Of Evolution
5. The Population Genetics Of Selection
6. Theorems Of Natural Selection: Results Of Price, Fisher, And Robertson
7. Interaction Of Selection, Mutation, And Drift
8. Hitchhiking And Selective Sweeps
9. Using Molecular Data To Detect Selection: Signatures From Recent Single Events
10. Using Molecular Data To Detect Selection: Signatures From Multiple Historical Events
11. Changes In Genetic Variance Induced By Drift
12. The Neutral Divergence Of Quantitative Traits
13. Short-Term Changes In The Mean: 1. The Breeder’s Equation
14. Short-Term Changes In The Mean: 2. Truncation And Threshold Selection
15. Short-Term Changes In The Mean: 3. Permanent Versus Transient Response

16. Short-Term Changes In The Variance: 1. Changes In The Additive Variance
17. Short-Term Changes In The Variance: 2. Changes In Environmental Variance
18. Analysis Of Short-Term Selection Experiments: 1. Least-Squares Approaches
19. Analysis Of Short-Term Selection Experiments: 2. Mixed-Model And Bayesian Approaches
20. Selection Response In Natural Populations
21. Family-Based Selection
22. Associative Effects: Competition, Social Interactions, Group And Kin Selection
23. Selection Under Inbreeding
24. The Infinitesimal Model And Its Extensions
25. Long-Term Response: 1. Deterministic Aspects
26. Long-Term Response: 2. Finite Population Size And Mutation
27. Long-Term Response: 3. Adaptive Walks
28. Maintenance Of Quantitative Genetic Variation
29. Individual Fitness And The Measurement Of Univariate Selection
30. Measuring Multivariate Selection
 - A1. Diffusion Theory
 - A2. Introduction To Bayesian Analysis
 - A3. Markov Chain Monte Carlo And Gibbs Sampling
 - A4. Multiple Comparisons: Bonferroni Corrections, False-Discovery Rates, And Meta-Analysis
 - A5. The Geometry Of Vectors And Matrices: Eigenvalues And Eigenvectors
 - A6. Derivatives Of Vectors And Vector-Valued Functions

Here are a few of the online reviews listed by Oxford Univ. Press.

A masterful synthesis of the growing points in selection analysis. * Stevan J. Arnold, Oregon State University, USA *

This book is a virtuoso synthesis of the theory and application of selection and evolution of complex traits. Much more than an advanced textbook, it is the most comprehensive treatment and synthesis of the theory and analysis of selection and evolution of quantitative traits to date. * Peter M. Visscher, University of Queensland, Australia *

This long-awaited volume gives an exceptionally com-

prehensive and thoughtful overview of the field, and will be invaluable to all those who are trying to understand the genetics of complex traits. As well as covering quantitative genetics, it gives a thorough treatment of the most recent methods for making inferences from DNA sequence data. * Nicholas H. Barton, Institute of Science and Technology, Austria *

The book is a fabulous resource; it will be the go-to place to learn about a broad variety of topics in population and quantitative genetics, from measuring differences among populations to estimating selection from genomic sequence data. A real strength of the book is the expert overview of the topics alongside pointers to the key papers for more details. * Sarah P. Otto, University of British Columbia, Canada *

Their 1998 book has been an essential and popular teaching and reference text for quantitative geneticists for 20 years. At last the long promised and awaited second volume is available, structured to provide both an introduction for the graduate student and a reference volume for the seasoned professional. The authors display both an impressive breadth and depth of knowledge and ability to explain it. * William G. Hill, University of Edinburgh, UK *

jbwalsh@email.arizona.edu jbwalsh@email.arizona.edu

Wikipedia upgrades

Wikipedia is the first port of call for most students, grant panellists journalists and policymakers, not to

mention the wider public. The WikiJournal of Science (www.WikiJSci.org) is an academic journal with an unusual feature: Published review articles are copied over to Wikipedia for added reach and exposure (articles are often read >100,000 times per year).

The journal couples the rigour of academic peer review with the extreme reach of the encyclopedia. It is therefore an excellent way to achieve public engagement, outreach and impact public understanding of science. Peer-reviewed articles are dual-published both as standard academic PDFs, as well as directly into Wikipedia. This improves the scientific accuracy of the encyclopedia, and rewards academics with citable, indexed publications. It also provides much greater reach than is normally achieved through traditional scholarly publishing.

Articles can either be on topics currently absent from Wikipedia, or be updates/overhauls of existing Wikipedia articles. Presubmission inquiries welcome to contact@wikijsci.org

Thomas Shafee

EiC of WikiJSci

Further info:

* WikiJSci Editorial Board (2018). The aims and scope of WikiJournal of Science. *WikiJournal of Science*, 1(1):1

* Shafee, T; Mietchen, D & Su A (2017). Academics can help shape Wikipedia. *Science*, 357(6351):557-558

* Shafee, T (2017). Wikipedia-integrated publishing: a comparison of successful models. *Health Inform*, 26(2):1
 “t.shafee@latrobe.edu.au” <t.shafee@latrobe.edu.au>

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UCalifornia Berkeley HumanEvolGenetics	63	UToronto 4 EvolutionaryBiol	80
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ARS-USDA Illinois FungalEvolutionaryBiology

Postdoctoral Position in Fungal Evolutionary Biology
NCAUR-ARS-USDA, Peoria, Illinois

We are searching for a highly-motivated postdoctoral associate with strong molecular and/or bioinformatic research experience with fungi or other microorganisms who can effectively utilize existing and incoming genome datasets to develop sequence-based classification tools for *Fusarium*, and to make inferences about evolutionary patterns and processes in this agriculturally important fungal genus. This position is part of the NSF-funded project "A Phylogenetic Revisionary Monograph of the Genus *Fusarium*" with colleagues at The Pennsylvania State University. Scientists in the Mycotoxin Prevention and Applied Microbiology (MPM) Research Unit at the USDA in Peoria have an outstanding record of discovery and publication regarding *Fusarium* biology, chemistry and evolution, and over 20,000 *Fusarium* cultures are available. Current *Fusarium* research projects

in the MPM Research Unit include phylogenomics of the genus, population genomics of key *Fusarium* pathogens and toxin producers, and the evolutionary dynamics of secondary metabolite gene clusters. Thus, opportunities exist for the postdoc to engage in these and other areas of interest. MPM scientists have generated genome datasets for more than 500 phylogenetically diverse *Fusarium* isolates and additional datasets will be developed for all known *Fusarium* species during this project. It will provide the postdoctoral associate with the opportunity to develop high-impact bioinformatics resources, and to utilize outstanding data resources for addressing key questions in fungal trait evolution. The postdoc will be working both with MPM scientists and an international community of PIs, Senior Personnel and project participants. They will participate in all phases of the project from design to publication. Salary and benefits are excellent, and because the position will be managed through the Oak Ridge Institute for Scientific Education (ORISE), it is open to both US and non-US citizens. This full-time position is funded for 3 years with annual renewal contingent on satisfactory performance. The anticipated start date is flexible, and could be as early as July 2018. The successful candidate must hold a PhD in Biology or related field by appointment start date, be proficient in both written and oral

English, and have experience in genome analyses and/or an excellent background in evolutionary biology. To apply, please email a single PDF to Kerry O'Donnell (kerry.odonnell@ars.usda.gov) that includes: (1) a cover letter with a short description of why you are interested in and qualified for the position, (2) a current CV that includes a list of peer-reviewed publications, and (3) names and contact information for three references. This position will remain open until filled.

"ODonnell, Kerry - ARS"
<Kerry.ODonnell@ARS.USDA.GOV>

BoiseStateU IntegrativeModeling

Position announcement

Post-doctoral position

Boise State University

Boise, Idaho, USA

Integrative modeling to forecast adaptive capacity of animal and plant species

*Position **Overview: *The Department of Biological Sciences invites applications for a post-doctoral researcher with expertise in modeling and evolution to develop quantitative models that integrate genomic, phenotype, and demographic rate data to forecast the adaptive capacity of species under different climate change scenarios. The post-doc will work with collaborative teams of ecologists, modelers, and geneticists across different institutions. The position will provide a unique opportunity to develop a transdisciplinary research program that addresses the National Science Foundations research priority of predicting phenotypes from genetic and environmental factors.

Key Responsibilities: The successful candidate will leverage data from the full cycle phenology project (full-cyclephenology.com) to forecast the adaptive capacity of wildlife and build capacity to extend the modeling framework to other species. In addition to modeling activities, the post-doc will lead and contribute to peer-reviewed publications, present findings at national meetings, and work with partners to extend modeling framework to other systems.

*Minimum **Qualifications:*

- Candidates must have obtained their PhD by the appointment start date: in mid-late September. - Demon-

strated statistical and programming skills with an emphasis on any of the quantitative areas: population genetics, agent-based models, integrated population models, size-structured population models, hierarchical Bayesian models. - Written and verbal communication skills. - The selected candidate must be able to meet eligibility requirements for work in the United States at the time appointment is scheduled to begin and to continue working legally for the proposed term of the appointment.

Preferred Qualifications:

- Evidence of creative problem solving - The ability to work well on teams and independently - Interest and understanding of ecological genomics, population dynamics, and evolutionary concepts. - Interest, experience, and/or ability to promote a climate of inclusion and equity

The successful candidate will be based at Boise, Idaho and have opportunities to interact with collaborators at Idaho State University, University of Idaho, University of California at Los Angeles, the Department of Defense, USGS, US Forest Service, and the Bureau of Land Management. The position is available for one year, with potential for renewal for subsequent years dependent on performance.

*Salary and benefits: *Salary will be based on qualifications and includes a benefits package including medical/dental/vision/life/LTD insurance, retirement plan, tuition benefits, sick leave, paid holidays, as well as other benefits.

*To apply for this this position: *Submit a single PDF by email that includes a cover letter that specifically address the qualifications listed above and a description of work experience, curriculum vitae, and contact information for 3 references to the following email address: julieheath@boisestate.edu. Please put evo postdoc in the subject line. Applications will be reviewed as they are submitted with final deadline of August 7.

About Boise and our University

The City of Boise: Boise is a mid-size city, located on the Boise River near the foothills of the Rocky Mountains. In national polls, Boise has been repeatedly named one of the best places to live because of surrounding natural beauty, access to outdoors, low cost of living, and low crime rates. Our region boasts numerous outdoor activities that include rivers, hot springs, skiing, and hiking. Boise provides residents with access to local wineries, a distillery, craft breweries, diverse dining that features ingredients from local farms and ranches as well as an active local and regional music scene and clubs for live entertainment. Boise also of-

fers a thriving art scene that includes Ballet Idaho, the Basque Center, the Boise Art Museum, Idaho Anne Frank Human Rights Memorial, nationally-renowned theater and performing arts companies, and cultural hotspots within a few blocks of downtown. To learn more about Boise: <http://www.cityofboise.org/> and <http://www.boise.org/> *Boise State University*: Boise State University, powered by creativity and innovation, stands uniquely positioned in the Northwest as a metropolitan research university of distinction. Learn more about Boise State at <https://go.boisestate.edu/join-our-team/>. Boise State University is committed to increasing the diversity of its workforce and academic program offerings and to strengthening sensitivity

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CornellU OatGenomics

The position is in the Plant Breeding and Genetics Section at Cornell University, and is part of a USDA Agriculture and Food Research Initiative grant to breed more nutritious oat. Oat is uniquely valued among grain crops for the health-promoting composition of its seeds. The project will leverage extensive genomic, transcriptomic, and metabolomic datasets collected in oat to develop and evaluate methods to improve the health-promoting composition of oat seed effectively. We will identify important causal loci and characterize new mutations affecting seed composition. The Plant Breeding & Genetics Section, within the School of Integrative Plant Science, trains interdisciplinary scientists in the elaboration of new breeding methods, the discovery of genetic mechanisms important for economically important traits, and the development of genetic stocks, germplasm, and varieties. Cornell University plant breeders are world leaders in innovative plant breeding research, teaching, and extension, and we collaborate globally.

This lab works with several crop species (wheat, oat, barley, cassava, and the brown algae sugar kelp) to develop genomic prediction methods and integrate them optimally within breeding schemes. We source tools from genomics, quantitative, statistical, and population genetics, and from machine learning and operations re-

search. With the Jannink lab, Dr. Michael Gore and Dr. Mark Sorrells provide leadership on the multiomic oat selection project.

In research for this project, the postdoc will collaborate with oat breeders at the Universities in Minnesota, Wisconsin and South Dakota, as well as a postdoctoral associate currently working on the project. We have characterized an oat diversity panel of 384 genotypes with high-density DNA marker data, RNA-seq gene expression data, and non-targeted LC-MS, GC-MS, and targeted fatty acid methyl ester data of mature oat seed. We will analyze these data to identify important genomic drivers of the mature oat seed metabolome. Results from this analysis will guide the sequencing of 80 target genomic segments in a population of 1,920 oat TILLING (Targeted Induced Local Lesions In Genomes) lines. TILLING lines mutated for putative metabolomic regulators will be evaluated to validate their function. We have also used these data to select 15 crosses among elite oat cultivars and will characterize 50 inbred progeny from each cross. We will assess whether results from the multiomic analysis of the diversity panel enables improved prediction among full-sib progeny for seed composition traits.

Term is one year renewable to three years contingent on performance and continued funding.

The candidate would be expected to contribute needed metabolomics expertise to the project. The postdoc responsibilities will therefore involve work on experiments with new oat lines and interpreting the output of metabolomic assays and connecting metabolite levels to gene expression and genotype through knowledge of biochemistry. In collaboration with other project personnel, the postdoc will conduct and interpret genome- and transcriptome-wide association studies. These studies should result in the identification of genomic regions targeted for sequencing in the TILLING population. Identified regions will also be used to inform genomic prediction models aimed at improving breeder selection of oat seed composition traits.

Position Requirements Ph.D. in plant biochemistry or metabolomics with experience or interest in breeding applications, or Ph.D. in plant or animal breeding with emphasis on biochemistry, metabolomics, nutritional science. Proven scientific writing ability and communication skills.

Preferred Specific Skills Genome-wide association studies and genomic prediction methods. High-dimensional data analysis. Programming skills in R or other quantitative / statistical scripting. Basic bioinformatics skills (sequence alignment, use of gene annotations). Basic notions of mating designs in breeding.

Candidates are encouraged to send a statement of interest, curriculum vitae, and contact information for three references. Submit all application materials to Academic Jobs Online at <https://academicjobsonline.org/ajo/jobs/11282>. Questions about the position can be addressed to Dr. Michael Gore at: mag87@cornell.edu. Review of applications will begin immediately and continue until the position is filled.

Diversity and Inclusion are a part of Cornell University's heritage. We are a recognized employer and educator valuing AA/EEO, Protected Veterans, and Individuals with Disabilities

Jean-Luc Jannink <jeanluc.work@gmail.com>

Halifax FisheriesGenomics

Postdoctoral Fellow positions with Fisheries and Oceans Canada on fisheries genomics in Halifax, NS, Canada.

Positions: Several postdoctoral fellow positions (3-4) are available at Fisheries and Oceans Canada (Halifax, NS) with the Bradbury Lab. Species of primary interest are Atlantic Salmon, Arctic Charr, Atlantic Cod, and Common Lumpfish but current projects include other anadromous fish and species of marine invertebrates as well. The lab's research is broadly concerned with the application of genomic tools to inform marine management and conservation.

Candidates must have a PhD in fisheries science, population genetics, genomics, oceanography or a related field.

Application: Please email Ian Bradbury (ibradbur@me.com) with (1) a letter describing your interests in this position and your previous research experience, and (2) a recent CV. Formal applications must be submitted through the Postdoctoral Research Program through Fisheries and Oceans Canada. Review of will applications begin right away with several positions available ASAP, and will continue throughout 2018.

Ian Bradbury <ibradbur@me.com>

Halle Germany Genomics HoneybeeResistance

Halle_Germany.Genomics.HoneybeeResistance

Postdoc project starting as soon as possible and lasting till 31st of March 2019 in the Molecular Ecology group at Martin-Luther-University, Halle-Wittenberg, Germany.

The aim of the project is to find genetic basis of honey bee *Apis mellifera* resistance to *Varroa destructor*. This will be done by using the latest methods in genomics, transcriptomics and proteomics. Thus representing a unique opportunity to gain experience in an area, which is of high demand in the research field.

The chosen postdoc is expected to work independently within the project framework. The skills should reflect the project description. The candidate will be familiar with standard molecular methods in the lab as well as bioinformatics and running scripts. Willingness to learn new methods is a must as well as ability to adapt to ever-changing circumstances. Excellent command of English in both writing and speaking is essential. Knowledge of German is beneficial but not must.

Information of the research group can be obtained from Dr. Jarkko Routtu, tel: +49 (0) 345 55 26382, email: [jarkko.routtu\(at\)zoologie.uni-halle.de](mailto:jarkko.routtu(at)zoologie.uni-halle.de)

<http://www.mol-ecol.uni-halle.de/staff/routtu-j/>
http://www.mol-ecol.uni-halle.de/research/genomics/-varroa_resistance/ Applications should be sent as soon as possible, subject line referring to "Postdoc resistance", together with your letter of motivation, CV, publication list, names of two referees in a single pdf file.

Jarkko Routtu <jarkko.routtu@zoologie.uni-halle.de>

HarvardU HIVDynamicsEvolution

The Program for Evolutionary Dynamics at Harvard University welcomes applications for a postdoctoral fellow to work in the field of infectious disease modeling. We are seeking a motivated and creative PhD-level scien-

tist with experience applying mathematics to biological systems.

In particular, we are seeking a postdoc to contribute to two major research efforts related to HIV/AIDS. One is an NIH-funded effort to develop mathematical models to predict the outcomes of new, potentially-curative treatment strategies for HIV infection. Another is a Gates Foundation funded project to use dynamic models to understand outcomes of antiretroviral therapy, including the risks of drug resistance, the influence of patient adherence, and the potential impact of new drug delivery mechanisms. We regularly work with data from experimental collaborators testing new therapies in vitro, in animal models, and in patients.

The successful candidate would also have the option to pursue independent research of mutual interest. More generally, we are interested in factors influencing the pathogenesis and evolution of infectious diseases, both at the individual and population levels, and in developing methods to infer mechanistic models from biological data. More information about our research can be found at <http://www.people.fas.harvard.edu/~alhill/> More information about the position can be found at : <https://academicpositions.harvard.edu/postings/7798> Inquiries can be directed to Alison Hill (alhill@fas.harvard.edu)

“alhill@fas.harvard.edu” <alhill@fas.harvard.edu>

Institut Pasteur Paris Virus Evolution Epidemiology

Postdoctoral position in virus evolution and epidemiology

We are looking for a computational biologist interested in pathogen evolution to join us to work on exciting projects combining molecular epidemiology and functional studies of arboviral infections. The Simon-Loriere lab is a junior group (G5) newly created in the Virology department of Institut Pasteur in Paris, France.

The aim of the current project is to study dynamics of arbovirus emergence or endemic circulation, and the underlying mechanisms, at the scale of individual outbreaks through the integrated analysis of genomic, spatial and temporal data.

Previous experience in computational analysis of viral sequence data, evolution and quantitative skills will be essential, ideally including familiarity with high-throughput sequencing and large genomics data sets.

The viral NGS data is generated by other members of the group, so the work is exclusively focused on data analysis and no lab skills are required. Knowledge of epidemiological models, phylodynamic approaches (including Bayesian methods), and pathogen evolution would be desirable but not essential. Scientific rigor, organizational skills, high motivation, English proficiency and ability to work collaboratively in an interdisciplinary environment are essential.

To apply: candidates should send in a single pdf: a cover letter including a brief description of their scientific achievements and research interests, how they would fit in a junior group, their CV and contact information for 3 references to etienne.simon-loriere@pasteur.fr.

The position will remain open until filled; the position is available immediately but the start date is negotiable. Funds are available for up to 3 years. Salary will be commensurate with experience according to the Institut Pasteur guidelines.

