
E v o l D i r

September 1, 2017

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

Foreword

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

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

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



Foreword	1
Conferences	2
GradStudentPositions	10
Jobs	39
Other	72
PostDocs	77
WorkshopsCourses	120
Instructions	136
Afterword	136

Conferences

ASABLondonZoo SexualSelection Dec7-8	2	Pittsburgh Evolution Sep9 TravelAwardsAbstractDead-	7
Asilomar AmNaturalist Jan5-9	3	line	7
Bolivia ConservationGenetics Jan14-28	3	SaoPaulo MarineInvertEvoDevo Dec3-16	8
HinxtonUK HumanEvolution Nov20-22	4	UCostaRica PolychaeteEvolution Jul17-19	8
Marseilles EvolutionaryBiol Sep26-29 CallForPosters	4	Ventura California PredatorPrey Jan28-Feb2	9
Medellin Colombia EvoDevo Oct9-13	4	Vienna ConservationGenetics Feb	10
NHM London YoungSystematists Dec1	6		
Oxford WildlifeConservation Sep25-27	7		

ASABLondonZoo SexualSelection Dec7-8

CONFERENCE ANNOUNCEMENT

The 2017 ASAB Winter meeting (Thursday 7th and Friday 8th December 2017):

Sexual selection: do we still need to test the alternatives?

Organised by Professor Nina Wedell and Dr David Shuker

ABSTRACT SUBMISSION NOW OPEN

The 30 years since the publication of Bradbury and Andersson's landmark "Sexual selection: testing the alternatives" has seen a wealth of new empirical data on the mechanisms and patterns of sexual selection, alongside major theoretical advances. However, some key concerns remain, including what drives the evolution of mate choice and how sexual selection and natural selection interact. Moreover, the very definition of sexual selection remains contested. In this meeting, we will explore the latest findings in sexual selection, in terms of both theory and experiment, to chart our progress in understanding this most beguiling of evolutionary

mechanisms, and to map the way forward for the next generation of sexual selection researchers.

Our invited speakers are Suzanne Alonzo, David Hosken, and Hope Klug, and we are also delighted that Christine Nicol will be presenting the 2017 Tinbergen Lecture during the meeting. We invite spoken and poster presentations encompassing the widest range of current work on sexual selection. Please note that due to space constraints, poster space will unfortunately be limited.

The meeting will be held at the Zoological Society of London, Huxley Lecture Theatre, London Zoo. As is traditional for the ASAB winter meeting, there is no registration and delegates need to organise their own accommodation and main meals. Tea and coffee will be provided both days, along with a wine reception on the evening of the 7th. We welcome those wishing to indicate their likely attendance however, and we are very pleased to announce that abstract submissions for spoken and poster presentations is now open (deadline 1st October 2017). An abstract submission form is available on our website: <http://asabwinter2017.weebly.com/> and only submissions using this form will be accepted. Presentations will be chosen blind to author(s) and host institution(s).

For further details, please visit our website (<http://asabwinter2017.weebly.com/>) or contact us on our dedicated conference email: asab2017@st-andrews.ac.uk

We very much look forward to seeing you in December,
Nina Wedell and Dave Shuker

David Shuker <dms14@st-andrews.ac.uk>

Asilomar AmNaturalist Jan5-9

Come celebrate 150 years of The American Naturalist!

The American Society of Naturalists is celebrating the 150th anniversary of the founding of The American Naturalist with a conference at the Asilomar Conference Center on the Pacific coast on 5-9 January 2018. Please visit <http://amnat150.org>. Registration will open on Tuesday, 1 August 2017. Because of the venue size, we can only accept 200 registrants for the conference, so don't delay. Submission of titles and abstracts for talks and posters must be made at the time of registration, so please have that information ready when you go to the registration webpage.

The American Society of Naturalists strives to advance knowledge of unifying biological principles by uncovering processes that generate and maintain patterns of biological diversity. These patterns and processes necessarily involve complex interactions between ecology, evolution, genetics, behavior, and physiology. Consequently, ASN emphasizes the value of interdisciplinary research and collaborations between diverse biologists to achieve conceptual unification across the biological sciences. This meeting will bring together a diverse array of biologists who might not normally encounter one another at separate discipline-specific meetings.

Come celebrate 150 years of The American Naturalist with us!

The American Society of Naturalists

<http://amnat150.org> "Mark.A.McPeck@dartmouth.edu"
<Mark.A.McPeck@dartmouth.edu>

Bolivia ConservationGenetics Jan14-28

*****VERSION EN CASTELLANO ABAJO*****

ACCEPTING APPLICATIONS for the XII Workshop on Conservation Genetics: New challenges in the An-

thropocene of the Conservation Genetics Network (Red de Genética para la Conservación - ReGeneC), Sucre - Bolivia, 14-28 January 2018.