Etienne SIMON-LORIERE <etienne.simon-loriere@pasteur.fr>

LMU Munich FernEvolution

Evolution of key traits in ferns

A postdoctoral position is open for application, starting immediately and until filled. Starting date is 10 October 2018. The research will involve analyzing ecological, morphological, and genetic data relevant to the evolution of ferns. Expertise available in our group includes an expert in the systematics and evolution of ferns, a postdoc in bioinformatics, a postdoc with expertise in chromosomal studies, and in-house access to a scanning electron microscope. We also have access to one of the World's largest herbaria and a top notch botanical garden. Participation in various basic botany courses taught in German is required. The postdoc will benefit from the broad range of methods and expertise available in the Munich plant systematics center, which will help them develop and carry out cutting-edge projects and thus their future career options.

To apply, please send your letter of motivation, cv, and the names of two referees to marlehnert@yahoo.com or renner@lmu.de

For more details email on our research:

<https://scholar.google.de/citations?user=->

vEvoCaMAAAAJ&hl=en <https://scholar.google.com/citations?user=uzOGmTgAAAAAJ&hl=de> Susanne Renner <renner@lmu.de>

Montpellier PopGen

. Project— title:— Demographic inference under the coalescent in a spatial continuum.

. Principal investigator: Stephane Guindon (CNRS)
 . Associate— investigator: Raphael Leblois (INRA).
 . Host institution: CNRS-University of Montpellier, France. . Funding:— ANR. . Net salary: ~2100 euros/month (including health insurance). . Starting date: October 2018.

A— 24 month postdoc— position— in— population genetics— is available— at the— University— of Montpellier, France.— The successful— candidate will— join the “Methods and— Algorithms in Bioinformatics” group and work— in close collaboration with other Montpellier-based research teams.

The main objective of the project is to develop, implement and apply original inference techniques for fitting the spatial Lambda-Fleming-Viot model, i.e., a coalescent model in which individuals are spatially distributed along a continuum, as opposed to discrete demes. A particular emphasis will be put on proposing techniques that are able to cope with genomic data. Preliminary work suggests that sequential Monte Carlo algorithms applied to SNP data could serve as a basis to build efficient inference techniques. Modern simulation-based approaches, such as random forest ABC [2], the summary likelihood— method [3] and deep-learning techniques [4] will also be considered.

Application of the proposed methods to simulated and real-world whole genome data will then reveal the ability of the new techniques to estimate population density and migration rate from the analysis of geo-referenced genetic data.

The ideal candidate— for the proposed project will have— a PhD in population genetics or statistical phylogenetics,— although pure statisticians and physicists— interested— in molecular evolution should— also apply. Good— skills in data— analysis with modern tools— and programming languages (R and/or— Python and/or Java or C/C++) are essential.

Montpellier is a vibrant city on the Mediterranean coast with a large student community. Cycling to the sea

takes about 30 minutes and the back country offers breathtaking landscapes (~30 minutes drive north of the city). It is about 3h from Barcelona and Paris by train.

Please—send—CVs—and—inquiries—to—Stephane—Guindon (guindon@lirmm.fr) and Raphael Leblois (raphael.leblois@inra.fr).

[1] Demographic inference under the coalescent in a spatial continuum.— S Guindon, H Guo, D Welch. *Theoretical population biology* 111, 43-50

[2] Pudlo, P., Marin, J.-M.,— Estoup, A., Cornuet, J.-M., Gautier, M. and Robert, C. P. (2015) Reliable ABC model choice via random forests. *Bioinformatics* 32 (6): 859-866.

[3] Rousset, F., Gouy, A., Martinez-Almoyna, C., Courtiol, A. (2017) The summary likelihood method and its implementation in the Infusion package. *Mol. Ecol. Resources*, 17 :110-119.

[4] Sheehan, S., Song Y. (2017) Deep Learning for population genetic inference. *PLoS Comput Biol* 12(3): e1004845. doi:10.1371/journal.pcbi.1004845

Stephane Guindon <stephane.guindon@lirmm.fr>

NTNU Taiwan AdaptationSpeciation

Postdoc Position in Adaptation and Speciation (NTNU, Taipei, Taiwan)

A two-year postdoc is available on August 1, 2018 for an innovative and motivated person to work on the adaptation of *Pachyrhynchus* weevils or the speciation of endemic *Psolodesmus* damselflies.

Project:

The position is funded by the MOST (Ministry of Science & Technology, Taiwan) grants focused on testing hypotheses about the adaptation of aposematic colours in *Pachyrhynchus* weevils and the process of species formation in two subspecies of *Psolodesmus* damselflies.

1. Aposematism of Weevils

Pachyrhynchus weevils are a group of brilliant, metallic-coloured weevils distributed in the Old World tropics. Recent studies showed that the conspicuous colouration of these weevils function as effective warning signals for their hard bodies to prevent predacious pursuit by lizards. We are interested in studying the adaptation,

evolution, and spatio-temporal dynamics of interactions between vertebrate predators and aposematic prey using these weevils.

Related articles:

Wang, L-Y., W-S. Huang, H-C. Tang, L-C. Huang and C-P. Lin* (2018) Too hard to swallow: A secret secondary defence of an aposematic insect. *Journal of Experimental Biology* 221.

Tseng, H-Y., W-S. Huang, M-L. Jeng, R.J.T. Villanueva, O.M. Nuneza and C-P. Lin* (2018) Complex inter-island colonization and peripatric founder speciation promote diversification of flightless *Pachyrhynchus* weevils in the Taiwan-Luzon volcanic belt. *Journal of Biogeography* 45: 89-100.

Chen, Y-T., H-Y. Tseng, M-L. Jeng, Y-C. Su, W-S. Huang and C-P. Lin* (2017) Integrated species delimitation and conservation implications of an endangered weevil *Pachyrhynchus sonani* (Coleoptera: Curculionidae) in Green and Orchid Islands of Taiwan. *Systematic Entomology* 42: 796-813.

Tseng, H-Y., C-P. Lin*, J-Y Hsu, D.A. Pike and W-S. Huang* (2014) The functional significance of aposematic signals: geographic variation in the responses of widespread lizard predators to colourful invertebrate prey. *PLoS ONE* 9(3):e91777.

2. Damsselfy Speciation

We focus on a damsselfy species, *Psolodesmus mandarinus*, with two subspecies differ in their distribution and wing pigmentations in Taiwan. It provides a great opportunity to evaluate the relative importance of natural and sexual selection in damsselfy divergence. The project will incorporate a wide range of techniques, including a whole-island field survey, behavioural studies, manipulation experiments, population genetics and genomic analysis to investigate the divergence in damsselfies.

A description of the research project:

<https://sites.google.com/site/yuhsunhsu/research?pli=1> Requirement:

1. The postdoctoral fellow will be responsible for either leading a hypothesis-driven field/laboratory experiment, or the analyses of genomic-scale DNA sequence data sets. The applicant is also encouraged to develop an independent project based on applicant's expertise and the study systems.
2. The successful applicant must have demonstrated expertise in behavioral ecology, population genetics, phylogenetics, genomics, or computational statistics.
3. Preference will be given to candidates with:

- (1) Background in behavioral ecology studies,
- (2) Experience of high performance computing,
- (2) The ability to develop and apply statistical or computational methods to solve biological problems,
- (3) Expertise in research on adaptation, speciation, theoretical models of evolution, or trait divergence.

Application:

To apply, please contact Chung-Ping Lin by email (treehopper@ntnu.edu.tw), and attach a single PDF file containing: 1) a cover letter, 2) a CV, 3) a brief 2-page statement of research interests, and how your skills can contribute to project objectives, and 4) contact information for three references.

Salary & Deadline:

The position will be available from 2018/08 to 2020/07. Start date is flexible. Funding is available for at least 2 year with a potential extension of 3 years, pending on the performance and funding.

A monthly post-doc salary of about \$55,000 NTD (\$1,900 USD) will be offered, including retirement plan, health benefits, and a year-ending bonus of 1.5-month salary. The average living cost in Taiwan is about 1/2 of that in the USA.

The position will remain open until a suitable candidate is found.

More information:

Chung Ping Lin's lab: <http://web.ntnu.edu.tw/~treehopper/> Department of Life Science: <http://www.biol.ntnu.edu.tw/> National Taiwan Normal University: <http://www2.ntnu.edu.tw/en/index.php> Chung-Ping Lin Department of Life Science National Taiwan Normal University Taipei, Taiwan <http://web.ntnu.edu.tw/~treehopper>

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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>

PurdueU PlantEvolGenetics

Postdoctoral position in plant ecological and evolutionary genetics at Purdue University

A postdoctoral position is available in the Oakley lab at Purdue University to study the genetic and physiological

mechanisms of fitness tradeoffs across environments. We use a combination of field experiments in native habitats and experiments in controlled growth chambers to investigate the links between sequence polymorphism, molecular phenotypes, organismal phenotypes, and ultimately fitness in contrasting environments. Current and future work will incorporate transcriptomic and metabolomic approaches to studying genotype by environment interactions for fitness. Additional research in the lab is focused on the evolutionary ecology and genetic basis of heterosis and outbreeding depression. Development of new research directions building on these broad themes is strongly encouraged. There is a vibrant community of interdisciplinary plant biologists at Purdue (<https://ag.purdue.edu/cpb/faculty/>), providing ample opportunity for interaction and new collaborations.

Research activities will include (but are not limited to): Leading growth chamber experiments to estimate freezing tolerance & lifetime fitness, and combining this data with differential expression analyses using RNAseq; 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 CRISPR-CAS9 lines, near isogenic lines, 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 or plant genetics. The ideal candidate will have an interdisciplinary skill set, having some combination of wet lab, bioinformatic, and experimental biology experience. A strong foundation in R, and at least a basic familiarity with bioinformatic analysis on a cluster 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 August-September 2018 is preferred, but this is negotiable.

Applicants should send (as a single PDF attachment): CV, a letter summarizing research interests, accomplishments, and fit to the lab and project, and the names and contact information for two professional references. Review of applications will begin June 15, 2018 and will continue until a suitable candidate is found.

Chris Oakley oakleyc@purdue.edu <https://dev.btny.purdue.edu/labs/oakley/> oakleyc@purdue.edu

RoyalVetCollege London AnimalEvolutionaryGenomics

We wish to recruit a highly motivated, postdoctoral scientist to carry out a BBSRC funded project in the laboratory of Dr. Denis Larkin. The project is focused on developing and applying new methods and algorithms to study genome and chromosome evolution in mammals and other animals using whole-genome sequences and existing algorithms (e.g., Damas et al. *Genome Res.* 2017. 27(5):875-884; Kim et al., *Proc Natl Acad Sci USA.* 2013. 110 (5)). The post holder will use cutting edge computational and laboratory approaches to generate chromosomal assemblies for sequenced genomes, study chromosomal structures and differences between mammalian and other vertebrate genomes in attempt to identify species- and clade-specific genome signatures.

Applicants must have a Ph.D. and a track record of success, as indicated by first-author publications in international journals. They must possess excellent organisation skills and be capable of individual initiative and of interacting as part of a team. Applicants with extensive practical experience in bioinformatics or computer science, programming, visualization, handling of large data sets, high-performance computing are encouraged to apply. The post will involve collaboration with a wide range of academic partners both within the EU and worldwide.

Experience in programming, bioinformatics and comparative genome analysis is essential. Applicants should have a minimum of a degree and preferably a higher degree in a relevant subject.

The Royal Veterinary College has the largest range of veterinary, para-veterinary and animal science undergraduate and postgraduate courses of any veterinary school in the world and is one of the largest veterinary schools in Europe.

Prospective applicants are encouraged to contact Dr. Denis Larkin, Comparative Biomedical Sciences Department on +442071211906 or email: dlarkin@rvc.ac.uk

We offer a generous reward package.

For further information and to apply on-line please visit our website: <https://jobs.rvc.ac.uk/Vacancy.aspx?ref=CBS-0084-18> Job reference CBS-0084-18

Deadline for applications July 25th, 2018 [RVC

Logo - link to RVC Website] < <http://www.rvc.ac.uk> > [Twitter icon - link to RVC (Official) Twitter] < <http://twitter.com/RoyalVetCollege> > [Facebook icon - link to RVC (Official) Facebook] < <http://www.facebook.com/theRVC> > [YouTube icon - link to RVC YouTube] < <http://www.youtube.com/user/RoyalVetsLondon?feature=mhee> > [Pinterest icon - link to RVC Pinterest] < <http://pinterest.com/royalvetcollege/> > [Instagram icon - link to RVC Instagram] < <http://instagram.com/royalvetcollege> >

“dlarkin@rvc.ac.uk” <dlarkin@rvc.ac.uk>

SorbonneU BarnaclePopulationGenetics

A postdoc position is available at the Roscoff Biological Station of Sorbonne University, France.

See details: http://www.sb-roscoff.fr/en/2018/05/18/-call-postdoctoral-position?lab_id=115&group_id=All

For application, please send a letter of motivation and a detailed curriculum vita by e-mail before the 15th of June 2018 to: Eric THIEBAUT (thiebaut@sb-roscoff.fr) and Didier JOLLIVET (jollivet@sb-roscoff.fr)

Christophe Lejeusne <christophe.lejeusne@sb-roscoff.fr>

Taipei Taiwan AvianGenomics

Postdoctoral Position in Avian Genomics (Academia Sinica, Taipei, Taiwan)

Research project: This postdoctoral position is available in Chih-Ming Hung’s research group at Biodiversity Research Center, Academia Sinica in Taiwan. This position is aimed at biologists in the area of evolutionary genomics. The main focuses of our research projects are to study the genomic bases of avian ecological adaptation or breeding behavior and understand their evolutionary mechanisms. The postdoctoral fellow will analyze population genomic and transcriptomic data of several bird species and prepare manuscripts for publication. Independently developing research within the project framework is also encouraged.

Requirement: 1. A Ph.D. in biology, bioinformatics, or a relevant field 2. Successful applicants must have strong background in molecular ecology, population genomics and/or bioinformatics. 3. Applicants with the following experiences are preferred: (a) experienced in whole genomic or trancriptomic analyses and (b) familiar with at least one programming language (Perl, Python or R).

Salary & Condition: This position is for one year, and renewable upon satisfactory progress. The starting date is flexible although August 1st, 2018 is preferred.

The monthly salary will be between \$ 58,000 ~ 63,000 NTD (\$ 1,920 ~ 2,090 USD) depending on research experiences. The position also offers health benefit and a year-ending bonus of 1.5-month salary. The average living cost (including housing) in Taipei, Taiwan is about \$ 20,000 ~ 28,000 NTD (\$ 660 ~ 930 USD).

Academia Sinica has dynamic research environment and cutting-edge research facilities. Taiwan is a subtropical island with beautiful beaches and mountains.

Application: To apply, please send (1) a motivation letter describing your qualification, experiences and research interests, (2) a C.V. and (3) names and contact information of 3 references to Dr. Chih-Ming Hung (cmhung@gate.sinica.edu.tw). The review of applications will start on July 1st, and the position will remain open until a suitable candidate is found.

Contact & Further information: Chih-Ming Hung, Assistant Research Fellow Biodiversity Research Center, Academia Sinica 128 Academia Road Sec.2, Nankang, Taipei 115, Taiwan Email: cmhung@gate.sinica.edu.tw Tel: 886-2-2787-2297 Webpage: <http://www.biodiv.tw/-index.php/en/people/faculty/dr-chih-ming-hung#lab-pi> cmhung <cmhung@gate.sinica.edu.tw>

UAlberta FishPoPulationGenetics

Post-Doctoral Position (1 or 2 yrs.) - Population genetics of endangered freshwater fishes in the Canadian Prairies

A postdoctoral fellowship is available in the Fisheries and Aquatic Conservation Laboratory led by Dr. Mark Poesch at the University of Alberta. This position is aimed at a population genomicist, regardless of taxa. Genetic marker data (SNPs and microsatellite data) has been collected for several freshwater fish species at risk, including the Athabasca Rainbow Trout (Endangered), Western Silvery Minnow (Endangered) and

Mountain Sucker (Threatened). The post-doctoral fellow will help analyze this data examining population structure, genetic diversity and introgression to aid in the management of these species. This project is fully funded for up to two years (after satisfactory review of the candidate's performance after one year).

Candidate must have a Ph.D. at the time of commencing the position. Experience with population genomics is essential. Candidates interested in this position should send an email to Dr. Mark Poesch (poesch(at)ualberta.ca) with cover letter clearly articulating how this research builds on their experience, specific skills and date of availability. Please note review of applicants will not commence until July 2, 2018. This competition will remain open until a suitable candidate is found. Start date is negotiable but ideal start date is fall 2018. The candidate will receive a salary of \$45,000 per year plus benefits.

The University of Alberta is consistently rated as one of the top 5 universities in Canada, and one of the top 100 universities worldwide. Located in Alberta's capital city, Edmonton (population of 1.2 million people), the University of Alberta provides a dynamic mixture of a large research intensive university, urban culture and recreation. More than 39,000 students from across Canada and 144 other countries participate in nearly 400 programs and 18 faculties (<http://www.why.ualberta.ca/-ualbertain1minute>).

Contact Information:

Dr. Mark Poesch Associate Professor, Fisheries and Aquatic Conservation

University of Alberta,

Department of Renewable Resources 751 General Services Building, Edmonton, Alberta, T6G 2H1 Ph: 780-492-4827 Email: Poesch(at)ualberta.ca

Website: <https://poeschlab.ualberta.ca/> Corey Davis <cordavis@ualberta.ca>

UArizona GGSimpsonFellow

A postdoctoral position is available in the Badyaev Lab at the Department of Ecology and Evolutionary Biology of University of Arizona. This is an excellent opportunity for a productive and creative scientist to work on outstanding problems in evolutionary biology of their own choosing and collaborate on the lab's existing projects. The position is supported by the G.G. Simpson Postdoctoral Fellowship, established to honor Prof. G.G. Simpson's work at the Department. The position leverages the considerable technical strength and intellectual rigor of EEB at University of Arizona to provide just the right combination of freedom and opportunities for professional growth. Of particular interest are candidates interested in collaboration on the ongoing projects below, each offering opportunities for creative experimental, comparative, and modeling studies:

1) Identification and analysis of cell lineages during ontogenetic changes that accompany evolution of diverse beak configurations. Requires expertise (or strong desire to be trained) in one of the following: immunohistochemistry, analysis of RNAseq data, histology, vertebrate embryology, population genetics/genomics. 2) Analysis of metabolic network evolution across avian taxa, with specific focus on the topological and flux aspects of network controls. Requires expertise in one of the following: biochemistry, network and dynamic systems theory, phylogenetic network analysis.

Both sets of projects are enabled by the data generated by the lab's long-term studies of house finch populations across Montana and Arizona. Thus, there are also unlimited opportunities to participate in field research in spectacular places for applicants so inclined.

The position comes with a salary of \$47,659 per academic year with full benefits, an additional research allowance of \$5,000, and is renewable for up to two years. Tucson, and southeast Arizona in general, is hard to match in terms of biological and cultural diversity and its stunning landscapes and limitless outdoor opportunities.

The start date is flexible, but anticipated to be in Fall 2018 or when the suitable candidate is identified. Candidates should apply online at: <http://uacareers.com/-postings/29780> submitting 1) cover letter outlining proposed research and potential projects for collaborations,

2) a description of research experience (2 pages max), 3) CV with the contacts of three references, and 4) reprints of three most significant publications combined in a single file. Review of applications will begin 1 July 2018 and continue until the position is filled.