Application deadline: October 1st, 2017. See "Preinscripciones" <http://regenec.org/taller/ene2018/-preinscripcion/> for application process details.

This 15-day intensive graduate course is directed primarily at Latin American postgraduate students and young professionals. Fluency in Spanish or Portuguese is required. Participating faculty confirmed to date represent six Latin American countries (Argentina, Bolivia, Brazil, Chile, Colombia, and Venezuela), and a wide array of scientific perspectives within this emerging field.

The course combines discussion sessions, hands-on data analysis, and in-depth review and presentation of ongoing research by participating students, with formal lectures in project design, marker choice, statistical analysis, phylogenetics, phylogeography, and population genetics. Throughout the course, we emphasize practical applications to the real-world process of conservation.

The course is organized by ReGeneC (<http://regenec.org/>, @ReGeneC.institutional) and the San Francisco Xavier University of Chuquisaca (USFX) (<https://www.usfx.bo>). So far, we have received financial support from The American Genetic Association (@theAGA.org).

For more information, please visit our website <http://regenec.org/taller/ene2018/> or send an email to asistenciaregenec@gmail.com or regenec@gmail.com

PREINSCRIPCIÓN ABIERTA para el XII curso intensivo de la Red de Genética para la Conservación (ReGeneC): "Nuevos desafíos en la época del Antropoceno", Sucre - Bolivia, 14 - 28 de enero de 2018.

Fecha límite: 01 de octubre de 2017. Ver la sección "Preinscripciones" en <http://regenec.org/taller/ene2018/preinscripcion/> para detalles del proceso de postulación.

Este curso intensivo de 15 días está dirigido principalmente a estudiantes de posgrado y jóvenes profesionales latinoamericanos. Para tomarlo se requiere tener fluidez en castellano o portugués. Los profesores participantes confirmados hasta el momento representan a seis países latinoamericanos (Argentina, Bolivia, Brasil, Chile, Colombia y Venezuela), con una amplia gama de enfoques dentro de este campo emergente.

El curso combinará sesiones de discusión, clases prácticas de análisis de datos, así como la revisión profunda y presentación de las investigaciones en curso de los estudiantes. Incluye temáticas como diseño de proyectos, selección de marcadores, análisis estadísticos acordes

con la pregunta a responder, filogenia, filogeografía y genética de poblaciones. A través del curso, se hará énfasis en aplicaciones prácticas al proceso de conservación en el mundo real.

El curso es organizado por ReGeneC (<http://regenec.org/>, @ReGeneC.institucional) y la Universidad San Francisco Xavier de Chuquisaca (USFX) (<https://www.usfx.bo>). Hasta el momento contamos con el apoyo financiero de The American Genetic Association (@theAGA.org).

Para más información, visite nuestro sitio web <http://regenec.org/taller/ene2018/> o contáctenos por correo electrónico en las siguientes direcciones: asistenciaregenec@gmail.com o regenec@gmail.com

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, Ñuñoa, Santiago, Chile

< <http://cursos.ciencias.uchile.cl/cienciasecológicas/index.html> >* < https://www.researchgate.net/profile/Elie_Poulin >* < <http://www.ciencias.uchile.cl/ecologia/jml/> ><http://www.ieb-chile.cl/>

Phone: (56)-2-29787298 E-mail: epoulin@uchile.cl

Elie Albert Poulin <epoulin@uchile.cl>

HinxtonUK HumanEvolution Nov20-22

Reduced rates for students: Bursary deadline 12 September

Name: Human Evolution: Fossils, Ancient and Modern Genomes conference Dates: 20-22 November 2017 Location: Wellcome Genome Campus Conference Centre, Hinxton, CB10 1RQ, UK Website: <https://coursesandconferences.wellcomegenomecampus.org/events/item.aspx?e=651> This new conference will celebrate the maturity of the ancient DNA field. The meeting will bring together genomic specialists, palaeontologists, archaeologists, primatologists, medical geneticists and other researchers interested in human evolution.

We will explore the use of genomic tools and large-scale analysis of ancient nuclear DNA to deciphering population mixing, complex migration patterns, microbiome evolution and the role of adaptive introgression in hu-

man evolution.

Best wishes

Anaid

-

Dr Anaid Diaz

Tel: +44 (0)1223 494860 Wellcome Genome Campus Advanced Courses and Scientific Conferences | Wellcome Genome Campus | Hinxton | Cambridgeshire | CB10 1RQ

Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is 215 Euston Road, London, NW1 2BE.

anaid.diaz@wellcomegenomecampus.org

Marseilles EvolutionaryBiol Sep26-29 CallForPosters

Dear all , the evolutionary biology meeting at Marseilles program (scientific , social events..)

is available on aeeb.fr web site (follow the evolutionary biology meeting link)

5 spots are available for poster presentations

best regards

Pierre

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

Medellin Colombia EvoDevo Oct9-13

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

Topics in the plenary sessions include:

- Animal and plant developmental biology
- Stem cells, Neurobiology, Medicine and Development
- Post-embryonic development and regeneration
- Evo-Devo and Next Generation Sequencing

Confirmed speakers include:

Nobel Awardee

Sir John Gurdon, Gurdon Institute, UK; University of Cambridge

The stability and reversal of cell differentiation

Karen Sears, University of Illinois, USA

>From genome to phenome: The developmental basis of mammalian variation

Enrique Amaya, The University of Manchester, UK

A conserved role for reactive oxygen species during early embryonic development and appendage regeneration

Maria Barna, Stanford University, USA

Bio-imaging of tissue patterning and cellular communication during embryonic development

Jeremiah Smith, University of Kentucky, USA

Developmentally programmed rearrangement of the lamprey genome

Sylvain Marcellini, Universidad de Concepcion, Chile

Junk or func? Contribution of mobile elements to the osteoblastic gene regulatory network

Siobhan Brady University of California Davis, USA

Regulation of root morphogenesis and cell type development in the face of a changing environment

Joseph Arboleda- Velasquez, Schepens Eye Research Institute, USA

Therapeutic antibody targeting of Notch3 signaling prevents mural cell loss in CADASIL.

Jesus Chimal-Monroy, Universidad Nacional Autonoma de Mexico

Digit patterning is controlled by an antagonism between retinoic acid and TGF beta

Karen Echeverri, University of Minnesota, USA

Molecular mechanisms of spinal cord regeneration

Randall Voss, University of Kentucky, USA.

Transcriptional Investigation of Positional Memory in Axolotl Limbs

Rodrigo Nunes da Fonseca, Universidade Federal do Rio

de Janeiro, Brazil

Evolution and multiple roles of the Pancrustacea specific transcription factor zeldain insects

Miguel Concha, Laboratory of Experimental Ontogeny, Chile

Novel roles of extra-embryonic tissue in directing early embryo morphogenesis in vertebrates

Patrizia Ferretti, University College London, Institute of Child Health, UK

Stem cells in health and disease: from animal to human models.

Robb Krumlauf, Stowers Institute for Medical Research, USA

Hox genes: Regulating the balance between pluripotency and differentiation

Veronica Di Stilio, University of Washington, USA

Reconstructing the ancestral role of flowering meristem identity genes in a non-flowering plant

Brigitte Galliot, Universite de Geneve, Switzerland

Regeneration and slow aging, what role for autophagy?

Marianne Bronner, Caltech, USA

Gene regulatory and signaling events in neural crest development

Vivian Irish, Yale University, USA

Petal development: a twist in fate

Luis Alfredo Cruz Ramirez, CINVESTAV. Langebio, Mexico

Unraveling the role of RETINOBLASTOMA-RELATED in Stem Cell maintenance and Asymmetric Cell Division along land plant phylogeny

Igor Schneider, Universidade Federal de Para, Brazil

Deep evolutionary origin of tetrapod limb regeneration

Lee Niswander, University of Colorado, USA

Using mouse and human iPSC modeling to reveal the causes of neural tube defects

Carole La Bonne, Northwestern University, USA

Stem Cells, Gene Regulatory Networks and the Evolution of Vertebrates

Robert Reed, Cornell University, USA

Developmental genetics of butterfly wing pattern evolution

Robert Sablowski, John Innes Centre, UK

Cell size regulation and organ patterning in the shoot

meristem

Maria Angela Nieto, Instituto de Neurociencias, Alicante, Spain

Epithelial plasticity in health and disease

Jose Garc a- Arraras, University of Puerto Rico, Rio Piedras

Understanding regeneration; a visceral reaction

Cristina Ferrandiz Instituto de Biolog a Molecular y Celular de Plantas, UPV, CSIC, Spain

A stylish story of carpel evolution

Claudia Torres Farfan, Universidad Austral de Chile

Light pollution during gestation induce maternal chromodisruption and long-term effect in the offspring, increasing the risk of chronic disease.

Roberto Mayor, University College London, UK

Chemical and mechanical cues control collective cell migration

Katia del Rio- Tsonis, Miami University, USA

Epigenetic signatures during chick retina regeneration

Alejandro Sanchez Alvarado, Stowers Institute for Medical Research, USA

The life cycle of regeneration

Joachim Wittbrodt, Centre for Organismal Studies - Heidelberg, Germany

Activating the regenerative potential of Muller glia cells in a regeneration-deficient retina

— / —

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>

NHM London YoungSystematists Decl

19th YOUNG SYSTEMATISTS' FORUM

Friday, 1 December 2017, 9:30 am

Venue: Flett Lecture Theatre,

Natural History Museum, London, UK

The annual Young Systematists' Forum represents an

exciting setting for Masters, PhD and young postdoctoral researchers to present their data, often for the first time, to a scientific audience interested in taxonomy, systematics and phylogenetics. This well-established event provides an important opportunity for budding systematists to discuss their research in front of their peers within a supportive environment. Supervisors and other established systematists are also encouraged to attend.