Questions regarding the search may be sent to Alex Badyaev (abadyaev@email.arizona.edu)

“abadyaev@email.arizona.edu”
<abadyaev@email.arizona.edu>

UArizona PlantEcolGenomics

A postdoctoral research position funded by the National Science Foundation is available to work in the Department of Ecology and Evolutionary Biology at the University of Arizona (Tucson, AZ, USA) with Dr. Katrina Dlugosch (@DlugoschLab, <http://-dlugoschlab.arizona.edu/>) and collaborator Dr. David Baltrus (@surt_lab, <http://cals.arizona.edu/research/-baltruslab>) at the University of Arizona on the ecological genomics of evolution along a growth-defense trade-off in the invasive plant yellow starthistle (*Centaurea solstitialis*). We are using greenhouse experiments, microbial culturing, plant immune function assays, microbiome sequencing, plant population genomics, plant QTL mapping, plant RNAseq analyses, and selection experiments to study the evolution of species interactions during range expansion and their impact on the spread of invading plant populations. In addition, there will be opportunities for the postdoc to propose new research directions, and to be involved in the mentoring of undergraduate students from underrepresented groups in research on plant-microbe interactions. We are seeking outstanding postdoctoral researchers with interests and experience in these areas.

The position is for one year, with reappointment for up to two additional years subject to satisfactory performance. Start date can be as early as Aug 2018, but a start date any time in the 2018/2019 academic year is negotiable. Review of applications will begin immediately and continue until filled.

Minimum qualifications *PhD in Biology or a related field *Experience producing and analyzing molecular genetic data *Authorship of peer-reviewed publications of research in a field related to the position *Strong communication skills *Ability to work independently and in a team

Preferred Qualifications (Some combination of these is highly desirable): *Experience rearing plants in the greenhouse or growth chamber *Experience preparing plant DNA for next-generation sequencing *Experience with QTL mapping *Experience with RNA extraction and RNAseq library preparation *Experience with microbiome sequencing *Experience with bioinformatic analyses of genomic data *Experience culturing bacterial colonies *Experience with assays of plant defense functions

To apply, submit a cover letter, statement of interest, curriculum vitae, and contact information for three references to job #30244 at <http://uacareers.com/postings/>. Inquiries about the positions may be directed to Dr. Katrina Dlugosch (kdlugosch@email.arizona.edu).

Katrina Dlugosch <katrina.dlugosch@gmail.com>

UArizona PlantMicrobeGenomics

A postdoctoral research position funded by the National Science Foundation is available to work in the Department of Ecology and Evolutionary Biology at the University of Arizona (Tucson, AZ, USA) with Dr. Katrina Dlugosch (@DlugoschLab, <http://-dlugoschlab.arizona.edu/>) and collaborator Dr. David Baltrus (@surt_lab, <http://cals.arizona.edu/research/-baltruslab>) at the University of Arizona on the ecological genomics of evolution along a growth-defense trade-off in the invasive plant yellow starthistle (*Centaurea solstitialis*). We are using greenhouse experiments, microbial culturing, plant immune function assays, microbiome sequencing, plant population genomics, plant QTL mapping, plant RNAseq analyses, and selection experiments to study the evolution of species interactions during range expansion and their impact on the spread of invading plant populations. In addition, there will be opportunities for the postdoc to propose new research directions, and to be involved in the mentoring of undergraduate students from underrepresented groups in research on plant-microbe interactions. We are seeking outstanding postdoctoral researchers with interests and experience in these areas.

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Minimum qualifications: *PhD in Biology or a related field *Experience producing and analyzing molecular genetic data *Authorship of peer-reviewed publications of research in a field related to the position *Strong communication skills *Ability to work independently and in a team

Preferred Qualifications (Some combination of these is highly desirable): *Experience rearing plants in the greenhouse or growth chamber *Experience preparing plant DNA for next-generation sequencing *Experience with QTL mapping *Experience with RNA extraction and RNAseq library preparation *Experience with microbiome sequencing *Experience with bioinformatic analyses of genomic data *Experience culturing bacterial colonies *Experience with assays of plant defense functions

To apply, submit a cover letter, statement of interest, curriculum vitae, and contact information for three references to job #30244 at <http://uacareers.com/postings/>. Inquiries about the positions may be directed to Dr. Katrina Dlugosch (kdlugosch@email.arizona.edu).

Katrina Dlugosch <katrina.dlugosch@gmail.com>

UCalifornia Berkeley DiseaseEvolution

Postdoctoral Scholar 'V Integrative Biology - Boots Lab - UC-Berkeley

A position for a theoretical postdoctoral scholar in disease ecology and evolution is available to join the Boots lab at Berkeley. Infectious disease continues to cause a major burden to human health, cause significant damage in agriculture and are ubiquitous in nature. Our lab is interested in understanding the evolution and ecology of infectious disease and applying this knowledge to their management and control. We develop ecological and evolutionary theory and test the theory in insect-virus model systems in the lab and the field. In addition, we apply ecological and evolutionary theory by building epidemiological models of human tropical disease, specific ecological models of wildlife disease and developing evolutionarily rational disease intervention and control strategies. Responsibilities:

The position will focus on developing ecological and evolutionary models of infectious disease dynamics. The specific projects will be developed between the postdoctoral scholar, Boots and their collaborators Current

projects include understanding the ecological implications and evolutionary drivers of multi-mode transmission dynamics in collaboration with Janis Antonovics at UVA, including the integration of models with field data. Other current work in the lab includes the evolution of bee disease, the role of population structure and management practice in the evolution of infectious disease, evolutionarily rational disease intervention and the evolutionary implications of the microbiome. There is the opportunity to develop novel projects within these areas with the Bootslab and their wider network of collaborators.

Minimum/Basic Qualifications Required (At the time of application):

Candidates must have completed all degree requirements except the dissertation or be enrolled in an accredited Ph.D or equivalent degree program in ecology, evolution or a related field

Additional Required Qualifications (By start date):

Ph.D or equivalent in ecology evolution, or related field, with a track record of publication in peer-reviewed journals.

Preferred Qualifications (By start date):

Excellent writing and communication skills.

Appointment:

This position reports to Dr. Michael Boots. The initial appointment will be at 100% time for one year with the possibility of extension based on satisfactory performance and availability of funding. The approximate start date of this position will be August 2018.

Salary: \$48,216-V \$58,560 depending on qualifications. This position provides full benefits.

To Apply: Apply online at <https://aprecruit.berkeley.edu/apply/JPF01757> Interested individuals should submit application documents as PDFs, which includes, an updated curriculum vitae (required), and names with contact information for at least 3-5 individuals who have agreed to provide a reference for this specific position (required) and a cover letter (required). (Letters of reference may be requested of the finalists).

Specific questions regarding the recruitment can be directed to Terri Leong, HR Partner, terri.leong@berkeley.edu

This recruitment will remain open until filled.

All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are provided

via a third party (i.e., dossier service or career center), to the UC Berkeley statement of confidentiality (<http://apo.berkeley.edu/evalltr.html>) prior to submitting their letters.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: <http://policy.ucop.edu/doc/4000376/-NondiscrimAffirmAct>. The department is interested in candidates who will contribute to diversity and equal opportunity in higher education through their work.

Michael Boots <mboots@berkeley.edu>

UCalifornia Berkeley HumanEvolGenetics

Recruitment Period

Open date: April 17th, 2018 Next review date: June 6th, 2018

Apply by this date to ensure full consideration by the committee. Final date: June 6th, 2018

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

Description:

The Moorjani Lab (<https://moorjanilab.org/>) at University of California, Berkeley has a post-doctoral position available for motivated candidates with background in statistical population genetics and/or data science.

Our lab focuses on using statistical and computational approaches to study questions in human genetics and evolutionary biology. A central aim in the lab is to understand the impact of evolutionary history on genetic variation and to apply this knowledge to learn about human history and biology. To this end, we use genetic data from ancient specimens and present-day species to learn about: (1) when key events (such as introgression and adaptations) occurred in human history, (2) how different evolutionary processes such as mutation rate evolve across primates, and (3) how we

can leverage these patterns to identify genetic variants related to human adaptation and disease. The research in the lab involves both development of new methods and large-scale genomic data analysis.

Responsibilities:

A successful candidate will develop and apply computational approaches to large genomic datasets to characterize patterns of population history and evolution. The main responsibilities include conducting research, attending regular lab meetings and journal clubs, and preparing research results for publication and presentations at scientific meetings. Opportunities may also exist for mentoring graduate and undergraduate students.

Minimum/Basic Qualifications required at the time of application:

- Completion of all doctoral degree requirements except the dissertation in genetics, computational biology, biostatistics, population genetics or related fields.

Additional Qualifications (required by start date):

- PhD or equivalent degree in genetics, computational biology, biostatistics, population genetics or a related field.

- Knowledge of statistics and population genetics theory.

- Demonstrated record of research productivity and publications.

- Programming experience (e.g. C/C++, Python/ Perl, R or other programming languages)

Preferred Qualifications:

Experience with large-scale genomic data analysis.

Salary: This is a full-time position. Salary is commensurate with qualifications and experience.

How to apply:

To apply, please go to the following link: <http://apptrkr.com/1205272> Applicants should submit the following materials:

- A cover letter
- A curriculum vitae
- Statement of Research (One-page summary of research interests)
- Contact information for 3 references

Letters of reference are not required at this time. We will seek your permission before contacting your references. All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are provided via a third party (i.e., dossier service or

career center), to the UC Berkeley statement of confidentiality: <http://apo.berkeley.edu/evalltr.html> . This position will be open until filled. The anticipated start date is June 2018. The appointment is for a duration of one year with the possibility of annual renewal up to three years. Please address inquiries to Maria Ruiz, maruiz@berkeley.edu.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: <http://policy.ucop.edu/doc/4000376/-NondiscrimAffirmAct> . Job location

Berkeley, CA

Requirements

Documents

-

Curriculum Vitae - Your most recently updated C.V.

-

Cover Letter

-

Statement of Research - One-page summary of research interests

References 3 references required (contact information only)

Jessica Godoy JobElephant.com | 800.311.0563 | jessica@jolephant.com Online Ads-Print Ads-Analytics-Automation-Expert Consultation. Recruitment Advertising. SolvedA

Jessica Godoy <jessica@jolephant.com> Jessica Godoy <jessica@jolephant.com>

UCalifornia Berkeley PupfishSpeciation

Postdoctoral position(s) on the genomics, function, and ecology driving adaptive radiation and multiple fitness peaks in Caribbean pupfishes

The Martin Fish Speciation Lab at the University of California Berkeley Museum of Vertebrate Zoology (starting

January 2019) seeks a postdoc for integrative studies of adaptive phenotypes and fitness in a sympatric radiation of trophic specialist pupfishes. Pupfishes present a rare opportunity to investigate the recent origins of spectacular adaptive radiation and the evolution of novel niches (e.g. scale-eating) localized to a single Bahamian island despite thousands of similar Caribbean environments. Our lab also investigates Cameroon crater lake cichlids, one of the most celebrated examples of sympatric speciation in nature, and the role of gene flow in their diversification.

A multi-year position is available (initial 12 month appointment with the possibility of renewal for four more years). This research is funded by both NIH and NSF grants. Start date is flexible, but must be after January 2019. Salary is scaled to the standard NIH postdoctoral rates.

This is a highly flexible position and we are seeking postdoctoral applicants with interests/expertise in any of the following areas: *speciation genomics, functional morphology, quantitative genetics, or craniofacial development*.

Ongoing potential projects in the lab include:

- 1) Estimate the genetic architectures of novel adaptive traits within Caribbean pupfishes using a combination of QTL mapping crosses, divergence mapping from whole genome resequencing, GWAS, allele-specific expression, and analyses of selective sweeps and introgression.
- 2) Measure the relationship between genotype, phenotype, and fitness across a complex fitness landscape estimated from the growth and survival of F2 hybrid pupfish placed in field enclosures on multiple Bahamian islands.
- 3) Functional and high-speed kinematic analyses of scale-eating performance in the wild and across a phenotypic continuum of laboratory hybrids.
- 4) Validation of candidate regulatory variants using in situ hybridization and CRISPR knockouts in the pupfish system.

The postdoc will have the option to participate in fieldwork in the Bahamas and/or Cameroon, but previous field experience is not necessary and participation is not required.

Required qualifications:

Ph.D. or equivalent degree in biology, evolution, genetics, bioinformatics, or related field. Publication of work based on dissertation. Programming experience in R or python. No pipetting experience necessary as this position is for downstream data analysis.

UC Berkeley has a world-class community of integrative biologists studying adaptive radiation spanning the Department of Integrative Biology, the Museum of Vertebrate Zoology, the Department of Environmental Science, Policy, and Management, the Department of Molecular and Cell Biology, the Center

for Theoretical Evolutionary Genomics, and more. UC Berkeley offers competitive salaries, excellent benefits, and is an equal opportunity employer. The City of Berkeley and the surrounding San Francisco Bay Area is known for its progressive values, vibrant social and cultural scene, and beautiful surrounding environment.

The University of California is an Equal Opportunity/Affirmative

Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age, or protected veteran status. Applicants from under-represented backgrounds are especially encouraged to apply.

Interested candidates should submit a cover letter detailing their interest in the position and relevant experience along with their CV, PDFs of two recent publications, and contact information for three references to Chris Martin at chmartin@unc.edu

This position is open until filled, but please apply within the next four weeks for full consideration. Please feel free to contact me at the above email address with any questions.

Christopher Martin

Assistant Curator of Ichthyology, Museum of Vertebrate Zoology

Assistant Professor, Department of Integrative Biology
University of California, Berkeley

<http://labs.bio.unc.edu/martin/> @fishspeciation

Christopher Martin <chmartin@unc.edu>

UdeChile 2 GenomicBiodiversity

I am pleased to inform you that we are now offering *two postdoctoral fellowships* in “Universidad de Chile”, on the biogeography of: (1) the microbiota in Antarctic and sub-Antarctic areas, and (2) marine fauna in the Southern Ocean.

These calls are made in the context of the PIA Conicyt Chilean project “Genomics insight into the past and present of Antarctic Biodiversity: a tool to assess the fate of a unique ecosystem in a changing world (GAB)”

.

Feel free to distribute this announcement widely.

Please, find as attached files the two different calls.

Complete application guidelines are available in: *<http://www.ciencias.uchile.cl/concurso%20academico.html>

Sincerely yours, Elie Poulin

Dr. Elie POULIN Laboratorio de Ecología Molecular (LEM) Instituto de Ecología y Biodiversidad (IEB) Departamento de Ciencias Ecológicas Facultad de Ciencias, Universidad de Chile Las Palmeras 3425 CP 7800003, Iquique, Santiago, Chile

*https://www.researchgate.net/profile/Elie_Poulin

<http://www.ieb-chile.cl/> Phone: (56)-2-29787298

E-mail: epoulin@uchile.cl

Elie Albert Poulin <epoulin@uchile.cl>

UEdinburgh HIVPhylogeneticEpidemiology

Postdoctoral Research position: Phylogenetic Epidemiology and Phylodynamics of HIV in Africa

The Institute of Evolutionary Biology at the University of Edinburgh seeks to appoint a Postdoctoral Researcher to work with Andrew Rambaut’s group, using virus genomic data to understand the phylodynamics, epidemiology, and molecular evolution of HIV in long-term patient cohorts and the generalised epidemic in Sub-Saharan Africa.

The successful applicant will be working closely with

project collaborators at Oxford, Johns Hopkins, UCL and the Africa Health Research Institute (AHRI), as part of the PANGAEA-HIV consortium studies. Funded by the Bill and Melinda Gates Foundation this project aims to improve our understanding of HIV epidemiology in order to design targeted HIV control strategies and to understand impact of HIV interventions. The consortium's goal is to analyse HIV-1 phylogenetic data, to identify the individual and population drivers, hubs, sources, sinks and dynamics of epidemic spread, and to translate that to information that is directly actionable in HIV prevention. The applicant will undertake analyses of over 15,000 HIV genomes and associated epidemiological data, developing state-of-the-art statistical models and tools to advance this goal.

Candidates will have a PhD in a relevant field (computational biology, computer science, mathematical biology or statistics), will have expertise in phylodynamics, molecular evolution or phylogenetic epidemiology of viruses, strong skills in computational biology, statistics or sequence data analysis and an interest in infectious disease research in a public health context. The candidates will have a track-record of publishing in peer-reviewed, academic journals and excellent communication skills.

The post is full-time until October 2021.

Please include a CV and supporting statement with details of how you meet the knowledge, skills and experience required.

See the following link for more details and application:

https://www.vacancies.ed.ac.uk/pls/corehrrecruit/-erq_jobspec_version_4.jobspec?p_id=044074 Informal enquiries to Prof. Andrew Rambaut (a.rambaut@ed.ac.uk).

Andrew Rambaut Institute for Evolutionary Biology Ashworth Laboratories, University of Edinburgh, Edinburgh, EH9 3FL, UK

contact V a.rambaut@ed.ac.uk | <http://tree.bio.ed.ac.uk> | tel +44 131 6508624

Andrew Rambaut <a.rambaut@ed.ac.uk>

UFlorida Butterfly Moth Phylogenomics

Postdoc, Kawahara Lab, University of Florida, Gainesville, FL USA.

A 2-year postdoc in phylogenomics is available on the evolution of butterflies and moths, as part of two funded National Science Foundation projects (NSF DEBNERC and NSF GoLife). The postdoc may also have the opportunity to work on collaborative bat-moth projects with Jesse Barber and his team at Boise State University.

The selected postdoc will work at the Florida Museum of Natural History, on the University of Florida main campus in Gainesville, FL, USA. The selected candidate will need to be able to communicate well in verbal and written English, have a strong understanding of phylogenetic methods, solid publication record, and have computational experience in phylogenomic and/or comparative methods. Candidates should also be interested in training students, writing grants and be motivated to use genomic high-throughput sequencing data. The selected candidate will join a team of postdocs, graduate students, undergraduates, and staff scientists in the Kawahara Lab. The postdoc will also work closely with local and international collaborators.

Required: 1) A Ph.D. in molecular evolution, systematics, evolution, bioinformatics, genomics, or related field. 2) Strong publication record. 3) Familiarity with analyzing next generation sequencing data, computer programming/scripting in Python, Perl, Java, C++, R or other language. Candidates with background experience in phylogenomics, biogeography, dating analyses will be highly considered.

Salary: \$47,500-\$50,000 USD plus benefits. The appointment can be up to 2 years, but will be made on a yearly basis given satisfactory progress.

Start date: Position available September 1, 2018 or until the position is filled.

How to apply: To ensure full consideration, please email the following to Akitō Kawahara at kawahara@flmnh.ufl.edu: (1) a cover letter, (2) your updated CV, and (3) 3 letters of support from 3 mentors/colleagues, sent directly to kawahara@flmnh.ufl.edu. The cover letter and updated CV should be merged into a single PDF. The cover letter should describe your previous research and training, your qualifications for the postdoc as detailed in this advertisement, and should explain how this postdoc position will further your long-term research/career aspirations. Specify in the email subject line: "Postdoc_KawaharaLab"

Evaluations of applicants will begin on Aug. 1, 2018, and continue until the position is filled.

About the University of Florida The University of Florida (UF) is one of the nation's leading research institutions with 35,000 undergraduates, 15,000 graduate students, and over 4,500 faculty and academic

staff. UF offers all resources of a top research university to study evolution, genomics, and systematics. The Florida Museum of Natural History (FLMNH) serves as the iDigBio HUB, and is now one of the primary centers for research in evolutionary biology and biodiversity.

The FLMNH is also closely tied to the UF High-Performance Computing Center (HPC) and HiPerGator2 (<https://www.rc.ufl.edu/>) allowing for the chosen postdoc to utilize this rich computational resource. UF also has a state-of-the-art genome sequencing facility at the Interdisciplinary Center for Biotechnology Research (ICBR), the Florida State Collection of Arthropods (FSCA), and collections of the McGuire Center for Lepidoptera and Biodiversity. The Kawahara Lab also has strong ties to UF's the Department of Biology, Department of Entomology and Nematology, School of Natural Resources and Environment, Department of Wildlife Ecology and Conservation, School of Forest Resources and Conservation, and Department of Microbiology and Cell Science.