Prizes will be awarded for the most promising oral and poster presentation as judged by a small panel on the day.

Registration is FREE.

Send applications by e-mail to YSF.SystematicsAssociation@gmail.com, supplying your name, contact address and stating whether or not you wish to give an oral or poster presentation. Please also tell us your academic stage - e.g., Masters, PhD or postdoc. Space will be allocated subject to availability and for a balanced programme of animal, plant, algal, microbial, molecular and other research. Non-presenting attendees are also very welcome - please register as above.

Again the YSF will be held the day after the Molluscan Forum (<http://www.malacsoc.org.uk/-MolluscanForum.htm>) also at the Natural History Museum. This has been arranged so both meetings can be attended, although if attending both you will have to register for both meetings separately.

Abstracts must be submitted by e-mail in English and in Word format no later than Friday 3 November 2017. The body text should not exceed 150 words in length. Title, authors, and their professional affiliations should be included with the abstracts. If the presentation is co-authored, the actual speaker (oral) or presenter (poster) must be clearly indicated in BOLD text.

If you have presented a talk at the YSF before, we ask that you submit only for a poster presentation, as speaker slots are limited and we want to give as many people a chance as possible. Similarly, if you are presenting at both the YSF and MF, we ask that you not apply for speaking slots in both (or let us know so we can assess).

All registered attendants will receive further information about the meeting, including abstracts, by e-mail one week in advance. This information will also be displayed on the Systematics Association website (www.systass.org).

Ellinor Michel <e.michel@nhm.ac.uk>

Oxford Wildlife Conservation Sep25-27

First Annual Wildlife Trade Symposium: Evolving perspectives on demand for illegal wildlife products

This three-day event is being organised by the Oxford Martin Programme on the Illegal Wildlife Trade and co-hosted with generous support from San Diego Zoo Global and TRAFFIC. The first day of the Symposium, September 25th will set the scene for subsequent days, showcasing a series of invited presentations, panel discussions and an open poster session themed on:

Diverse approaches to illegal wildlife trade research

Linking the supply and demand for wildlife products

Changing wildlife consumption onto a legal, sustainable path

September 26th & 27th will consist of in-depth interactive sessions covering a range of methodological and conceptual challenges of the illegal wildlife trade more broadly. Delegates will have the opportunity to select and register in advance for sessions in which they wish to participate, customising their schedule for both days. Sessions will be confirmed closer to the date and sign-up will be on a first-come first-served basis.

September 26th will feature an evening debate on the Illegal Wildlife Trade chaired by BBC journalist John Simpson.

More information about the event can be found here:

<http://www.illegalwildlifetrade.net/2017symposium/>

If you would like to upload a poster abstract you can do so here:

<http://www.illegalwildlifetrade.net/2017symposium/-submissions/> Wildlife Trade Symposium
<symposium@illegalwildlifetrade.net>

Pittsburgh Evolution Sep9 Travel Awards Abstract Deadline

Abstract submission for the Three Rivers Evolution Event (TREE) ends on midnight August 1st - You have just over 24 hours to submit and edit your submission!

Thanks to funding from SMBE, we are now offering small (up to \$200) travel awards to facilitate attendance by those with limited travel resources.

Please register, submit abstracts, and apply for awards here: <https://sites.google.com/view/tree2017> Already registered? You may revise your information until the August 1st deadline, using the link provided on your initial registration, or use the registration link to apply for awards only by selecting 'yes' on the questions about having previously registered and submitted an abstract.

What is TREE?

The Three Rivers Evolution Event (TREE) is a conference sponsored by SMBE and ASN that aims to bring together researchers from Western Pennsylvania and the surrounding areas to share and discuss research in all aspects of evolutionary biology. The research of attending members is expected to span viruses, microbes, plants, invertebrates and vertebrates, and include ecology, anthropology, epidemiology, developmental biology, zoology, theoretical, applied, urban ecology, paleontology, and many other specialized research areas. Researchers of all stages, institutional affiliations, and related fields (including ecologists, anthropologists, paleontologists, and similar fields) are welcome to present. We are excited at the diversity of current registrants, which as of this writing includes 104 scientists from 33 institutions, and 71 submitted abstracts!

When and Where: Saturday, September 9th, 2017 at the University of Pittsburgh.

The TREE organizing committee

Sebastian Echeverri

Dr. Wynn Meyer

Melissa Plakke

Dr. Avery Russell

Dr. Martin Turcotte

Dr. Caroline Turner

Contact us at biotree2017@gmail.com

biotree2017@gmail.com

SaoPaulo MarineInvertEvoDevo Dec3-16

Dear Colleagues,

It is my pleasure to announce the third Comparative Embryology of Marine Invertebrates (CEMI) Course that will take at CEBIMAR (Centro de Biologia Marinha da Universidade de São Paulo) in São Sebastião, Brazil from Dec 3rd - Dec 16th, 2017. It is a two-week intensive graduate level course to study in depth local marine invertebrate species.

Registration for the course is 16 USD (free for USP students). Your dorm, simple breakfasts every day, and lunches from Mon-Fri, will be covered by the organizers. Transportation from São Paulo to São Sebastião before and after the course will also be covered by the organizers. You will only be in charge of your own dinners during the two weeks of the course, as well as week-end meals. Estimate to spend approx. 12-13 USD per meal.

Please, forward the link below to any graduate student that may be interested. Application deadline is September 15th!

CEMI Course Info: <http://zoologia.ib.usp.br/-evodevo2/index.php/biz5765/> Cheers, Federico

Federico D. Brown Professor Doutor Departamento de Zoologia Instituto Biociencias Universidade de Sao Paulo Ramal direto: +55 11 3091.0950 <http://www.ib.usp.br/zoologia/evodevo> Federico Brown <fdbrown@usp.br>

UCostaRica PolychaeteEvolution Jul17-19

Dear colleagues,

We are delighted to announce the V Latin American Symposium of Polychaeta (V SILPOLY), to be held on the campus of the University of Costa Rica (UCR), San Jose Costa Rica, during July 17-19, 2018.

Both the Center of Marine Research in Marine Sciences and Limnology (CIMAR) and the Museum of Zoology

at UCR would like to invite students and professionals studying annelid polychaetes to present their exciting research to our community. The V SILPOLY will highlight the research being made in Latin America and it is inclusive to all of those interested in annelid biology.

Previously held in Brazil, Argentina, Venezuela and Mexico, V SILPOLY will be the first SILPOLY to be held in Central America. We invite people from all of the Americas and the rest of the world to participate.

Research themes will include, but will not be limited to, evolution, taxonomy and systematics, paleontology, ecology, diversity, genetics, reproduction and development of polychaetes. We also open our door to researchers studying sipunculans, echiurans, oligochaetes and leeches.

Important deadlines:

Abstract submission: January 15, 2018

Communication to authors about acceptance of abstracts: March 15, 2018

Early registration: Before June 1, 2018

Late registration: After June 1, 2018

More information regarding the abstract and poster format can be found in our website: <http://www.cimar.ucr.ac.cr/simposios/v-simposio-latinoamericano-polychaeta-2018.html>

Information about registration can be found at <https://www.horizontes.com/en/about-horizontes/-meetings-and-events-2/v-latin-american-symposium-of-polychaeta>

Please follow our facebook: <https://www.facebook.com/vsilpoly/>, twitter: <https://twitter.com/VSilpoly18CR?lang=en> and research gate: <https://www.researchgate.net/project/Organization-of-the-V-Latin-American-Symposium-of-Polychaeta> or contact us at: vsilpoly@gmail.com

Organizing committee:

Jeffrey Sibaja-Cordero jeffro.alejandro@gmail.com

Victoria Bogantes-Aguilar vikbogantes79@gmail.com

Allan Carrillo-Baltodano acarrillobaltodano@clarku.edu

Jose A. Vargas-Zamora jose.vargas@ucr.ac.cr

Sponsoring institutions:

Centro de Investigacion en Ciencias del Mar y Limnología (CIMAR) and Museo de Zoología,

Universidad de Costa Rica

“Carrillo Baltodano, Allan”
<ACarrilloBaltodano@clarku.edu>

Ventura California PredatorPrey Jan28-Feb2

TITLE: Predator-Prey Interactions Gordon Conference:
Registration now open BODY:

Third Gordon Research Conference on Predator-Prey
Interactions

January 28 - February 2, 2018, Ventura, California

<http://www.grc.org/programs.aspx?id=16781> 2018
Theme: "Scaling Across Space and Time"

Gordon Research Conferences are recognized as the "world's premier scientific conferences", where leading investigators from around the globe meet biennially for a full week of intense discussion of the frontier research in their field. We have an outstanding list of confirmed speakers and contributors (below). Our meeting is capped at 200 people, and filling up fast; so please register soon!

The neurobiology of responses to risk in individual prey can, when aggregated across a population, profoundly affect surrounding ecosystems. Similarly, researchers are increasingly aware of how quickly selection and epigenetic forces can shift prey phenotypes and alter future interactions with predators. In both cases, the connections between small-scale (within an individual or at a single point in time) and large-scale (across ecosystems or generations) processes illustrate how exploring the 'linkage map' of predator-prey interactions across scales can identify new fields of research and synergize the collaborations necessary to address them. We have targeted the most exciting advances in predator-prey work across multiple fields, with each speaker agreeing to share their latest unpublished findings. In order to encourage active participation from everyone at the conference, all attendees are strongly encouraged to present a poster on their work.

The complete program is available, along with further details concerning registration, at our website (<http://www.grc.org/programs.aspx?id=16781>).