For additional information about the lab, visit: <http://www.flmnh.ufl.edu/mcguire/kawahara/> Akito Y. Kawahara Associate Curator/Associate Professor Florida Museum of Natural History McGuire Center for Lepidoptera and Biodiversity University of Florida 3215 Hull Road Gainesville, FL 32611 USA 352.273.2018 kawahara@flmnh.ufl.edu

“kawahara@flmnh.ufl.edu” <kawahara@flmnh.ufl.edu>

UFlorida MNH Phyloreferencing

We are seeking a postdoctoral fellow to support the Phyloreferencing project < <http://phyloref.org/> > by developing and advocating driving biological research use cases, and to coordinate these with large research projects in comparative biodiversity. Our ideal candidate is a biologist by training with strong expertise in systematic biology, and a deep interest in research questions that benefit from enabling a phylogenetic (as opposed to a taxonomic) perspective for integrating biodiversity data at a level that depends on computation.

The Phyloreferencing project aims to create the data standards and computational resources to render phylogenetic clade definitions < <https://doi.org/10.2307/2992353> >, specifically their semantics, fully computable. A major part of our effort is to build an ontology of published and peer-reviewed phylogenetic clade definitions expressed in the Web Ontol-

ogy Language (OWL) < https://en.wikipedia.org/wiki/Web_Ontology_Language >, as well as the machine reasoning capabilities to resolve such definitions to clades in a given phylogenetic tree, including at the scale of the synthetic Open Tree of Life.

One role of the postdoc is to provide critical guidance and inform prioritization of software development efforts by developing, advocating, and ideally pursuing compelling research questions as use cases. As part of being compelling, such use cases should demonstrate how the phylogenetic view that phyloreferencing enables for linking data is different from traditional solutions to this problem (such as identifying clades manually, or using taxonomic checklists and synthetic taxonomy backbones).

The other major role of the postdoc is to serve as an ambassador of the project both to the comparative biodiversity research community at large, as well as in particular to select research projects (such as NSF GoLife < https://www.nsf.gov/funding/pgm_summ.jsp?pims_id=5129 >-funded projects, or the ARBOR < <http://arborworkflows.com/> > project) that could benefit from our technologies for integrating or communicating trait data with other biodiversity data resources at a large-scale. We expect that as a result at least some of our driving research use cases would be informed by or even actively coordinated with such projects, and the postdoc initiating and leading deeper collaborations would be welcome.

By rendering the semantics of phylogenetic clade definitions fully computable, phyloreferencing also enables computationally reproducing, disambiguating, and evaluating the effect of changing such clade definitions, features lacking in or made very difficult for taxonomic name-based approaches. Candidates with research ideas that take particular advantage of these features are equally encouraged to apply. More generally speaking, we are particularly interested in how you might incorporate phyloreferencing into your own research projects, current or future.

The Phyloreferencing project is a collaboration between Dr. Nico Cellinese (Florida Museum of Natural History, University of Florida) and Hilmar Lapp (Center for Genomic and Computational Biology, Duke University) funded by the National Science Foundation. The postdoc will be based in the lab of Dr. Cellinese, but will work closely with both PIs. Starting date is negotiable. Salary is \$50,000.

Qualifications:

* PhD in Biology or a related field. * Strong background in Systematic Biology required. You should be

well versed in all aspects of theoretical phylogenetics and related topics. * Programming experience in languages popular in scientific computing (e.g., Python, JavaScript) is useful (and thus preferred) but not required. * Similarly, prior exposure to or familiarity with ontologies and ontology languages (in particular, OWL) is useful but not required. * Excellent communication and writing skills, and ability to interact productively with other projects' PIs and personnel.

How to apply:

Please submit a letter of interest and CV, together with the names and contact information of three academic references, to Dr. Nico Cellinese (ncellinese@flmnh.ufl.edu). All other inquiries should also be directed to Dr. Cellinese. The position will remain open until filled.

The University of Florida is an Equal Opportunity Employer.

Nico Cellinese, Ph.D. Associate Curator, Botany & Informatics Joint Associate Professor, Department of Biology

University of Florida Florida Museum of Natural History
354 Dickinson Hall, 1659 Museum Rd. Gainesville, FL
32611-7800, U.S.A. Tel. 352-273-1979 Fax 352-846-1861

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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>

UGeorgia InsectVirusSymbiosisDevelopment

Postdoctoral position on insect-viral symbiosis

This NSF-funded position is for research on evolution, development, symbiosis and insects. Specifically, the lab has funding for work on developmental events that guide insect-microbe interactions using parasitoid wasps as a study system: wasps that lay eggs in other insects and consume them during development. Several lineages of wasps have acquired associations with beneficial symbiotic viruses that are specifically produced in wasp reproductive tracts and are injected into host insects. There, they play vital roles in preventing hosts from mounting effective defenses against the developing parasitoid. The production of virus in wasps is very

tightly timed and coincides with specific stages of wasp development. The lab is seeking an energetic postdoc with interests in some of these topics and a strong background in one or more of the following: developmental biology, evolutionary biology, genomics, or molecular genetics. The position is in the Entomology department at the University of Georgia and is available immediately but the start date is negotiable.

Gaelen Burke leads a friendly and interactive team of driven, creative, scientifically curious, and smart researchers. We are committed to diversity, to the career success of team members, and to a supportive and productive approach to research and mentoring. Check out our website, (<http://blog.caes.uga.edu/burkelab/>) for more information on our lab.

If you are interested in joining our group, please send an email to Gaelen Burke (grburke@uga.edu) with a single file including CV, statement of research interests, and the names, phone numbers, and email addresses of three references. Women and underrepresented minorities are particularly encouraged to apply. Applications will be reviewed by 1 July 2018 and will continue to be accepted until the position is filled.

Gaelen R Burke

@gaelenburke Assistant Professor The Department of Entomology 120 Cedar St 419 Biological Sciences Building The University of Georgia grburke@uga.edu

Gaelen R Burke <grburke@uga.edu>

UGothenburg AvianCarotenoidColoration

Postdoc: UGothenburg.AvianCarotenoidColoration

WANTED: A highly motivated and self-driven postdoc, with strong evolutionary and molecular genetics background, to join the ECCO (Evolution of Colour Communication) lab at the Dept. of Biological and Environmental Sciences, University of Gothenburg, Sweden. ECCO (P.I. Staffan Andersson) explores sexual selection, evolution and diversification of the spectacular breeding plumages of African weaverbirds (Ploceidae), in particular carotenoid coloration and elongated tails in the widowbirds and bishops (Euplectes spp.). In collaboration with researchers in UK, Norway and South Africa, the focal areas are at present; 1) Evolutionary genetics and physiology of carotenoid metabolism and pigmentation, and 2) Phylogenetic and comparative analyses

of coloration and sexual dichromatism in weaverbirds. Depending on background, talents and interests, the successful candidate may be involved in either of these interacting approaches, as applied to a suggested project on Coevolution of color signals and color vision, as well as to other ongoing or emerging projects. **QUALIFICATIONS:** PhD in biology, a genuine interest in the intersection of behavioral ecology and evolutionary genetics, ability to conceive and write research papers, extensive PhD or postdoc experiences of either or both molecular genetic labwork (spec. qRT-PCR) and computational biology (bioinformatics, statistics, comparative methods). A background in biochemistry (spec. HPLC and LC-MS) is valued, so also proficiency in one or more programming or scripting languages (spec. R, Python), and database management (spec. PostgreSQL). Other relevant qualifications include reflectance spectrometry, field ornithology (watching, handling, and sampling birds), and social and communicative skills. **POSITION:** The postdoc is funded by a tax-free 2-year scholarship from the Carl Tryggers Foundation, amounting to 23,000 SEK per month. Starting date: ASAP, but not later than 1 October, 2018 **APPLICATION:** Before the DEADLINE 30 JUNE, 2018, submit an e-mail to staffan.andersson@bioenv.gu.se with subject heading 'ECCO PDRA' followed by your last name, and attach a SINGLE PDF FILE including the following documents: i) A cover letter describing your research background and interests, suitability for the position, and which aspects of the ECCO research you are most interested in, ii) A detailed CV including a publication list and other achievements, iii) Contact details (letters welcome, but optional) of two or three reference persons who can be contacted by phone or e-mail. Prospective candidates will be invited for interviews in person or by Skype. For more information contact staffan.andersson@bioenv.gu.se. BioEnv, University of Gothenburg, Box 463, 40530 Goteborg, Sweden. +46-317863647 (office), +46-708-641959 (cell)

Staffan Andersson Professor, Animal Ecology Dept of Biological and Environmental Sciences, University of Gothenburg Email: staffan.andersson@bioenv.gu.se Skype: [euplectes](https://www.skype.com/en/people/euplectes) Phones: +46-317863647 (office), +46-708641959 (mobile) OrderID: 3130BANSTA (on all invoices!) Invoices: Box 115, 40530 GÅ-TEBORG Deliveries: Medicinaregatan 18, 413 90 GÅ-TEBORG Snail-mail: Box 463, 405 30 GÅ-TEBORG

Staffan Andersson <staffan.andersson@bioenv.gu.se>

UGuelph PDF PhD MacroInvertGenomics

Postdoc & PhD student positions, Hajibabaei lab, Centre for Biodiversity Genomics & Department of Integrative Biology, University of Guelph, Canada.

Ecological genomics of macroinvertebrates to assess watershed health across Canada

Postdoctoral fellow: A 3-year postdoc position is available as the main project coordinator and data analyst to conduct environmental DNA (bulk samples, water) analysis of macroinvertebrates in Canadian watersheds. The position involves design and coordination of sampling, genomics and bioinformatics analysis with emphasis on ecological/environmental analysis using Illumina MiSeq/NovaSeq data as well as data integration and visualization. A background in molecular ecology/evolution, familiarity with high throughput sequence analysis, ability to work at the command-line in a Linux environment, knowledge of a scripting language (ex. Python) and R is required. Experience with large-scale multi-investigator project/data management is an asset. Preferred starting date: October 2018.

PhD student: A PhD student position is available to conduct ecological genomics research (DNA metabarcoding, transcriptomics) on macroinvertebrate communities from Canadian watersheds. The position involves optimizing protocols (metabarcoding/transcriptomics, bioinformatics) to generate comparative data to study environmental responses of freshwater benthic taxa. An MSc in biological sciences (molecular evolution/ecology, genetics or related fields) is required but applicants with a BSc and an exceptional academic/research record will also be considered. Preferred starting date: January 2019

Guelph is located about one hour from Toronto. Because of its relatively low crime rates, clean environment and generally high standard of living, Guelph is consistently rated as one of Canada's best places to live.

The University of Guelph is committed to equity in its policies, practices, and programs, supports diversity in its teaching, learning and work environments, and ensures that applications for members of underrepresented groups are seriously considered under its employment equity policy. All qualified individuals who would contribute to the further diversification of our University

community are encouraged to apply.

Please send a copy of your CV, a cover letter and names/contact information for three references to: Mehrdad Hajibabaei (mhajibab@uoguelph.ca). Please indicate the title of the position you are applying for in the subject line of your email. We will start reviewing applications on July 15, 2018.

Mehrdad Hajibabaei <hajibabaei@gmail.com>

UHelsinki EvolutionaryEcol

The University of Helsinki has an international academic community of 40,000 students and staff members, and it offers comprehensive services to its employees, including occupational health care and health insurance, sports facilities, and opportunities for professional development. The International Staff Services office assists employees from abroad with their transition to work and life in Finland. The Organismal and Evolutionary Biology Research Programme is situated at the Viikki science park and belongs to the Faculty of Biological and Environmental Sciences of University of Helsinki.

The Organismal and Evolutionary Biology Research Programme (OEB) invites applications for a

1,5 YEAR POST DOCTORAL RESEARCHER POSITION in Evolutionary Ecology

in the research group of Marjo Saastamoinen (<http://www.helsinki.fi/life-history-evolution>), as part of the ERC funded META-STRESS project. The successful applicant will be part of the

Research Centre for Ecological Change at the University of Helsinki.

Our Life-History Evolution research group is a dynamic team with several post docs and PhD students and we are part of the OEB with its vibrant and collaborative research community of experimental, computational, and theoretical labs that all share a common interest in Evolutionary Biology. Cutting edge infrastructure is available at all levels, including high-performance computer clusters, a next-gen sequencing facility, as well as molecular labs. We collaborate with research groups at Cambridge University, Stockholm University, and UCL among others.

The project, initiated in 2015, aims to understand the mechanisms that allow organisms in the wild to cope with environmental stress. Working with the large

metapopulation of the Glanville fritillary butterfly gives a unique opportunity to study processes operating from genes within individuals all the way to metapopulation-level dynamics (> 20 years of data; e.g. Kahilainen et al. GCB). In this project ecological and experimental studies are integrated with molecular approaches to unravel the significance of different mechanisms - candidate genes, epigenetic inheritance and intestinal microbial communities - potentially influencing individual responses to environmental challenges.

In addition to exceptional demographic and ecological resources, substantial genomic data is also available for this species, including a whole genome sequence (Ahola et al. 2014 Nature Comm) and linkage map (Rastas et al. 2013 Bioinformatics) for which a new version is underway and ready to be utilized. Some available experimental and genomic data, including across land PoolSeq, RNA Seq and sequence data of mothers and their offspring exposed to different stressors, and SNP genotype data from 20,000 individuals genotyped for both known candidate genes and neutral loci across hundreds of populations (Fountain et al. 2016 PNAS, Fountain et al. 2018) is potentially available for the candidate. There is also an option to generate/collect new experimental and/or genomic data within the framework of the META-STRESS project.

The successful candidate should have PhD / postdoctoral experience within the fields of evolutionary biology, evolutionary genetics, microbiology or similar, and a strong interest in working with natural populations. Excellent written and verbal communication skills in English, and the ability to think independently and creatively are required. The candidate must demonstrate ability to work as part of a team, and participate in supervision of more junior group members.

The starting date is flexible but preferable no later than September 2018 (funding is available until end of March 2020), with a probationary period of six months. The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal work performance. Starting salary will be 3300 euros/month, depending on the appointee's qualifications and experience.

Please submit your application using the University of Helsinki Recruitment System via the link Apply for the position (<https://www.helsinki.fi/en/open-positions/postdoctoral-researcher-in-evolutionary-ecology>). Applicants who are employees of the University of Helsinki are requested to leave their application via the SAP HR portal. Please attach the following documents as

a single pdf file: your CV with publications included and a letter (max 2 pages) with a description of your research interests and, in particular, why you would be a suitable candidate for the project. The application letter should also contain possible starting dates and contact information of two persons who can provide a reference letter based on request.

— / —

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>

UInnsbruck Bioinformatics 2

Second announcement – application deadline 22 June 2018

MOLECULAR ECOLOGY, DEPARTMENT OF ECOLOGY, UNIVERSITY OF INNSBRUCK PostDoc position

We seek to hire a PostDoc with training in bioinformatics. This is a 31-months position at the Molecular Ecology group of the Department of Ecology, starting from 2 July 2018 ideally.

Centering on the Alpine Space, the group's mission is interdisciplinary research, embedded in international collaboration networks. A list of research topics can be found at: < http://www.uibk.ac.at/ecology/forschung/molecular_ecology.html.en >. The successful candidate will participate in resequencing individual transcriptomes and genomes of the ant *Tetramorium alpestre* to identify signatures of aggressiveness vs. nonaggressiveness.

Responsibilities 1. SNP calling in individual genomes using Illumina data and the reference genome 2. searching for genomic signatures by genome-wide association study and by searching for genomic footprints of selective sweeps 3. searching for signatures in individual transcriptomes using Illumina data and the annotated genome 4. editome analyses 5. provision of advice / training to other group members in analysing high-throughput sequencing data and participation in other bioinformatics tasks as need arises in the group 6. participation in manuscript writing 7. contact and collaboration with scientists and laboratory technicians at the Faculty of Biology in Innsbruck and internationally

Selection criteria A. PhD degree in bioinformatics or a related field B. published research experience in bioinformatics, preferentially in identifying genomic and transcriptomic signatures of phenotypic traits C. excellent skills in the maintenance of Linux systems for bioinformatic purposes D. proficiency in Python, R, scripting languages E. experience in the use of relevant software packages for genome and transcriptome analysis (e.g. Bowtie2, Trinity) and genealogy reconstruction (e.g. BEAST, RevBayes) F. ability to work as part of a multi-disciplinary team G. ability to work independently H. very good knowledge of English

Salary The annual gross salary is Euro 51,955.40 for a 40 h/week employment for 31 months. Extension to 37 months and corresponding reduction of the weekly working hours are possible and welcome. The contract includes health insurance and 5 weeks of holidays annually.

How to apply To apply, please submit by E-mail to <florian.m.steiner@uibk.ac.at>: a cover letter, systematic point-by-point replies as to your readiness for the responsibilities and how you meet the selection criteria, a brief statement of research interests, your curriculum vitae, and your complete list of publications. Also, arrange for at least one letter of recommendation to be sent to <florian.m.steiner@uibk.ac.at> Applications must be written in English. Review of applications will begin immediately and continue until 22 June 2018 the latest. The University of Innsbruck is striving to increase the percentage of female employees and therefore invites qualified women to apply. In the case of equivalent qualifications, women will be given preference. An offer of employment is contingent on a satisfactory pre-employment background check.

The research institution and its environment Detailed information about the Molecular Ecology group can be found at < https://www.uibk.ac.at/ecology/forschung/molecular_ecology.html.en >. The University of Innsbruck has a long-standing and internationally renowned tradition in life sciences and offers a vibrant research atmosphere. It has close to 30,000 students and 4,500 staff members. Innsbruck is situated in the Alps and very close to Switzerland, Germany, and Italy; scenery and outdoor recreation are fantastic.

More information needed? For more information, please contact: Florian M. Steiner <florian.m.steiner@uibk.ac.at>

Assoc.-Prof. Dr. Florian M. Steiner

Department of Ecology University of Innsbruck Technikerstr. 25 6020 Innsbruck, Austria Phone: +43 512 507-51752 Fax: +43 512 507-

51799 http://www.uibk.ac.at/ecology/forschung/-molecular_ecology.html.en “Steiner, Florian Michael” <Florian.M.Steiner@uibk.ac.at>

ULausanne FungalSymbionts

The following position in our group is being re-advertised due to the lack of a suitable applicant.

Postdoctoral position 'V Epigenetic versus Genetic and Variation in Fungal Symbionts and How it Affects Plant Growth (Uni. Lausanne, Switzerland)

Job Description: A position is available in the Sanders' group to study the role of epigenetic versus genetic variation in mycorrhizal fungi on plant growth. Our research indicates that variation in mycorrhizal fungi is associated with large differences in plant growth. We will study this in more detail to find out which aspects of genetic or epigenetic variation in these fungi causes high growth rates in plants (especially cassava).

It is intended that the results of this project will be combined with research in the field where our work is leading to real solutions to increase production of food in areas of the world where starvation is a major problem. More information about our work can be found at <http://people.unil.ch/iansanders/> The project is part of a wider collaboration between the University of Lausanne, Dr Marco Pagni at the Vital-IT center of the SIB Swiss Institute of Bioinformatics and Prof. Alia Rodriguez at the National University of Colombia.

Your skills and qualifications: Candidates must be highly motivated, have a PhD (or expect to have very soon), and have knowledge in one or more of the following fields: genetics; plant or fungal molecular biology; epigenetics; quantitative or population genetics. Sound knowledge of bioinformatics would be an advantage and an interest in solving problems in an analytical way. The successful candidate should also have good interpersonal skills and an ability to work well in a team.

Job information: The position is available as soon as possible and is initially for 1 year (100% contract), renewable for a maximum of 4 more years (depending on the number of years since your PhD). Preference will be given to someone who recently obtained a PhD. Most of the postdoc' s time will be dedicated to research, but a contribution to teaching is expected, including the possibility of supervising master students. Formally, the contract stipulates : 70% Personal research, 25%

Participation to teaching activities, 5% Maintenance of lab equipment or other institutional tasks

Applications: To apply you must upload a CV and motivation letter in English, including the names of 2-3 referees, to the University of Lausanne job portal at:

<https://bit.ly/2HP24on> Applications must be received not later than 19th July 2018. Informal enquiries may be made by email to ian.sanders@unil.ch. Previous applicants need not apply.