Sessions and Confirmed Speakers

Predator-prey interactions in the field and lab

Joel Berger, Caroline Blanchard (speakers)

Jacqueline Blundell & Evan Preisser (discussion leaders)

Evolutionary underpinnings of predator-prey interac-

tions

John Orrock, Catherine Matassa, Robyn Crook, Robby Stoks (speakers)

Sonny Bleicher (discussion leader)

Predators at the landscape level

Elizabeth Madin, Trisha Atwood, Stephanie Periquet

Shelby Rinehart (discussion leader)

Prey responses to predator cues

Ted Stankowich, Grant Brown, William Resetarits, Mark Berry

Adam Crane (discussion leader)

Neural responses to predators

Gwyneth Card, Rupshi Mitra, Cornelius Gross

Newton Canteras (discussion leader)

Neurobiology of fear

Ken Lukowiak, Arun Asok, Gal Richter-Levin, Marta Moita

Wen Han Tong (discussion leader)

Carnivores in natural and managed landscapes

Doug Smith, Justin Suraci, Mathew Crowther

Rebecca Selden (discussion leader)

Transgenerational impacts of stress

Tracy Langkilde, Michael Sheriff, Brian Dias, Regina Sullivan

Michael Clinchy (discussion leader)

Past, present, and future directions in fear and predator-prey research

James Estes, Liana Zanette

Maud Ferrari & Ajai Vyas (discussion leaders)

Evan Preisser, Professor & Chair Dept. of Biological Sciences, University of Rhode Island 9 E. Alumni Ave., Kingston RI 02881 USA (401) 874-2120; preisser@uri.edu; <http://web.uri.edu/preisserlab> Evan Preisser <preisser@uri.edu>

Vienna ConservationGenetics Feb

We are organizing a conservation genetics meeting in Vienna next February: <https://consngen18.nhm-wien.ac.at/> Frank Priv.-Doz. Dr. habil. Frank E. Zachos Naturhistorisches Museum Wien Säugetiersammlung Burgring 7 1010 Wien, Österreich

Tel. +43-(0)1-52177-550 Fax +43-(0)1-52177-234

Zachos Frank <frank.zachos@NHM-WIEN.AC.AT>

GradStudentPositions

AustralianNatU AlpinePlantPhenotypicPlasticity . 11	TrentoU FEM Italy MetagenomesEvolution 26
AustralianNatU InsectGenomes 11	TrentoU MosquitoEvolution 27
Berlin EvolutionOfVirulence 12	TU Braunschweig AmphibianSpeciesDelimitation . 27
Bialowieza Poland BisonDiseaseEvolution 13	UEasternFinland HumanEvolutionaryBiology 28
Budapest EvolutionaryGenomics 14	UHaifa CircadianClockMolEvol 29
CIBIO Portugal Biodiversity 15	UIceland SpeciationEvolReprodBar 30
FUBerlin EcoEvoInsectImmunity 16	UJyvaskyla 4 EvolutionaryBiology 31
ICETA Portugal ConservationGenetics 17	UNewOrleans EvolutionaryPhysiology 31
IGB Berlin FunctionalGenomics 18	UNotreDame EvolutionEcology 31
JagiellonianU EvolutionaryPhysio 19	UPittsburgh EvolutionaryEcol 32
LaurentianU Canada WolfCoyoteEvolution 20	UQueensland UExeter EvolGenomicsNutritionAgeing 33
MaxPlanck Germany 2 AvianCulturalEvolutionEcol 20	UTokyo PlantEvolutionaryEcol 33
MonashU EvolutionaryEcologyDisease 21	UTulsa 2 EvolBiol 34
MPIO Seewiesen EvolutionCognition 22	UValencia ViralEvolution 35
Museum BonnGermany 2 Ricefish 22	UWestGeorgia EvolutionaryBiol 35
NewZealand FinfishGenomics 23	UWollongong EvolutionFishSociality 36
SouthDakotaStateU GrasslandCommunityPhylogenetics 24	UWurzburg 2 EvolAmbrosiaBeetles 37
TexasTechU RatEvolution 24	UZurich SexChromosomeEvolution 37
Toulouse DemographicInference 25	

AustralianNatIU AlpinePlantPhenotypicPlasticity

PhD positions in alpine plant evolutionary ecology

We are seeking highly-motivated PhD students for projects on the evolutionary ecology of Australian alpine plants, based at the Research School of Biology in the Australian National University. The projects will suit students with interest and knowledge in plant evolutionary ecology, environmental physiology and/or ecological and evolutionary genetics.

Project descriptions: 1. The epigenetic and ecophysiological basis of plasticity in an Australian alpine herb in response to warming. Phenotypic plasticity, or the ability to change phenotype with environment, is the most important process determining the immediate response of natural populations to environmental change, and yet our mechanistic understanding of the process is limited. Using large-scale temperature-manipulation experiments on an Australian alpine herb, the waxy bluebell (*Wahlenbergia ceracea*), these PhD projects will identify the (epi)genomic and ecophysiological mechanisms driving phenotypic plasticity in a range of phenotypic traits in response to temperature. Supervisors Prof Adrienne Nicotra (ANU), Prof Loeske Kruuk (ANU) and A. Prof Christina Richards (Uni South Florida, USA).

2. The adaptive potential of woody plants in the Australian Alps How do shrubs disperse and spread across the landscape and how is this reflected in their evolutionary genetic history? These projects combine cutting edge population genomic and classic plant ecology approaches and to assess patterns of genetic structure in several key alpine shrub species and assess how these patterns reflect underlying ecological processes. Projects will make use of next generation sequencing techniques and bioinformatics in the Genome Discovery Unit at the Biomolecular Resources Facility (ANU), as well as fieldwork in Australia's Snowy Mountains, Kosciusko National Park. Supervisors: Dr Susanna Venn & Prof Adrienne Nicotra (ANU) and Prof Ary Hoffmann (Univ Melbourne).

Suitable applicants need to be highly motivated with strong academic and research backgrounds; some background in plant evolutionary ecology, environmental physiology and/or ecological and evolutionary genetics is required. Demonstrated ability to conduct fieldwork and independent research experience are highly desirable. Interested students must apply for admission and scholarship online at the Australian National University.

Successful applicants will receive scholarship stipend, tuition fee waiver, and research funds including computer and travel grants.

Location: We're based in the Division of Ecology & Evolution in the Research School of Biology, Australian National University, Canberra, Australia. The facilities and intellectual environment are outstanding and the Nicotra and Kruuk labs are lively, hard-working and inquisitive places. We strive to do excellent, fundamental research that is relevant in the context of rapid global change.

Application deadline: Applications for international students are due by August 31 and for Australian citizens and permanent residents or New Zealand citizens are due October 31, for an early 2018 start.

To apply, please contact Adrienne.Nicotra@anu.edu.au or Loeske.Kruuk@anu.edu.au, including a CV, a brief letter outlining your research interests, and details of two academic referees. For further information on ANU scholarships, go here: <http://biology.anu.edu.au/-education/degree-programs#ees> and click the 'Higher Degree by Research' button.

Professor Adrienne Nicotra Division of Ecology & Evolution Research School of Biology The Australian National University Canberra, ACT 2601, Australia www.biology.anu.edu.au/Adrienne_Nicotra Loeske Kruuk <loeske.kruuk@anu.edu.au>

AustralianNatIU InsectGenomes

A molecular view of Australian biodiversity - exploring insect genomes for major shifts in functional genes

Use CSIRO's collection resources in combination with DNA barcodes, Whole Genome Shotgun sequences and 600 recently sequenced transcriptomes to build the tree of life for selected Australian insect groups, exploring genomes for functional genes within this evolutionary context.

With over 1 million named and many more undescribed species, insects provide more than 80% of the biodiversity of life on earth. Insects have adapted to almost every terrestrial habitat on the planet, which is reflected by their vast morphological diversity. Far less well studied, yet even greater and crucial for adaptation, is their diversity at the molecular level.

New DNA sequence data are generated worldwide at an unprecedented scale, and exploring their diversity

in the context of an evolutionary framework could help answer many important questions: - How did the great diversity of insects evolve in Australia? - Are shifts in insect biology correlated with major changes in genomes, e.g., changes from host specialists to generalists with the expansion of gene families? - Can we use genomic information to predict the potential of a species to develop into a pest? - How many new species are probably hidden in our collection and still await discovery?

The Australian National Insect Collection (ANIC) is home to 12 million specimens and is the by far largest repository of Australia's biodiversity. As part of CSIRO's Environomics Future Science Platform, the ANIC has started to generate low coverage whole genome sequence data for selected groups for the purpose of species identification and discovery. This will be feasible in a high-throughput fashion due to robotics and cutting-edge technology like Acoustic Liquid Handling in our lab.

You will be part of a collaborative team at CSIRO and ANU (Research School of Biology) and have access to our lab infrastructure, supercomputers, collection and molecular data, which will include unpublished low coverage whole genome shotgun (WGS) data for several thousand species, unpublished transcriptomes of 600 species and published data (e.g. 1,000 transcriptomes of 1KITE). By combining and analysing these data phylogenetically, you will reconstruct branches of the Australian 'Tree of Life'. Based on this tree, you will have the opportunity to explore transcriptomes and genomes for major changes in functional genes. To follow promising leads, you will also generate your own genome and transcriptome data as needed.