Ian Sanders <ian.sanders@unil.ch>

UM StLouis PlantSpeciation

Postdoctoral Researcher in Plant Molecular Phylogenetics

I am looking for a postdoctoral researcher to join my lab at the University of Missouri - St. Louis. The NSF-funded project involves constructing a species-level phylogeny for the Neotropical genus *Burmeistera* (Campanulaceae) using high-throughput sequencing approaches (targeting low-copy nuclear regions with enrichment probes and genome-skimming for plastomes). Results will be used to test the relative roles of pollinator-mediated, gametic, and postzygotic reproductive isolation in the diversification of *Burmeistera*. Candidates should have experience with plant molecular phylogenetics, including labwork and bioinformatics analysis of next-gen data, and an interest in plant speciation and/or pollination biology. Successful applicants will also be encouraged to carry out his or her own research projects related to work done in the Muchhala Lab (see www.umsl.edu/~muchhala). The start date for the position is flexible, from August of 2018 to January 2019. Funding is available for one year, with renewal for up to three years given satisfactory progress.

St. Louis is a vibrant Midwestern city that boasts an exceptional quality of life, combining a low cost of living with a variety of cultural attractions including parks, museums, and lively music and art scenes. The University of Missouri - St. Louis has strong local ties with the Missouri Botanical Garden, the Saint Louis Zoo, Washington University, St. Louis University, and the Donald Danforth Plant Science Center, and annual retreats (sleec.weebly.com) bring together ecologists and evolutionary biologists from these and other local institutions. The Department also houses the Whitney R. Harris World Ecology Center, established to promote

international research, particularly in tropical regions.

Review of applications will begin on July 20th. Informal inquiries are welcome: muchhalan@umsl.edu. Submission online at <http://www.umsl.jobs>: click 'Faculty' tab, 'Get Started' tab, then search '26783' (the Job ID #). Applicants must combine application materials, including 1) a short statement (one to two pages) on previous experience, research interest, and motivation for applying, and 2) a curriculum vitae, into a single PDF or Microsoft Word document and upload as a resume attachment. Additionally, have three recommendation letters sent to muchhalan@umsl.edu. For questions about how to apply, please call (314) 516-5258, or if you are experiencing technical problems, please email psrsupport@umsystem.edu.

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Nathan Muchhala, Ph.D. Assistant Professor Department of Biology University of Missouri -St Louis One University Blvd, R428 Research Hall St Louis, Missouri 63121 (314) 516-6672 <http://www.umsl.edu/~muchhalan/> "Muchhala, Nathan" <muchhalan@umsl.edu>

UMunich LichenPopulationGenomics

Postdoctoral position: "Population genomics and gene expression in lichens"

A three-year postdoctoral position is available in the laboratory of Dr. Silke Werth at the University of Munich.

The lab focuses on population genomics and gene expression. Our research topics currently include: 1) evolution of lichenized fungi 2) gene flow among populations of lichenized fungi 3) gene expression in lichenized fungi and their photobionts under thermal stress conditions.

The candidate will work in a DFG project on *Lobaria pulmonaria* lichens funded for three years. The candidate must be proficient in programming, preferably in Python, R and Shell. Additional essential skills are analytical skills with respect to population genetic analyses, physical ability to perform field work, and excellent manuscript writing skills. Candidates with familiarity with lichen biology or statistics analytical skills will rank higher. Applicants should have a doctorate in the field of bioinformatics, population genetics or compa-

table. The deadline for application is 15th July, 2018. The successful applicant is expected to start the appointment as soon as possible. For further information, contact Silke Werth, +49 89 2180 74754, email: werth@bio.lmu.de. To apply, the following papers are needed. Please send them in one pdf file to the following email address: Tanja.Ernst@lrz.uni-muenchen.de ——— A letter of motivation ——— Certificates attesting to education (PhD and MSc, or equivalent) ——— List of publications ——— CV ——— Contact information for 3 references

The salary for the position will be in accordance with the in-house rules for hiring post-doctoral fellows at LMU Department Biology I. The initial contract will be for one year, with the possibility of two extensions of one year.

Information on the research environment at University of Munich can be found here:— www.en.biologie.uni-muenchen.de More information on relocation to LMU can be found at the International Office homepage: www.en.uni-muenchen.de/about_lmu/contact/-int_office/index.html – Prof. Dr. Silke Werth University of Munich Systematic Botany and Mycology LMU Biozentrum Großhaderner Straße 2-4 82152 Planegg-Martinsried Germany Phone: +49 89 2180 74754 Silke Werth <werth@bio.lmu.de>

Werth <werth@biologie.uni-muenchen.de>

UNewHampshire TreeMicrobialDiversity

The Garnas lab (<http://mypages.unh.edu/garnaslab>) seeks a highly motivated postdoctoral scientist to study 1) patterns and consequences of microbial diversity in the beech bark disease (BBD) pathogen complex and associated bark communities; and 2) impacts of divergent life histories among the dominant BBD associates on pathogen gene flow and population structure across the range of the disease. Within this framework, the successful candidate will be encouraged to develop their own ideas to advance basic understanding of fungal evolution in the context of a complex, multi-organism decline disease.

Brief background Beech bark disease (BBD) is a widespread decline disease arising from complex interactions among a non-native scale insect and at least two putatively native pathogens that differ in key aspects

of their biology and ecology. Recent work also suggests that associated microbes may play a role in disease development and/or attenuation. In addition to being highly relevant ecologically (e.g., to wildlife and to forest stand development), the BBD system represents fertile ground for scientific inquiry, with many key questions that are currently unexplored.

Details of the position and skills sought The ideal candidate will have both experience and a proven publication record that demonstrates a keen interest and background in population genetics, microbiome sequencing and bioinformatics as well as facility with the core concepts of eco-evolutionary dynamics. The research is primarily lab and bioinformatics-based using comprehensive collections across the range of the disease. Fungal isolation and culture curation will also be required. Experience working with fungi is preferred but not required.

Start date negotiable but must be no later than October 1, with an earlier start date preferred. Salary is \$48,000 plus benefits. Funding is for one year with reappointment subject to satisfactory performance.

Interested applicants should send the following as a single pdf file to jeff.garnas@unh.edu: - CV - Statement of purpose that summarizes research goals/interests/trajectory and relevant experience - 2-5 relevant publications, with an annotated list of the applicant's role/contribution for each - Contact information for three references Application review will begin immediately; the position is open until filled.

"Garnas, Jeff" <Jeff.Garnas@unh.edu>

UNorthCarolina Charlotte PlantComparativeGenomics

Postdoctoral position in plant comparative genomics/transcriptomics at UNC Charlotte

A postdoctoral position is available in the newly established Cooper lab at University of North Carolina at Charlotte to study the genomic architecture of complex traits underlying divergent phenotypes in the crop species *Sorghum bicolor*. I am seeking a candidate with bioinformatics experience to analyze existing genomics and transcriptomics data sets, as well as generate new datasets related to understanding the genetics of both adaptive and agronomically important traits. The main goals of this research project are to: i) Explore the relationship between structural rearrangements in the

genome and changes in gene expression that may relate to phenotypic differences; ii) Look for networks of co-expressed genes and their upstream regulators; iii) Perform comparative genomics among multiple varieties and species to search for parallel mechanisms under selection.

This work will involve some greenhouse activities as well as some molecular lab work to collect and extract materials for sequencing, but it will predominantly focus on computational analyses. Prior experience with plants and/or with extraction techniques is desirable, but not required. The development of new research directions building on the broad themes of dissecting complex traits and improving methods for comparing and integrating -omics data sets is strongly encouraged. To see past projects and get an idea of the type of research I do, go to eacooper400.github.io.

My lab will be based at the North Carolina Research Campus (<https://transforming-science.com/>) just north of Charlotte, NC, which houses scientists from multiple North Carolina North Carolina universities and corporations to create a unique and exciting interdisciplinary environment with state-of-the-art genomics facilities, providing ample opportunity for interaction and collaboration.

A Ph.D. in Bioinformatics, Computational Biology, Quantitative Genetics, Population Genetics, Evolutionary biology or related discipline with prior experience analyzing genomics data is required. Candidates must have a strong foundation in R, python, perl, or another coding language, and experience using a computing cluster is highly desirable.

The funding for this position can support up to 3 years, with a preferred start date of September 2018, but this is negotiable.

To apply, please submit a cover letter and CV through the UNCC jobs website, at the following link: <https://jobs.uncc.edu/postings/22426> Contact Info:

Liz Cooper, Ph.D. Department of Bioinformatics and Genomics University of North Carolina at Charlotte
Email: lizcooper@uncc.edu

"eecooper4@clemson.edu" <eecooper4@clemson.edu>

UNorthCarolina Greensboro MicrobialEvolution

Postdoctoral position: *Speciation and Recombination in Bacteria*

A two-year postdoctoral position is available in the laboratory of Dr. Louis-Marie Bobay at the University of North Carolina Greensboro.

The lab focuses on microbial evolution and genomics. Our research topics currently include: 1) the evolution of recombination in bacteria and archaea 2) the processes of speciation in microbial populations and 3) the evolution of gene diversity in prokaryotes. To find out more details about our research, you can visit: <https://louismariebobay.wixsite.com/bobaylab> The lab is primarily computational. The candidate must be proficient in programming, preferably in Python. The ideal candidate would have experience in bioinformatics, evolution, microbiology, and metagenomics.

To apply, email Louis-Marie Bobay at ljbobay@uncg.edu. Please include a CV, a short research statement and the name and email address of at least two referees.

To find out more information about Greensboro, North Carolina you can visit: <https://realestate.usnews.com/-places/north-carolina/greensboro> Louis-Marie Bobay

– Louis-Marie Bobay, PhD Assistant Professor Department of Biology - EBER 102-117 Univ. of North Carolina at Greensboro Greensboro, NC 27403 USA Website: <https://louismariebobay.wixsite.com/bobaylab> Louis-Marie Bobay <ljbobay@uncg.edu>

UPotsdam AdaptiveGenomics

The University of Potsdam, Faculty of Science, Institute of Biochemistry and Biology, Research Unit of Evolutionary Adaptive Genomics is seeking to fill the following position possibly by 01.10.2018:

Academic Staff Member

Postdoctoral position in the Evolutionary Adaptive Genomics group

The Institute for Biochemistry and Biology at the University of Potsdam is seeking to fill a position for a post-doctoral researcher (TV-L E13) in the research group of Prof. Hofreiter. We are seeking a highly motivated candidate with a strong background in Evolutionary Biology, preferably in research areas such as evolutionary genetics, evolutionary genomics or evolutionary bioinformatics. Organismal zoologists with motivation to extend their skill set towards genomic analyses are also welcome to apply. Candidates need to have a PhD in biology, bioinformatics, biochemistry or molecular biology. They should have an excellent publication record and ideally experience with grant acquisition and teaching. The successful candidate is expected to apply for grants in Germany or abroad. The position comes with a teaching requirement of 11h per week during the semester and the candidate is expected to supervise undergraduate (mandatory modules) as well as graduate students. Teaching of bachelor students has to be performed in German. Consequently, good command of German in both written and spoken form is required. Teaching includes courses in zoology and molecular biology and will be organized in a way that leaves time for research.

The successful candidate will work in an active, interdisciplinary and stimulating environment and will have access to state-of-the-art equipment and techniques in genetic and genomic research, including a group owned Illumina Nextseq500 sequencing system and a 10xGenomics Chromium system. The group is part of the University Research Center “Functional Ecology and Evolution” and is collaborating with a number of international research groups. For more information visit our webpage (<http://www.uni-potsdam.de/-ibb-genomics/index.html>) or contact Prof. Hofreiter (michael.hofreiter@uni-potsdam.de).

The contract should start 1st October 2018. The position will initially be restricted to 2 years. Extension for a further 3 years is possible.

Applications including a motivation letter and research plan (no more than 2 pages), CV (no more than 3 pages), list of publications, teaching experience, copies of degree certificates, and names of two referees should be submitted by 15th July 2018 as a single pdf-file to michael.hofreiter@uni-potsdam.de.

Michi Hofreiter <michi@palaeo.eu>

UppsalaU FungalPhyloinformatics

I am hiring a post doc to work on evolutionary processes shaping the diversity of fungi with focus on ectomycorrhizal fungi. The add is available at <http://www.uu.se/en/about-uu/join-us/details/?positionId=210086> and there is a link at the bottom of this page to submit your application.

Martin Ryberg Systematic Biology Uppsala University Uppsala

Martin Ryberg <martin.ryberg@ebc.uu.se>

UppsalaU HostAdaptationBacteria

POSTDOCTORAL FELLOW IN EVOLUTIONARY MICROBIOLOGY, BIOINFORMATICS We are recruiting a postdoctoral fellow to Lionel Guy's research group at Uppsala University.

PROJECT Our group is studying the evolution of host-adaptation in bacteria. We are currently focusing on the Legionellales order, which contains representatives at several stages of host adaptation. We are gathering a number of novel genomes through extended sampling, metagenomics and data mining. The goal of this project is to extend the current dataset, analyze it, to shed light on the evolution of Legionellales in particular, and on the evolutionary transitions in host adaptation in general.

FORM One-year post-doctoral fellowship (SEK 288 000, circa USD 34 000, per annum); extension for a second year available. Candidates who are employees of Uppsala University, or have been in the two years before the start of the fellowship, are not eligible.

Starting date: to be discussed.

BASIC SKILLS AND QUALIFICATIONS - A PhD in evolutionary biology, molecular evolution, microbiology or related topic. - Experience with high-throughput sequencing data, metagenomics, comparative genomics, and molecular evolution tools. - A documented experience of team work and collaborative projects.

DESIRED QUALIFICATIONS - Programming experi-

ence.

APPLICATION To be sent by email to lionel.guy@imbim.uu.se, latest on June 30th, 2018. Applications (in one single document) should include: - Letter of motivation - Resume - Publication list - Names and contact information of two references or two letters of reference.

HOST INSTITUTION The group is located at the Department of Medical Biochemistry Microbiology, Uppsala University. The host department is a very strong and stimulating research environment, counting over 250 researchers in over 30 groups, and is conducting world-leading research in antibiotic resistance.

Uppsala University is a comprehensive research-intensive university with a strong international standing. Our mission is to pursue top-quality research and education and to interact constructively with society. Our most important assets are all the individuals whose curiosity and dedication make Uppsala University one of Sweden's most exciting workplaces. Uppsala University has 40,000 students, 7,000 employees and a turnover of SEK 6.5 billion.

CONTACT Lionel Guy, M: lionel.guy@imbim.uu.se, P: +46 18 471 42 46, W: <http://www.imbim.uu.se/research-groups/infections-and-defences/guy-lionel/>

Lionel Guy, PhD, Assistant Professor Department for Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden phone: +46 18 471 4246; postal address: Box 582, SE-751 23 Uppsala lionel.guy@imbim.uu.se

Lionel Guy <guy.lionel@gmail.com>

URegina FishAdaptation

Postdoc: Molecular physiology of adaptation to thermal stress in fish

A two-year, MITACS and NSERC CRD-funded, post-doctoral position to study transcriptomic responses to embryonic and early life history thermal stress in fish is available in Dr. R. Manzon's Lab at the University of Regina. The ideal candidate will have a strong background in bioinformatics and transcriptomics and/or fish physiology and developing an understanding of how cellular responses lead to changes at the whole organism or population levels.

The successful applicant will help develop an indepen-

dent research program examining the short- and long-term effects of thermal pollution on embryonic and early life history stages of Lake Whitefish using modern transcriptomic and genomics tools. Within this framework there will be ample opportunity to develop novel and independent research avenues. This position is part of a large project involving four Principal Investigators at three different institutions (Dr. C. Somers, U. Regina; Dr. J. Wilson, McMaster; Dr. D. Boreham, NSOM), several postdoctoral fellows and many graduate and undergraduate students who meet annually and work very closely with each other and our industrial partner, Bruce Power.

The Manzon research group is a dynamic, productive and very close knit group that works as a team on a variety of different research projects and are generous with their time to help others in the group. Maintaining this environment is a key priority, thus the successful candidate will be a hard-working team player who appreciates the value of helping others in the group and is willing to accept help when required. There will be opportunities for both formal and informal mentorship opportunities of graduate and undergraduate students and as such it is expected that the successful candidate will take on a leadership role in the group. Information on the Manzon group can be found at: <https://www.uregina.ca/science/biology/people/faculty-research/manzon-richard/index.html> or <https://www.facebook.com/SaskFishPhysResearch/> Applications including a cover letter, CV, names and contact details of 3 academic references and unofficial transcripts should be sent to Dr. Richard Manzon at richard.manzon@uregina.ca. The ideal start date will be late fall of 2018, but is negotiable. Review of applications will begin August 1st, 2018 and continue until the position is filled.

Richard G. Manzon, Ph.D.

Professor

Department of Biology

University of Regina

3737 Wascana Parkway

Regina SK S4S 0A2

Ph: 306-337-2417

Fax: 306-337-2410

Richard Manzon <richard.manzon@uregina.ca>

USDA BatonRouge HoneybeeBioinformatics

Biologist (Computational Bioinformatics) USDA-ARS, Honey Bee Breeding, Genetics and Physiology Research Unit, Baton Rouge, LA

Summary: The incumbent will be assigned to the USDA-ARS Honey Bee Breeding, Genetics and Physiology Research Unit in Baton Rouge, LA. The incumbent will conduct bioinformatics analyses related to whole genome sequencing, transcriptomics and molecular marker development and verification in honey bees. The overarching goal of this work is to increase our understanding of the variation across different stocks of honey bees to better inform decisions for marker development as a selection tool for breeding programs. As such, the incumbent will be able to address broader questions and explore new hypotheses including identifying stock-related genomic signatures, examining differential selection pressure across stocks, and determining genetic underpinnings of traits of interest. Additional projects will likely be explored stemming from other ongoing projects, including RNAseq of susceptible or resistant bees, or other research avenues to be explored by the incumbent.

Requirements/Qualifications: - U.S. Citizens and Permanent Residents seeking U.S. Citizenship. - A Ph.D. is required that was obtained within the last four years - Knowledge and skills in conducting genome-wide association studies, RADseq, RNAseq is highly desirable. - Proficiency in R statistical software and experience writing scripts for analysis of genomic data is highly desirable.

Salary

\$61,218 to \$79,586 per year

Open & closing dates

6/04/2018 to 12/31/2018 (or until the position is filled)

The following information is required of all applicants:

-- Announcement number, title, and grade(s) of the position

-- Full name, mailing address (including zip code) and day and evening phone numbers (with area code)

-- A one-page abstract of Ph.D. dissertation

-- A resume of any honors or awards received; mem-

berships in professional or honor societies; invitations to make presentations at scientific/technical meetings; scientific society office and committee assignments; presentations (other than invitations); and publications.

.. A list of names, addresses, and phone numbers of persons familiar with your stature, contributions, and recognition.

.. Indicate country of citizenship

..Copy of DD Form 214, Certificate of Release or Discharge from Active Duty (Only if claiming veterans preference. Visit the following web site for additional information: <http://www.opm.gov/employ/veterans/html/vetguide.asp>)

..SF-15 (Application for 10-point Veterans Preference) plus the supporting documentation required by this form (if claiming 10-point veteran's preference). Visit <http://www.opm.gov/forms/html/sf.aspto> obtain the form.

Applications may be mailed, faxed, or e-mailed to the appropriate address and/or facsimile number listed below:

Mail: USDA-ARS-HBBGPRU Attn: Michael Simone-Finstrom, Ph.D. 1157 Ben Hur Road Baton Rouge, LA 70820

E-mail: Michael.simonefinstrom@ars.usda.gov

Phone: 225-767-9293; Fax: 225-766-9212

Refer to full job posting at: <https://www.usajobs.gov/GetJob/PrintPreview/501355400> - - - Michael Simone-Finstrom Research Molecular Biologist USDA-ARS Honey Bee Breeding, Genetics, and Physiology Research < http://www.ars.usda.gov/main/site_main.htm?modecode=60-50-05-00 > 1157 Ben Hur Rd Baton Rouge, LA, 70820

Phone: (225) 767-9293

“SimoneFinstrom, Michael - ARS”
<Michael.SimoneFinstrom@ARS.USDA.GOV>

UStrasbourg SquirrelEvolution

2-year Postdoctoral Fellow position in Animal Physiology and Behavioural Ecology with Dr Vincent A Viblanc and Dr F Stephen Dobson at the University of Strasbourg, Institut Pluridisciplinaire Hubert Curien, France.

Social networking in the Columbian ground squirrel: a bio-logging approach linking animal behavior to individual health and ageing

Ageing is likely influenced by social biology in group-living organisms. However, the mechanisms of interaction between social stressors and stress-related health issues are poorly studied, and the impact of social stress on organismal fitness is virtually unknown. Our research will integrate the links among social stressors, physiological stress indicators, and individual fitness in a colony of ground squirrels observed since 1992. Columbian ground squirrels (*Urocitellus columbianus*) are semi-social sciurid rodents that inhabit sub-alpine meadows of the Rocky Mountains of Canada and the northern US. They have a matrilineal social system where related individuals overlap both spatially (kin clusters) and over generations. Our current research indicates that individual fitness benefits are acquired by co-breeding with neighbours that are close kin. However the consequences of social heterogeneity on individual physiology and health are unknown.

In this project we will explore the effects that the social environment has on adult phenotype, using a bio-logging approach to measure individual social contacts both above and below ground. We will use an innovative approach, via large scale deployment of >80 novel contact collars coupled with 3D-accelerometers and magnetometers to establish continuous networks of social interactions throughout the breeding season, and connect individual social attributes to their underlying physiology (glucocorticoid stress hormones, oxidative stress markers, immunity markers and telomere dynamics). More information on the MamTag project can be found here.

Research will be based at the Institut Pluridisciplinaire Hubert Curien (Strasbourg, France, website), and field-work will be carried out in the Sheep River Provincial Park (Alberta, Canada, website). The applicant should have a keen interest in working with free-living mammals in outdoor conditions.

The post-doctoral fellow will be responsible for implementing the first stage of the MamTag project. This will include (1) standardization and pre-analysing accelerometer, magnetometer and contact data collected in 2018 (Dec 2018-Mar 2019), (2) deploying loggers and collecting data (including physiological samples) in the field (Apr-Jul 2019), (3) analysing logger signals and developing programming routines to establish social contact networks and animal behaviour (Aug-Mar 2020). The post-doctoral fellow will also assist with the supervision of a PhD student associated with the project, whose research will focus on the social determinants of fitness. The second year of the project will be used to analyse physiological samples at the IPHC and the Centre for the Neurobiology of Stress, University of Toronto, and publish the results.

For this post-doctoral project we are seeking someone who works well in a team environment; who is mobile, creative, highly motivated; and who has a keen interest in integrating animal physiology, behavioural and evolutionary ecology. Our ideal candidate will have a proven record of working on complex signal analyses (accelerometer, compass and environmental data) and developing specific toolboxes for signal analyses (strong expertise in signal processing with Matlab/R/Python). Previous experience working in the field (long hours outdoors, animal handling) and in the lab (ELISA, RIA) is preferred but not essential; the willingness to learn such techniques is, however, required. The candidate should have excellent written and oral communication skills in English and an excellent publication record.

The successful applicant will be mainly based in the Department of Ecology, Physiology & Ethology (DEPE) at the University of Strasbourg, France, under the joint supervision of Dr Vincent A Viblanc and Dr F Stephen Dobson. The DEPE is a lively Department where the post-doctoral fellow will benefit from interaction with a thriving community of postgraduate students, postdocs and researchers in animal physiology, marine biology and behavioral ecology. Furthermore, the applicant will integrate with an international team, and will thus benefit from the interaction and support of research partners, including Rudy Boonstra (University of Toronto), Dominique Filippi (Sextant Technology, New Zealand), and François Criscuolo (IPHC CNRS). The applicant will participate in University of Strasbourg Institute for Advanced Studies (website) actions such as seminars and related activities.

Strasbourg is one of Europe's most attractive cities, being 1h45 by train from Paris, 1h by plane from Amsterdam and Scandinavia, and at

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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>

UtahStateU EvolutionCommunity

Hello,

I'm looking for a post-doc with experience in community ecology or evolutionary biology, who is interested in analysing the co-occurrences and associations of many taxonomic groups using NEON data. The position is fully-funded, and includes money to travel to conferences and working groups.

A copy of the funded proposal that outlines the project and instructions for application are available online (<http://pearselab.com/join-the-lab/>). I'm happy to answer any questions over email (will.pearse@usu.edu).

Thanks,

Will Pearse

—
Assistant Professor of Biology, Utah State University Office: +1-435-797-0831; Room BNR-139 Skype: will.pearse

“will.pearse@usu.edu” <will.pearse@usu.edu>

UTexas Austin EvolutionaryBiology

In connection with a new research collaboration and award, the research groups of Howard Ochman and Mark Kirkpatrick (Department of Integrative Biology, UT Austin) are seeking two postdoctoral research associates with experience in evolutionary biology, phylogenetics, population genetics, bioinformatics, and/or genomics.

The general theme of this research is to resolve the underlying structure of bacterial species and to elucidate to the process of bacterial speciation using a variety of approaches. Projects may be strictly computational (and involve the development of phylogenetic methods and theory) or experimental (including genetic, genome and microbiome analysis).

The start date is flexible, preferably within calendar year 2018, although later dates can be accommodated. Salary is \$49,000 to \$52,000 per year depending on experience, plus a full benefits package is included. Initial appointments would be for 1 year, with potential to extend to 2 or 3 years. UT Austin offers a very stimulating research environment with outstanding facilities and infrastructure. Austin is a vibrant city with many options for recreation and cultural activities.

If interested, please send a resume and a brief statement of research interests and career goals to Kim Hammond: kim.hammond@utexas.edu. Please include the names and contact information for three references familiar with your scientific work. Queries about the project can also be directed to either H. Ochman (howard.ochman@austin.utexas.edu) or M. Kirkpatrick (kirkp@austin.utexas.edu).

howard.ochman@austin.utexas.edu

UToronto 4 Evolutionary Biol

The Department of Ecology and Evolutionary Biology at the University of Toronto invites applications for four different Postdoctoral Fellowships for 2018-2019: Banting, Liber Ero, EEB, FAS.

Area of Research: Ecology and/or Evolution, broadly defined.

Description of duties: The Fellow will collaborate with the advisor(s) on research that is mutually agreed upon by all parties and the Fellow will publish the results in scientific journals.— The Fellow will be a fully participating member in the Department.

Application Instructions: All individuals interested in any of these positions must first contact and obtain the agreement of a—faculty advisor (or co-advisors). For some of these fellowships, only full-time faculty members at the St. George (downtown) campus of the University of Toronto are eligible to serve as advisors. For the Banting Postdoctoral Fellowship competition, the first deadline is July 5, 2018.

See this website for details on deadlines, criteria, etc. for each of the four different postdoctoral fellowship competitions (details will be added to the website when they become):

http://www.eeb.utoronto.ca/about-us/employment/-postdocs/Overview_Postdoctoral_Positions.htm For

Closing date, Salary, Expected start date, Term, Required qualifications: See details on the website listed above.

FTE (full time equivalent):— 100%

The University of Toronto is a leading academic institution in Canada with over 60 faculty members specializing in ecology and evolution.

Strong links exist between the Department of Ecology and Evolutionary Biology and the Royal Ontario Museum, the Centre for Global Change, and the School of the Environment. The University owns a nearby field station dedicated to ecological and evolutionary research (the Koffler Scientific Reserve, www.ksr.utoronto.ca). The department also has a partnership with the Ontario Ministry of Natural Resources that helps provide access to infrastructure, including lab facilities in Algonquin Provincial Park (www.harkness.ca), funding, and long-term data sets. Genomic analyses are supported by a number of high-performance computing resources, multi-lab bioinformaticians, as well as staff at the Centre for the Analysis of Genome Evolution and Function.

The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from racialized persons / persons of colour, women, Indigenous / Aboriginal People of North America, persons with disabilities, LGBTQ persons, and others who may contribute to the further diversification of ideas.

Asher D. Cutter Professor and Associate Chair Undergraduate Department of Ecology and Evolutionary Biology University of Toronto 25 Willcocks St. Toronto, ON, M5S 3B2

tel: 416-978-4602 email: asher.cutter@utoronto.ca
<http://labs.eeb.utoronto.ca/cutter> Asher Cutter
 <asher.cutter@utoronto.ca>

UTurku Microbial Evolution

Dear All,

I have an open postdoc position for 3 year, starting September 1st 2018. Aim of the project is to investigate eco-evolutionary dynamics in multispecies microbial (bacteria + protist) communities and how antibiotic resistance evolves in the presence of species interactions. Person who I am looking for must have a PhD degree from a relevant field and experience in working with microbes in laboratory setting, preferably a background

in experimental evolution or microbial ecology.

Keywords: evo-evolutionary dynamics, experimental evolution, community dynamics, AMR, microbiology / microbial ecology.

Deadline for the applications is end of June. Detail how to apply: (job ID 5916) <http://www.utu.fi/en/-university/come-work-with-us/open-vacancies/Pages/-home.aspx> Best regards,

Teppo Hiltunen Associate Professor University of Turku Finland

“Hiltunen, Teppo” <teppo.hiltunen@helsinki.fi>

Vanderbilt Univ EvolutionBiologicalClocks

Postdoctoral Position: Evolution of Circadian Rhythms in Bacteria

Vanderbilt University, Nashville, USA: Laboratory of Dr. Carl Hirschie Johnson

The Position: Dr. Johnson is seeking a highly motivated postdoctoral fellow to study the evolution of circadian (daily) clocks in bacteria by experimental and bioinformatics methods, including the use of an innovative experimental evolution approach.

Background: The field of circadian clocks received the Nobel Prize in Physiology or Medicine in 2017 for its progress towards understanding the mechanism of circadian oscillators. While these biological clocks display conserved properties from bacteria (especially cyanobacteria) to fungi, plants, insects, and vertebrates (including humans, of course), practically nothing is known about their evolution or about the selective pressure(s) that led to the evolution of these fascinating biological timekeepers. The laboratory of Dr. Johnson led the discoveries of circadian clocks in bacteria, in particular major contributions to the mechanism of the circadian system in cyanobacteria. Moreover, Dr. Johnson's laboratory is the major (and practically the only) laboratory that has provided experimental support for the fitness advantage of circadian clocks (see PMID: PMC21132; PMID:15324665; and PMID: PMC3633149).

The Project: Inspired by studies from other laboratories of bacterial experimental evolution to relatively simple selective pressures, the Johnson Laboratory has undertaken an experimental evolution approach using *E. coli* (that does not exhibit circadian phenomena) under a

variety of rhythmic environmental regimes to evolve clock-like behavior. This experimental evolution has been conducted for eight years by the technician in the laboratory, and is now exhibiting interesting phenotypes that need a conscientious and motivated postdoctoral fellow to characterize and analyze. The methodology will include genetic/bioinformatic methods (genome sequencing, analysis of adaptive mutations, RNAseq, etc.), physiological/imaging methods (to most fully characterize phenotypes using luminescent and/or fluorescent reporters), proteomic methods (analyzing gene expression patterns), and metabolomic methods (temporal changes in metabolism in response to rhythmic environments).

In addition to the experimental evolution project, the candidate will also be involved in analyses of the adaptive significance and mechanism of biological timekeeping in purple bacteria and cyanobacteria (see PMID: PMC4794148). For an overall introduction to these research questions, see our review in Nature Reviews in Microbiology (PMCID: PMC5696799).

The Candidate: The ideal candidate has strong motivation and should ideally be driven by a passion for evolutionary biology. Expertise in genetic technology with bacteria and bioinformatics is a plus. The position requires the ability to independently take responsibility for the project, as well as strong teamwork & communication skills, problem-solving abilities, reliability, and effective time management.

Research environment and location: There are excellent facilities and collaborations available within the Vanderbilt University system, including other laboratories that study circadian clocks (e.g., the labs of Doug McMahan, Terry Page, and Beth Malow) and evolutionary biology in microbes (e.g., the labs of Antonis Rokas, Seth Bordestein, and Ann Tate). Nashville is an exciting city with a low cost of living and many artistic opportunities (especially music) as well as close proximity to nature.

For more information about the Johnson Laboratory, see our website: <http://www.cas.vanderbilt.edu/-johnsonlab/> Interested applicants should contact Dr. Carl Johnson at: carl.h.johnson@vanderbilt.edu. Please send a CV, your research interests, and a list of at least three referees.

Selected relevant publications from the Johnson Laboratory:

Ishiura, M., S. Kutsuna, S. Aoki, H. Iwasaki, C. R. Andersson, A. Tanabe, S. S. Golden, C. H. Johnson, and T. Kondo. 1998. Expression of a gene cluster *kaiABC* as a circadian feedback process in cyanobacteria. *Science* 281: 1519-1523.

Ouyang, Y., C.R. Andersson, T. Kondo, S.S. Golden, and C.H. Johnson. 1998. Resonating circadian clocks enhance fitness in cyanobacteria. *Proc. Natl. Acad. Sci. USA* 95: 8660-8664.

Woelfle, M.A., Y. Ouyang, K. Phanvijhitsiri, and C.H. Johnson. 2004. The adaptive value of circadian clocks: An experimental assessment in cyanobacteria. *Current Biology* 14: 1481-1486.

Mori, T., D.R. Williams, M.O. Byrne, X. Qin, H.S. Mchaourab, M. Egli, P.L. Stewart, and C.H. Johnson. 2007. Elucidating the Ticking of an in vitro Circadian Clockwork. *PLoS Biology* 5: e93. PMID: PMC1831719

Johnson, C.H., M. Egli, P.L. Stewart. 2008. Structural Insights into a Circadian Oscillator. *Science* 322: 697-701. PMID: PMC2588432

Johnson, C.H., P.L. Stewart, and M. Egli. 2011. The Cyanobacterial

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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>

WashingtonU AmoebaBacterialSymbiosis

Postdoctoral position on amoeba - bacteria symbiosis available immediately

This position is for research on the farming symbiosis between the social amoeba *Dictyostelium discoideum* and certain Burkholderia bacteria. Specifically, we have funding for work on the existence and effect of partner choice, the effect of symbiont kin selection and kin recognition on the symbiosis, finding genes underlying the symbiosis in both partners, the molecular evolution of

these genes, the theory and measurement of mutualistic selection, and co-evolutionary specialization at the level of species and clone between an existing NSF grant, a newly funded one, and other resources. We are seeking an energetic postdoc with interests in some of these topics and a strong background in one or more of the following: evolutionary biology, social behavior, mutualism, microbial evolution, genomics, molecular genetics, and coevolution theory. The position is in the biology department at Washington University in St. Louis and is available immediately but the start date is negotiable.

David Queller and Joan Strassmann lead a friendly and interactive team of highly motivated, creative, and smart investigators. They are committed to diversity, to the career success of their team members, and to a collaborative and productive approach to research and mentoring. Check out our website, (<http://strassmannandquellerlab.wordpress.com/>) for more information on our lab, or Strassmann's blog (<http://sociobiology.wordpress.com>).

If you are interested in joining our group, please send an email to Joan Strassmann (strassmann@wustl.edu) with a single file including CV, statement of research interests, and the names, phone numbers, and email addresses of three references. Please specify which of the research areas appeal to you. Women and underrepresented minorities are particularly encouraged to apply. We will begin reviewing applications by 15 June 2018 and will continue to accept them until the position is filled.

Joan Strassmann

Joan E. Strassmann Charles Rebstock Professor of Biology Department of Biology Washington University in St. Louis One Brookings Drive Campus Box 1137 St. Louis MO 63130 phone: (314) 935-3527 fax: (314) 935-4432 cell: (832) 978-5961 skype: strassm e-mail strassmann@wustl.edu <http://strassmannandquellerlab.wordpress.com/> Blogs: <http://sociobiology.wordpress.com/> <http://slowbirding.wordpress.com/> <http://goodbyehouston.wordpress.com/> Twitter: @JoanStrassmann

Joan Strassmann <joan.strassmann@gmail.com>

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Barcelona AnatomicalNetworkAnalysis Oct22-26

Dear colleagues,

This course might be of interest for some people in this list: ANATOMICAL NETWORK ANALYSIS (ANNA), October 22nd-26th, 2018.

Place: Capellades, Barcelona (Spain).

Instructors: Diego Rasskin-Gutman (Cavanilles Institute of Biodiversity and Evolutionary Biology, Spain) and Borja Esteve-Altava (The Royal Veterinary College, UK).

Course overview

Anatomical Network Analysis (AnNA) is a framework for quantitatively characterizing the topological organization of anatomical systems using tools from Network Theory. AnNA is emerging as a new tool to identify developmental constraints, measuring morphological complexity and modularity, building morphospaces, and modelling the growth of anatomical structures.

This course is entitled to teach the main concepts of AnNA. Students will learn the basics of network analysis applied to morphological and anatomical systems: gathering information, building network models, analysing them, and interpret the outcomes of their analysis. This course combines theoretical introductions and practical

exercises using the free and open-source software R and RStudio.

Participants are encouraged to bring their own data for practising and for the supervised project session; anatomical networks will be provided by the instructors if needed.

This course is addressed to PhD students, postdocs and senior researchers.

More information and registrations: <https://www.transmittingscience.org/courses/systems-biology/-anatomical-network-analysis-anna/> With best regards

Sole

Soledad De Esteban-Trivigno, PhD. Scientific Director Transmitting Science <http://www.transmittingscience.org/> Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.org>

Barcelona NGS Jul2-6

SECOND CIRCULAR: postgraduate course "INTRODUCTION TO NEXT-GENERATION SEQUENCING: APPLICATIONS IN ECOLOGY AND EVOLUTION" in Barcelona (Spain) from 2nd to 6th July

Dear all,

here you can find information about the postgraduate course "INTRODUCTION TO NEXT-GENERATION

SEQUENCING: APPLICATIONS IN ECOLOGY AND EVOLUTION" (3 ECTS credits) which will take place in the Faculty of Biology (Universitat de Barcelona), Barcelona, from 2nd to 6th July. The Institut Botànic de Barcelona (CSIC), the Universidad Rey Juan Carlos and the IRBio-Universitat de Barcelona participate in the course organisation, with the support of the Fundación General CSIC and the EVOLTREE network.

The course is aimed at graduates, postgraduates and PhD students on Evolutionary Biology and related sciences, interested in knowing the new tools and the potential that is being developed with the new techniques of massive parallel sequencing. No specific training in bioinformatics is necessary although basic knowledge is desirable.

The main objective of this course is to show a battery of potential applications of the NGS by researchers who are currently working with this technological approach. As an introductory course, the main purpose is not looking for a complex or deep training in a specific technique, but to give a broad view of the available approaches.

The assistant to this course should end with the feeling of knowing the techniques and their applications, with the purpose of being able to assess which ones may be interesting for their research or on which to deepen in later stages.

The specific objectives are:

1. To present an updated information on the different NGS techniques and their applications, potential and complexity.
2. To provide basic training in the main software for each of the techniques, as well as in data processing, and give tips on how to expand knowledge. This includes from the quality analysis, edition and analysis of the files to the interpretation of results. We aim that, with this basic knowledge, the student can be trained later if he is interested in a specific aspect of the ones addressed (for example, attending specialized courses or self-taught).
3. To favour the contact between students interested in specific techniques with teachers and specialized personnel, for possible collaborations or training.

Please visit our website to have more information about the course content: <http://www.ibb.csic.es/en/formacio/col%C2%B7laboracions-en-docencia/curs-postgraduat/>

Online enrolment: <https://www.ub.edu/acad/-npost/fitxes/3/201711079.php> Enrolment deadline: 25/06/2018

FEW POSITIONS STILL AVAILABLE!

*Sonia Garcia * Institut Botànic de Barcelona (CSIC) Passeig del Migdia s/n | 08038 Barcelona | Tel. (0034) 932 890 611 | Fax (0034) 932 890 614 soniagarcia@ibb.csic.es | sphaeromeria@gmail.com skype: sonia.garcia31

Sonia Garcia <sphaeromeria@gmail.com>

Berlin Comparative Genomics Oct1-5

Course: Comparative Genomics

When: 1st - 5th October 2018

Where: Botanischer Garten und Botanisches Museum Berlin, Freie Universität Berlin, Königin-Luise-Straße 6-8, Berlin (Germany)

Instructors:

Dr Fritz J. Sedlazeck (<https://fritzsedlazeck.github.io/>)

Prof. Dr. Ingo Ebersberger (<https://scholar.google.com/citations?user=LOOY3kYAAAAJ&hl=en>)

Course overview

This course will introduce biologists and bioinformaticians into the field of comparative genomics. Different techniques will be introduced to identify single nucleotide polymorphism (SNP) and structural variations (SVs) as well as the annotation of these variations and the assessment for their functional impact.

Course format

The course is structured in modules over five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group.

TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at researchers interested in learning how to compare genomes and what can be learned from genomic similarities as well as variations. It will include information useful for both beginners and more advanced users. We will start by introducing general concepts of comparative genomics. On this basis, we

will then continue to describe all major analysis steps from the raw sequencing data via the identification of variations to an assessment of their impact on the phenotype.

Attendees should have a background in biology. There will be a mix of lectures and hands-on practical exercises using command line Linux. We will therefore dedicate one session to introduce basic and advanced Linux concepts for processing data on Amazon cloud (AWS). Attendees should have also some familiarity with genomic data such as that arising from NGS sequencing experiments.

LEARNING OUTCOMES

Identification of SNPs and SVs using de novo genome assembly and read mapping strategies

Assessment of strengths and weaknesses of the different DNA sequencing technologies, Illumina, Pacific Bioscience, Oxford Nanopore, for the detection of variations

Strengths and pitfalls of de novo assembly and mapping approaches for comparative genomics

Hands on experience of state of the art methods to compare multiple genomes

Annotation of variations and comparative genomics analysis

PROGRAM

Monday: Run your own de novo assembly

Lecture 1

General introduction File formats: FastQ, SAM, BAM Introduction in de novo assembly strategies, best practices and quality control

Lab 1

Setting up the computers/AWS instances Reads QC + trimming De novo assembly Computing General assembly statistics

Tuesday: Run a multi sample SVs comparison

Lecture 2

What are SVs and why are they important? Mapping of short and long reads Visualization SV calling

Lab 2

How to choose the appropriate short read mapper? Calling of SVs using de-novo and mapping based approaches Comparison of de novo based and mapping based results SV Visualization and quality control

Wednesday: Towards annotating the observed variations

Lecture 3

Gene prediction RNA-Seq mapping Repeat annotation Gene order analysis

Lab 3

QC and mapping of RNA seq data Annotate genome Visualize read mapping

Thursday: Identifying genes affected by SVs

Lecture 4

Gene order and their role in regulating gene expression The concept of shared synteny and regulation blocks Evolution of the gene set: Loss, duplication, fissions and fusion of genes

Lab 4

Annotation of variants Identification of orthologs/homologs across species

Friday: Predicting the functional consequences of genomic variations

Lecture 5

Assessment of gene function (e.g. GO analysis) Functional changes due to loss, SVs, cis-regulation Impact in pathways (e.g. KEGG)

Lab 5:

GO annotation and analysis Running your own pathway analysis

Lecture 6:

- Summary and discussion

For more information about the course, please visit our website: (<https://www.physalia-courses.org/courses-workshops/course33/>)

Here is the full list of our courses and Workshops: (<https://www.physalia-courses.org/courses-workshops/>)

"info@physalia-courses.org"

<info@physalia-

courses.org>

Berlin GWAS Oct22-26

GENOME-WIDE SIGNATURES OF SELECTION AND ASSOCIATION STUDIES

Berlin, 22nd-26th October 2018

General Topic: Genome-wide analysis of selection signatures and genotype-phenotype associations

INSTRUCTORS:

Dr. Pablo Orozco-terWengel (Cardiff University, Wales (UK))

<https://scholar.google.co.uk/citations?user=urqxLJgAAAAAJ&hl=en> Dr. Filippo Biscarini (CNR, ITA)

https://www.researchgate.net/profile/Filippo_Biscarini Overview

This course will introduce students, researchers and professionals into the field of using genomics data to identify meaningful genomic regions. The course comprises two approaches: one based only on genomic information, which will use populations genetics techniques to detect signatures of selection (both natural and artificial); the other approach will combine genomic and phenotypic data to identify genetic associations for specific phenotypes (i.e. GWAS, genome-wide association studies).

Format

The course is structured in modules over five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group.

TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at advanced students, researchers and professionals interested in learning how to make use of genomic information to study how selection has shaped the genome and how the genome influences measurable phenotypes. It will include information useful for both beginners and more advanced users. We will start by introducing general concepts of population genetics, which will take up most of the first half of the course; the second half of the course will be centered mainly on GWAS and related aspects.

Attendees should have a background in biology, specifically genetics. There will be a mix of lectures and hands-on practical exercises using R and the Linux command line, and bespoke software. Some basic understanding of R programming and the Linux environment will be advantageous. Attendees should have also some familiarity with genomic data such as those arising from NGS experiments, including genotyping-by-sequencing (GBS), and commercial genotyping platforms.

Please visit our website to have more information about the course content: <https://www.physalia-courses.org/courses-workshops/course36/curriculum-36/>

Here is the full list of our courses and Workshops: <https://www.physalia-courses.org/courses-workshops/>
Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR
info@physalia-courses.org <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 15771084054 <https://groups.google.com/forum/#!forum/physalia-courses> "info@physalia-courses.org" <info@physalia-courses.org>

Berlin LandscapeGenomics 26-30 November

Course: LANDSCAPE GENOMICS

Berlin, 26-30 November 2018

Botanischer Garten und Botanisches Museum
Berlin/Freie Universitat Berlin Konigin-Luise-Str. 6-8

<https://www.physalia-courses.org/courses-workshops/course17/> INSTRUCTORS:

Dr. Stephane Joost (Lab of Geographic Information Systems (LASIG), EPFL, Lausanne, Switzerland)

Oliver Selmoni, MSc (Lab of Geographic Information Systems (LASIG), EPFL, Lausanne, Switzerland)

Course overview

The course will provide an overview of the type of dataset that can be used for a landscape genomics analysis. Firstly, students will learn how to obtain environmental data from publicly available databases, how to process it with Geographic Information Systems (GIS) and how to use the latter to produce indicators able to describe the characteristics of the landscape. Next, the course will discuss the different approaches to obtain genetic data and subsequently show how to study genetic variation and population structure across space in the R environment. Students will be given an overview of the different statistical approaches to study local adaptation, and will be trained in using two of them, Sambada and LFMM. The course will also cover the critical task of the interpretation and validation of the results. Finally, the course will consider the crucial aspects and good habits to account for when planning a landscape genomics experiment (e.g. sampling design).

Targeted Audience & Assumed Background

This course is aimed at all biologists, ecologists, geneticists, veterinarians that want to implement the landscape genomics approach in their own studies of evolutionary biology and conservation. Even though the course is not intended for a specialized audience, basic knowledge in evolutionary biology and population genetics would help. Students will learn how to use GIS, but basic computer skills are desirable (e.g. in the R environment). A basic understanding of statistics is also necessary.

Teaching Format

The course is organized in ten learning sessions. During the first two sessions, the course will provide a contextualization of the research field. Then, students will be guided through a landscape genomics experiment with sessions that couple brief theoretical introductions with practical work.

Please visit our website to have more information about the course content: <https://www.physalia-courses.org/courses-workshops/course17/> Here is the full list of our courses and Workshops: <https://www.physalia-courses.org/courses-workshops/>
Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR
info@physalia-courses.org <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 15771084054 <https://groups.google.com/forum/#!forum/physalia-courses> "info@physalia-courses.org" <info@physalia-courses.org>

Berlin PythonDataVisualization Oct15-19

Course: Data Manipulation and Visualization with Python

Berlin, 15th-19th October 2018

(<https://www.physalia-courses.org/courses-workshops/course38/>)

INSTRUCTOR:

DR. Martin Jones (founder, Python for biologists: (<https://www.physalia-courses.org/instructors/t1/>))

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 lead 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.

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.

Assumed Background

This workshop is aimed at researchers and technical workers with a background in biology and a basic knowledge of Python (if you've taken the Introductory Python course then you have the Python knowledge; if you're not sure whether you know enough Python to benefit from this course then just drop us an email).

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.

Please visit our website to have more information about the course content: (<https://www.physalia-courses.org/courses-workshops/course38/>)

Here is the full list of our courses and Workshops: (<https://www.physalia-courses.org/courses-workshops/>)

Carlo Pecoraro, Ph.D

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Berlin QGIS Jul2-4

Dear all,

we still have some places available for our course “Introduction to QGIS” which will be held in Berlin this July (2-4 July 2018).

Our instructor is Matteo Ghetta, Co-Founder of QGIS Italia. Matteo is working for the company Faunalia that operates since more than 10 years in the field of Geographic Information Systems (GIS) basing on free and open source software.

In this course, you will learn how to install and use QGIS, access and present the data, style the data and produce high quality layouts with high informative content.

Please visit our website for more information about the course: (<https://www.physalia-courses.org/courses-workshops/course35/>)

Many thanks, Carlo

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Berlin RADseq Jul2-6 Last2spots

Dear all,

we have the last 2 spots left for our course on RAD-seq data analysis with Dr. Julian Catchen and Dr. Josie Paris.

We will run the course in the beautiful botanical museum (<https://www.bgbm.org/>) in Berlin from the 2nd to the 6th of July.

The registration deadline is this Friday. For more information about the course, please visit our website:

<https://www.physalia-courses.org/courses-workshops/course16/> Best regards,

Carlo

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Berlin RADseq Jul2-6 LastCall

Dear all, last weeks to apply for our RAD-seq data analysis Workshop based on Stacks 2.0 this July (2nd-6th) in Berlin, with Dr. Julian Catchen (University of Illinois, Urbana-Champaign; (<http://catchenlab.life.illinois.edu/>)) and Dr. Josie Paris (University of Sussex, UK).

We have the last 4 places left and attendees are seated on a first-come, first-served basis.

In this course, we will introduce the different approaches for obtaining reduced representation genome sequencing data and will specially focus on the data analysis. We will cover all necessary steps to obtain genome variants from short read data that are informative for population genetics, phylogenetic and association studies.

This course is aimed at researchers and technical workers who are generating and/or analyzing reduced representation genome sequencing data (RAD-seq, ddRAD, 2bRAD, GBS, \$B!D(B). Examples demonstrated in this course will involve primarily non-model organisms and examples of applications of this data type for different purposes will be covered. Attendees should have a background in biology. We will dedicate one session to some basic and advanced Linux concepts. Attendees should have also some familiarity with genomic data such as that arising from NGS sequencers.

Please visit our website to have more information about the course content: (<https://www.physalia-courses.org/courses-workshops/course16/>)

Here is the full list of our courses and Workshops: (<https://www.physalia-courses.org/courses-workshops/>)

Best regards,

Carlo

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Crete
EvolutionGeometricMorphometrics
Sep10-14

Dear colleagues,

Early bird registration has been extended for the course “STUDYING EVOLUTION WITH GEOMETRIC MORPHOMETRICS - 3rd edition”

Instructor: Dr. Chris Klingenberg (Manchester University, UK)

Place: Heraklion, Crete (Greece)

Dates: September 10th - 14th

PROGRAM:

Monday, September 10th, 2018. —Review of some fundamental methods, introduction to MorphoJ. * Size and shape, Procrustes fit, visualization of shape changes. * Principal component analysis. * Distinguishing groups: Canonical variates and discriminant analysis.

Tuesday, September 11th, 2018. —A closer look at some properties of morphometric data. * Measurement error and outliers. * Symmetry and asymmetry. * Regression: Allometry and size correction.

Wednesday, September 12th, 2018. —Morphological integration and modularity. * Partial least squares. * Inferring developmental integration from fluctuating asymmetry.

Thursday, September 13th, 2018. —Phylogeny and comparative methods. * Mapping shape data onto phylogenies. * Comparative methods. * Advanced topics: Analyses across levels, evolutionary size correction.

Friday, September 14th, 2018. —Special topics and combined analyses. * Complex symmetries. * Comparing covariance matrices (matrix correlation, ordination

methods, etc.). * Putting things together: Multi-level analyses.

Morning sessions will be used for lectures and demonstrations of analyses (participants will conduct their own analyses with software and data provided to them).

Afternoon sessions will be devoted to work in small groups. The first four afternoons will be used for analysis of the participants’ data as small group projects. During the last afternoon, participants will give informal presentations of the group work. There would be an evaluation at the end of the course, based on the group work presentations.

More information and registrations: <http://bit.ly/transmitting-science-sctudying-evolution-with-gm> Best wishes

Sole

Soledad De Esteban-Trivigno,PhD. Scientific —Director Transmitting Science (<http://www.transmittingscience.org/>)

soledad.esteban@transmittingscience.org

Lisbon
MicrobialEcoEvolutionaryDynamics
Oct22-24

ABSTRACT DEADLINE EXTENSION!

We have extended the deadline for oral and poster abstract submission. The oral abstract submission deadline for the IGC Symposium 2018 MICROBIAL ECO-EVOLUTIONARY DYNAMICS is now Friday, June 29th at 11:59PM, and poster abstract submission deadline is Friday, August 31st, or until reaching carrying capacity.

For more information and to apply, please visit <http://microbial.eco-evo.science/>

If you have any questions, please contact The Organizing Committee at <http://microbial.eco-evo.science/> or [eco-evo\(AT\)mailbox.org](mailto:eco-evo(AT)mailbox.org).

Hermina Ghenu <hermina.ghenu@gmail.com>

MDIBL Maine Environmental Genomics Jul13-21

Subject: The Summer Workshop on Population-Scale Genomic Studies of Environmental Stress (EnGen 2018), July 13 - July 21, with scholarships still available

REGISTER SOON; scholarships and places are now very limited

Next-Generation Summer Course in Environmental Genomics at the Mount Desert Island Biological Laboratory

A technical course that provides participants with the skills needed to generate and analyze modern sequence data (DNA, RNA) through a hands-on approach that utilizes novel data to guide research into how environmental conditions affect gene responses and the fitness of organisms while accounting for population structure.

Date: July 13 - July 21, 2018. Number of participants: Restricted to 25. Only \$300 registration fee!

We are pleased to announce that this course is supported by the National Institutes of Health through the Big Data To Knowledge (BD2K) Program. Therefore, scholarships are available for US citizens or permanent residents, including room and board.

<https://mdibl.org/course/environmental-genomics-2018/> < <https://mdibl.org/course/environmental-genomics/> >

Please contact Joe Shaw (joeshaw@indiana.edu) and John Colbourne (J.K.Colbourne@bham.ac.uk) if you are a non-US citizen or permanent resident wanting to participate.

The faculty at MDI Biological Lab is pleased to again offer a training course in Environmental Genomics, aiming to better understand technologies and approaches used to discover how gene function is influenced by environmental conditions while accounting for variation that exists within and among natural populations. This course is built on the paradigm that the research field will most effectively grow by properly designing large-scale experiments enabled by drastically increased sample-throughput and lower sequencing costs. Most importantly, the bioinformatics challenges of manipulating and analyzing population-level genomics data must be addressed.â€œâ€œ

This course is designed to train the next-generation of

environmental scientists, which have included in past years: university professors, postdoctoral researchers, doctoral students and government scientists, representing institutions from North America and Europe. Most responded in the departure survey that the course curriculum, choice of technologies, and effectiveness provided sufficient training to either begin or enlarge an environmental genomics project in their own laboratories. All reported that they would recommend this course to a colleague.

This course trains researchers to design studies, and to collect and analyze RNA-Seq gene expression data. *Daphnia* is used for training because of its growing use as a model system for environmental genomics and for improving environmental health protection, yet the skills learned during the course will be applicable to all study systems with maturing genomics resources, including humans. Much time is devoted to guiding the current and future projects of attendees.

Ultimately, participants will be better positioned to incorporate these technologies into their own research laboratories, while better understanding how functional genomics and automation can be applied to ecology, evolution and environmental toxicology.â€œ

Mount Desert Island Biological Laboratory Old Bar Harbor Rd., Salisbury Cove, ME 04672 MDIBL - <http://www.mdibl.org> < <http://www.mdibl.org/> >

John Colbourne <J.K.Colbourne@bham.ac.uk> John Colbourne <J.K.Colbourne@bham.ac.uk>

Online UManchester Morphometrics Nov5-Dec14

Dear colleagues

I am pleased to announce this year's morphometrics course from the University of Manchester. This year's course will run in the six weeks from 5 November to 14 December 2018.

Course content: * Data acquisition: the kinds of data and the equipment used to collect them. * Definitions of size and shape * Geometric methods to characterise shape from a configuration of landmark points (Procrustes superimposition) * Statistics of variation, scatter plots, basic multivariate statistics * Principal component analysis * Measurement error and outliers * Shape transformations and 'warping' – the thin plate spline * Analysis of outline shapes * Distinguishing

between groups (taxonomy, clinical diagnosis, etc.) * Allometry and size correction * Influence of external factors on shape (ecomorphology, dose- response studies) * Symmetric forms and measurement of asymmetry. * Morphometric inferences on developmental processes * Morphological integration and modularity * Genetics of shape: analyses of resemblance between relatives, QTL analyses. * Phylogeny: examining the history of evolutionary changes of shape

Practice examples: As far as possible, practical exercises are provided to accompany the course content. These practice exercises consist of data sets and explanations on how to run the respective analyses using the MorphoJ software (http://www.flywings.org.uk/-MorphoJ_page.htm). Participants who already have their own data are encouraged to use those and to discuss them as part of the course. I hope there will be a bit of a 'workshop' feel to the course unit.

Group work: Participants will work in small groups to prepare web presentations of possible morphometric studies (wikis prepared by the groups). This activity stimulates discussion and provides a broad overview of the broad range of questions that can be addressed with morphometric methods.

Further information on the course and a link to the registration page can be found on the following website: <http://www.flywings.org.uk/MorphoCourse> Registration uses the university's e-store, which can process automatic *payments by credit card or debit card*. The deadline for registration via this site is the *29 October 2018*.

The direct link to the e-store is this: <https://estore.manchester.ac.uk/short-courses/-faculty-of-biology-medicine-and-health/school-of-biological-sciences/analysis-of-organismal-form/analysis-of-organismal-form?token=4b10ca6c5fa0d1b5273920a4b103520e> The fee for the course is GBP 360.00.

If you cannot pay by credit or debit card, or *if you require a formal invoice* (e.g. for reimbursement by your institution), you need to contact the Short Course Office in our faculty via this E-mail: ShortCourses-biosciences@manchester.ac.uk If you need to use this option, please do so as soon as possible, but definitely *well before October*.

Best wishes, Chris

—

Christian Peter Klingenberg School of Biological Sciences The University of Manchester Michael Smith Building Oxford Road Manchester M13 9PT United

Kingdom

Telephone: +44 161 275 3899 E-mail: cpk@manchester.ac.uk Web: <http://www.flywings.org.uk> Skype: chris_klingenberg

"cpk@manchester.ac.uk" <cpk@manchester.ac.uk>
"cpk@manchester.ac.uk" <cpk@manchester.ac.uk>

QuebecCity eDNAMetabarcoding Nov19-23

Workshop: eDNA Metbarcoding

When: 19-23 November 2018

Where: Institut de Biologie Integrative et des Systemes (IBIS), Laval University, Quebec City (Quebec), Canada

Instructors:

Dr. Vasco Elbrecht (University of Guelph, Canada)

Eric Normandeau (Laval University, Canada)

Website: <https://www.physalia-courses.org/courses-workshops/course40/> Course Overview

Obtaining environmental DNA (eDNA) from water, soil, air, gut content or other sample types holds great promises for biodiversity research and assessment. Targeted species specific markers, and broader, more inclusive metabarcoding approaches using universal primer sets can detect invasive and rare rare species, or the range of taxa present in ecosystems from trace amounts of DNA. eDNA can capture sample diversity using non-invasive or minimally invasive methods/techniques. However, due to the low quantity of DNA present in samples, these approaches often require specialized laboratory protocols, careful sample handling to prevent contamination, as well as specialized bioinformatic processing due to high levels of noise and the presence of non-target taxa.

After completing the workshop, students should be in a position to (1) understand the potential and capabilities of eDNA barcoding and metabarcoding, (2) run complete analyses of eDNA metabarcoding pipelines and obtain diversity inventories and ecologically interpretable data from raw next-generation sequence data and (3) design their own eDNA projects, including bioinformatic data analysis and planning of laboratory work. All course materials (including copies of presentations, practical exercises, data files, and example scripts prepared by the instructing team) will be provided electronically

to participants.

While this course will focus on eDNA metabarcoding, however targeted single species detection and other alternatives will also be explored, as they can sometimes be suitable metabarcoding alternatives.

Targeted audience & ASSUMED BACKGROUND

This workshop is mainly aimed at researchers and technical workers with a background in ecology, biodiversity or community biology who want to use molecular tools for biodiversity research, and researchers in other areas of bioinformatics who want to learn ecological applications for biodiversity-assessment. In general, it is suitable for every researcher who wants to join the growing eDNA community. This workshop will review mostly techniques and software useful for eukaryotic single species detection and eDNA metabarcoding. Other workshops focused on procedures currently used in bulk sample and microbial metabarcoding will be available from Physalia-courses. A survey will be provided 2 weeks ahead of the workshop, where participants can mention topics or aspects they are particularly interested in.

No programming or scripting experience is necessary, but some previous expertise using the Linux console and/or R will be most welcome. All examples will be run either in Linux or Mac environments. Please make sure to have linux installed if you bring a Windows based laptop. Among the software and tools we will be using is R or Rstudio (+ the JAMP & PrimerMiner package), FastQC, Usearch, Vsearch, Cutadapt, and mBRAVE.net. No prior knowledge of these software packages is required.

TEACHING FORMAT

The workshop is delivered over 5 days (see the detailed curriculum below). The lectures are interactive with active discussion where asking questions is strongly encouraged. A key aspect of this course are practical sessions in primer development, bioinformatic analysis of high throughput sequence data, and data visualization as well as a project planning exercise to apply what you learned in this course.

Session content: <https://www.physalia-courses.org/-courses-workshops/course39/curriculum39/>

Here is the full list of our courses and Workshops: <https://www.physalia-courses.org/courses-workshops/>
Should you have any questions, please do not hesitate to contact us: info@physalia-courses.org

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR

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QuebecCity PopulationGenomics Nov12-16

Workshop: Population Genomics

When: 12-16 November 2018

Where: Institut de Biologie Integrative et des Systemes (IBIS), Laval University, Quebec City (Quebec), Canada

Instructors:

Dr. Martin Taylor (University of East Anglia, UK)

Dr. Lewis Spurgin (University of East Anglia, UK)

Eric Normandeau (Laval University, Quebec City, Canada)

Website: <https://www.physalia-courses.org/courses-workshops/course39/> Course Overview

Next generation sequencing has revolutionized evolutionary biology allowing unprecedented resolution and insight into evolutionary questions that appeared intractable only a few years ago. The course will cover the basics of population genomic analysis from SNP data onwards and will cover the key analyses that may be required to successfully analyze a population genetic data set. The course will NOT cover steps prior to generation of a .vcf file or SNP data set such as NGS data demultiplexing, clustering and SNP calling (This is covered in detail in the Introduction to RADseq course). This course will introduce Linux and the command line environment, basic perl and python usage, file conversions and manipulation, population structure and differentiation in R, outlier analysis, landscape / seascape genomics and introgression. Having completed the course, students should have a good understanding of the software and methods available for population genomic analysis and be competent in population genomic analysis.

Targeted audience & ASSUMED BACKGROUND

This workshop is aimed at postgraduate students and early career researchers who are interested in using population genomic tools in their research. No previous experience of bioinformatics is required, but an under-

pinning in evolutionary biology and basic population genetics concepts such as Hardy Weinberg Equilibrium and F[ST] are desirable. The course will use a range of software including the Linux operating system and R.

TEACHING FORMAT

The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of a combination of lectures and practical exercises, with breaks at the organisers' discretion. There will also be time for students to discuss their own problems and data.

Session content: <https://www.physalia-courses.org/courses-workshops/course9/curriculumpg/>

Here is the full list of our courses and Workshops: <https://www.physalia-courses.org/courses-workshops/>
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Smithsonian ConservationGenomics Oct10-19

Reminder for: Bioinformatics Analysis for Conservation Genomics

October 10-19, 2018

Smithsonian-Mason School of Conservation, Front Royal, VA, USA

<https://smconservation.gmu.edu/programs/-graduate-and-professional/professional-training-courses/conservation-genomics/>

This new course is designed to provide attendees at any career stage with a theoretical understanding of the methods used in conservation genomics along with the practical skills necessary to design and carry out the analysis component of a conservation genomics study. While introduction to the theoretical aspects of each of the analytical steps will be given, the emphasis of the course will be on hands-on training, enabling the participants to complete the analysis steps behind a conservation genomics study. Thus, the course will follow the format of short lectures introducing each analytical step, followed by hands-on activities during which students will complete the corresponding analysis.

The course will begin with an overview of conservation genomics, comparison of different next generation sequencing platforms, and the analytical factors to consider when beginning a conservation genomics study. The rest of the course will focus on the bioinformatics analysis behind a conservation study including: genome assembly (trimming, assembly techniques, quality assessment), genome annotation, mapping low coverage genome data to a reference genome, SNP calling, demographic analysis, and estimation of genome-wide diversity. These steps will all be accomplished with real data used in a recent conservation genomics study and performed on the Smithsonian High Performance Computing Cluster (SI/HPC). By the end of the course, attendees will have acquired the necessary background and applied knowledge to implement genomic analyses for the conservation of endangered species.

The Smithsonian-Mason School of Conservation is a partnership between George Mason University and the Smithsonian Conservation Biology Institute (SCBI). All courses are intensive residential programs hosted in a sustainably-built Academic Center on the grounds of SCBI in Front Royal, Virginia, USA. All courses offer continuing education credits (CEUs) and some can be taken for graduate credit. Limited scholarships are available for eligible applicants. See our upcoming offerings below and check out our website (<http://SMConservation.gmu.edu>) for more course details and pricing.

Rebecca Dikow (dikowr@si.edu)

"Dikow, Rebecca" <DikowR@si.edu>

Switzerland AncientDNA Aug29-Sep1

Ancient DNA: A Time-machine to Study Evolution

While the sequencing of DNA extracted from fossils has been attempted since 1983, several technological revolutions such as rigorous lab practices and the availability of next-generation sequencing now make it possible to obtain high-quality ancient DNA data for many organisms. This opens up an unprecedented opportunity to include data from multiple time points when studying evolutionary processes such as past demographic events or the action of selection.

In this workshop we will explore the range of evolutionary questions that will benefit from ancient DNA,

and discuss important considerations in designing and executing research projects using ancient DNA, as well as best practices in analyzing ancient DNA data. While the ancient DNA field had arguably its largest impact on the study of human evolution, we want to focus on its broader implications: how can ancient DNA help to disentangle the effect of selection and demography? How should modern population genomic analyses be tailored to be applicable to ancient DNA? What are appropriate samples sizes for ancient DNA to make a real contribution? And the ultimate question for participants: would the inclusion of ancient DNA data make a difference in answering my evolutionary research questions?

Confirmed Speakers

- Dr. Aida Andres, UCL Genetics Institute, London, UK - Prof. Joachim Burger, Johannes Gutenberg University Mainz, Germany - Prof. Greger Larson, School of Archeology, University of Oxford, UK - Prof. Ludovic Orlando, Center for GeoGenetics, University of Copenhagen, Denmark - Dr. Maanasa Raghavan, Department of Zoology, University of Cambridge, UK - Prof. Montgomery Slatkin, University of California, Berkeley

Location

We will be on the Gemmi Pass, a remote alpine location in Switzerland on 2350m asl.

Costs

The costs for full board (three nights) is CHF 600 per person. But we offer 10 stipends of CHF 300.

Registration / more Information

See <https://www.cuso.ch/activity/?p=1128&uid=4093>
Daniel Wegmann <daniel.wegmann@unifr.ch>

Turkey ComputationalEcolEvolution Sep16-22

Hi,

The summer school is a joint venture of the evolutionary biology and ecology societies of Greece and Turkey. This will be the first summer school of its name and we are hopeful to turn it into an annual event. Hosting will alternate between Greece and Turkey and the first school will take place in Urla-Izmir 16 - 22 September 2018. All relevant information regarding the school can be found on our webpage (<https://->

aegeancompecoevo.wixsite.com/home).

If any further information is needed please do not hesitate to contact me.

Yours Sincerely İsmail SaĖlam

İsmail K. SaĖlam, PhD Assoc. Prof. Hacettepe University, Faculty of Science, Department of Biology Ecological Sciences Research Laboratories Beytepe, 06800, Ankara, Turkey Tel: + 90 312 780 5034 Fax: +90 312 299 2028 www.iksaglam.com ismail saglam <iksaglam@gmail.com>

Udine NGSDataAnalysis Jul25-27

The Institute of Applied Genomics, together with IGA technology services and the University of Udine is organizing an introductory course on NGS data analysis: "Data crunching: from hell to heaven" in Udine, Italy, 25-27 July 2018. For further info visit the website: <https://appliedgenomics.org/it/-dissemination/training-1/> Fabio Marroni, PhD IGA Technology Services, s.r.l. Istituto di Genomica Applicata, via J. Linussio 51 Phone +39 0432 629741 or +39 0432 558652 Fax +39 0432 603887 Web page: <http://www.fabiomarroni.altervista.org/> Fabio Marroni <marroni@appliedgenomics.org>

UK FunctionalEcology Nov26-30

Functional ecology from organism to ecosystem: theory and computation (FEER01)

This course will be delivered by Dr. Francesco de Bello, Dr. Lars Götzenberger and Dr. Carlos Carmona and will take places in Glasgow city centre from 26th - 30th November 2018.

Course Overview: The course will describe different aspects and methods in the field of functional ecology, combining theoretical lessons with hands-on real data. Lectures will provide the theoretical and mathematical basis for different applications of functional traits at organismal, community and ecosystem levels, with examples across different trophic levels. This will serve as a basis for exploring the practical tools to connect the

effect of land-use and climate change on biodiversity to the effect of biodiversity on to multiple ecosystem functions and ecological services. An overview of existing computational methods, including recent developments authored by the lecturers, will be provided during the course and the students will learn how to apply them using functions and scripts run in R. Students are welcome to apply these tools to their own data, or use the data provided, to be analysed during the course while benefiting from advice by the lecturers. As such, compared to other courses given by the lectures, this is a slightly more advanced and data oriented course which concentrates on detailed and practical aspects in functional traits related applications, especially computational ones. The aim of the course is to provide participants with a handy synthesis of existing concepts, tools and trends in functional ecology and guide them to apply these tools to their own field of interest. As the field of functional ecology is rapidly expanding, participants will be ready to exploit the potential of the main trait approaches.

Monday 26th - Classes from 09:30 to 17:30 - People's traits game - Introduction to functional ecology and key definitions - Environmental filtering and related community metrics - Overview on functional trait community metrics - Practical with 'community weighted mean' and solution to potential biases

Tuesday 27th - Classes from 09:30 to 17:30 - Species level analyses - Missing values and trait databases - Functional diversity indices (alpha, beta and gamma diversity) - Practical with functional diversity indices

Wednesday 28th - Classes from 09:30 to 17:30 - Trait evolution and the relevance of phylogenetic distance between species - Phylogenetic corrections - Combining functional and trait information - Practical on phylogeny and traits

Thursday 29th - Classes from 09:30 to 17:30 - Community assembly: theory - Community assembly: from species to community level analyses - Null-models - Practical on community assembly

Friday 30th - Classes from 09:30 to 16:00 - Effects of traits on ecosystem processes and services - The trait sampling game - Intraspecific trait variability: biological relevance and quantification - Practical on intraspecific trait variability

Email oliverhooker@prstatistics.com

Check out our sister sites, www.PRstatistics.com (Ecology and Life Sciences) www.PRinformatics.com (Bioinformatics and data science) www.PSstatistics.com (Behaviour and cognition)

1. May 21st - 25th 2018 INTRODUCTION TO PYTHON FOR BIOLOGISTS (IPYB05) Glasgow, Scotland, Dr. Martin Jones <http://www.prinformatics.com/course/introduction-to-python-for-biologists-ipyb05/>

2. May 21st - 25th 2018 INTRODUCTION TO REMOTE SENSING AND GIS FOR ECOLOGICAL APPLICATIONS (IRMS01) Glasgow, Scotland, Prof. Duccio Rocchini, Dr. Luca Delucchi www.prinformatics.com/course/introduction-to-remote-sensing-and-gis-for-ecological-applications-irms01/

3. May 28th - 31st 2018 STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR (SIMM04) Canada (QUEBEC) Dr. Andrew Parnell, Dr. Andrew Jackson www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm04/

4. May 28th - June 1st 2018 ADVANCED PYTHON FOR BIOLOGISTS (APYB02) Glasgow, Scotland, Dr. Martin Jones www.prinformatics.com/course/advanced-python-biologists-apyb02/

5. June 12th - 15th 2018 SPECIES DISTRIBUTION MODELLING (DBMR01) Myuna Bay sport and recreation, Australia, Prof. Jane Elith, Dr. Gurutzeta Guillera www.prstatistics.com/course/species-distribution-models-using-r-sdmr01/

6. June 25th - 29th 2018

— / —

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>

UK StatisticalModelling Jun21-25

Statistical modelling of time-to-event data using survival analysis: an introduction for animal behaviourists, ecologists and evolutionary biologists (TTED01)

<https://www.psstatistics.com/course/statistical-modelling-of-time-to-event-data-using-survival-analysis-tted01/>

This course will be delivered by Dr Will Hoppitt in Glasgow and will run from the 21st - 25th Jan 2019.

Course Overview:

Survival analysis is a set of statistical methods initially designed to analyse data giving the times at which individuals die, and assess the effect that different predictor variables have on the rate of death. However, its applications are much broader than this: it can be used

to analyse any time-to-event data. Ecologists and evolutionary biologists often encounter data of this kind. Often factors influencing survival itself will be of interest. But there are many other cases, e.g. what factors influence the time of first breeding? Or the time taken to reach maturity? Animal behaviourists too will encounter this type of data frequently, e.g. what factors influence the time it takes to learn a novel behaviour pattern? Or the time to respond to a stimulus? etc. And yet the techniques of survival analysis are not generally well known by researchers in these disciplines.

In this course, you will learn how to apply survival analysis models to quantify the effect that predictor variables (continuous or discrete) have on the rate at which events occur, and how to test hypotheses about these effects. We will focus on a flexible modelling technique called the Cox proportional hazards model, which makes minimal assumptions about the underlying probability distributions. You will learn how to fit and interpret these models, how to evaluate its assumptions, and how to extend it to model time dependent variables, random effects, multistate models and competing risks models.

Monday 21st - Classes from 09:30 to 17:30

Module 1: Statistical modelling of rates and times

Module 2: Parametric survival models and the Cox model

Tuesday 22nd - Classes from 09:30 to 17:30

Module 3: Fitting Cox models

Module 4: Interpreting Cox Models

Wednesday 23rd - Classes from 09:30 to 17:30

Module 5: Evaluating the proportional hazard assumption

Module 6: Stratified Cox models

Thursday 24th - Classes from 09:30 to 17:30

Module 7: Time dependent variables

Module 8: Frailty Models and Multistate models

Friday 25th - Classes from 09:30 to 17:30

Module 9: Competing risks models

Module 10: Open session

Email oliverhooker@psstatistics.com

Check out our sister sites,

www.PRstatistics.com (Ecology and Life Sciences)

www.PRinformatics.com (Bioinformatics and data science)

www.PSstatistics.com (Behaviour and cognition)

1. June 12th - 15th 2018

SPECIES DISTRIBUTION MODELLING (DBMR01)

Myuna Bay sport and recreation, Australia, Prof. Jane Elith, Dr. Gurutzeta Guillera

www.prstatistics.com/course/species-distribution-models-using-r-sdmr01/ 2. June 25th - 29th 2018

SPECIES DISTRIBUTION/OCCUPANCY MODELLING USING R (OCCU01)

Glasgow, Scotland, Dr. Darryl McKenzie (PROTEUS)

www.prstatistics.com/course/species-distributionoccupancy-modelling-using-r-occu01/

3. July 2nd - 5th 2018

SOCIAL NETWORK ANALYSIS FOR BEHAVIOURAL SCIENTISTS USING R (SNAR01)

Glasgow, Scotland, Prof. James Curley

<http://www.psstatistics.com/course/social-network-analysis-for-behavioral-scientists-snar01/>

4. July 8th - 12th 2018

MODEL BASE MULTIVARIATE ANALYSIS OF ABUNDANCE DATA USING R (MBMV02)

Glasgow, Scotland, Prof. David Warton

www.prstatistics.com/course/model-base-multivariate-analysis-of-abundance-data-using-r-mbm02/

5. July 23rd - 27th 2018

EUKARYOTIC METABARCODING (EUKB01)

Glasgow, Scotland, Dr. Owen Wangenstein

<http://www.prinformatics.com/course/eukaryotic-metabarcoding-eukb01/>

6. September 24th - 28th

INTRODUCTION TO MIXED (HIERARCHICAL) MODELS FOR LIFE SCIENCES USING R (IMLS01)

Glasgow, Scotland, Prof. Subhash Lele

<https://www.psstatistics.com/course/introduction-to-mixed-hierarchical-models-for-life-sciences-using-r-imls01/>

7. October 1st - 5th

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

Wageningen NL Animal Genomic Diversity Oct15-19

Characterization, management and exploitation of genomic diversity in animals

<https://www.wur.nl/en/Education-Programmes/-PhD-Programme/Graduate-Schools/Wageningen-Institute-of-Animal-Sciences/Show-1/Interactive-post-graduate-course-on-characterization-management-and-exploitation-of-genomic-diversity-in-animals-15-19-October-2018.htm> Wageningen University & Research organizes a 5-day interactive course from 15 to 19 October 2018, in the framework of the EU Horizon 2020 project IMAGE (Innovative Management of Animal Genetic Resources). The course consists of lectures during which various topics related to genomic diversity are addressed and of group work during which the participants will apply novel and exciting methods to their own genomic data.

Aim of the course Preserving genetic diversity is essential for sustainable animal populations. Learn to characterize, prioritize and conserve genetic diversity in animal populations, from both a genomic and a breeding perspective.

Target audience istudents - at least in their 2nd year i-docs and researchers interested in genomic diversity

Content of the course at a glance - Measures of genomic diversity - Diversity across breeds - Adaptive introgression - Functional genomics - Management of small populations - Prioritization for conservation - Optimal contributions - Setting up gene bank collections

Lecturers - Jack Windig, Wageningen University & Research (the Netherlands) - Gabor Meszaros, University of Natural Resources and Life Sciences (Austria) - Hendrik Jan Megens, Wageningen University & Research (the Netherlands) - Steffen Weigend, Friedrich Loeffler Institute (Germany) - Michele Tixier-Boichard, French National Institute for Agricultural Research (France) - Mirte Bosse, Wageningen University & Research (the Netherlands)

“Windig, Jack” <jack.windig@wur.nl> “Windig, Jack” <jack.windig@wur.nl>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email `evoldir@evol.biology.McMaster.CA`. Do not include encoded attachments and do not send it as Word files, as HTML files, as \LaTeX files, Excel files, etc. ... plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at `Golding@McMaster.CA` and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.