Supervisors: - Andreas Zwick, Australian National Insect Collection, CSIRO (Andreas.Zwick@csiro.au)
- Craig Moritz, Research School of Biology, ANU (craig.moritz@anu.edu.au)

For more information see: <http://cba.anu.edu.au/-opportunities/student-research/projects-opportunities/csiro-insect-collection-postgraduate>

Claire Stephens <claire.stephens@anu.edu.au>

Berlin EvolutionOfVirulence

Reminder of the recently advertised PhD position (application deadline: 22.08.17):

The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) is the largest freshwater ecology research institute in Germany. It is a member of the Forschungsverbund Berlin e.V. and the Leibniz-Association (www.wgl.de). The FVB manages 8 large research institutes in Berlin that have close links to all three universities in the German capital. IGB offers excellent laboratory and field facilities for interdisciplinary research, large-scale experimental facilities, and long-term research programs and data sets.

IGB invites applications for a

PhD position in Evolutionary Biology: "The Evolution of Virulence under Conditions of Frequent Multiple Infections"

The position is available from 1st January 2018 (or November/December 2017) and limited to 3 years.

— Project Description

Interactions between multiple parasite species (infecting the same host) can affect the evolutionary trajectory of virulence, with important ecological and epidemiological consequences. The goal of the proposed work is to elucidate implications of multiple infections on the evolution of (parasite) virulence. The successful candidate will use a combination of experimental evolution and field approaches to generate new and refined predictions regarding the virulence of parasites that spread into new habitats, where they encounter co-infecting parasites. He/she will use a model system consisting of the crustacean *Daphnia* and their microparasites. The proposed research is a collaboration between German and Israeli scientific teams: Prof. Justyna Wolinska from IGB and Freie Universität Berlin (<http://www.igb-berlin.de/en/profile/justyna-wolinska>) and Dr. Frida Ben-Ami from Tel Aviv University (<http://fridaslab.weebly.com/>), financed by the German Science Foundation (DFG). The position is mainly based in Berlin; however, a two-month research stay at the Tel Aviv University is planned. Funding for attending national/international conferences is available.

— Duties and responsibilities

— * laboratory experiments * field work (investigating

geographical patterns of co-infections) * advance statistical analyses of experimental (life history and genomic) and field (environmental and genetic) data

— Requirements

— * MSc degree in biology, bioinformatics or related field * strong background in evolutionary biology, population genetics or ecology * hands-on experience with experimental work * experience in molecular or genomic research would be an advantage * excellent analytical skills and very good knowledge in statistics * a basic knowledge in bioinformatics or programming would be advantageous * excellent communication and writing skills in English * good work ethic * creative thinking

Salary is paid according to the TVöD (65% position). In keeping with the IGB's policy regarding gender equality, female applicants are particularly encouraged. Severely disabled applicants with equal qualification and aptitude are given preferential consideration.

Enquiries or questions should be directed to Prof. Justyna Wolinska (wolinska@igb-berlin.de).

— Please upload complete application documents as a single pdf-file including CV, a letter of motivation, copies of relevant degrees and contact details of three referees no later than 22nd August 2017 via the IGB's (<http://www.igb-berlin.de/en/jobs>) online job-application facility (button "Apply online").

Justyna Wolinska

Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) Mueggelseedamm 301 12587 Berlin, Germany

Group Leader at the IGB & Professor for Aquatic Evolutionary Ecology at the Free University of Berlin

Phone: +49 (0)30 64181 686; Fax: +49 (0)30 64181 682; email: wolinska@igb-berlin.de

<http://www.igb-berlin.de/en/profile/justyna-wolinska-0>
<http://www.igb-berlin.de/en/disease-evolutionary-ecology> Justyna Wolinska <wolinska@igb-berlin.de>

Bialowieza Poland BisonDiseaseEvolution

Mammal Research Institute of the Polish Academy of Sciences in Białowieża seeks for a PhD student in a grant

“ Genetic background of a lethal posthitis disease in the

European bison males

Project Leader: Małgorzata Tokarska, PhD. Eng.

Requirements:

1. MSc degree in biology, evolutionary biology, molecular biology or related fields
2. good experience with standard molecular biology techniques
- 3 at least basic experience with any biostatistical softwares
4. team cooperation skills
5. fluent spoken and written English;
6. enjoyment from conducting the scientific studies and presenting the results;

Required documents:

1. CV
2. Information on the candidate's scientific experience (specialization, research techniques, and achievements (including list of publications and reports) (max. 500 words)
3. An opinion from the academic tutor or/and previous scientific employer

Conditions of employment: 30 month PhD student scholarship of 3000 PLN netto

The summary and objectives of the project

Posthitis (necrotic inflammation of the prepuce) is a severe disease of the European bison, which affects approx. 6 % of males a year. The disease is incurable and the affected animals are usually eliminated or otherwise the disease leads to penis autoamputation and death. The etiology of posthitis is unknown but recent studies on European bison using cattle tools indicated significant associations between certain cattle markers and the occurrence of the disease. A study by Oleński et al. (2015) has shown the existence of genetic background of posthitis in the European bison but the cross - species character of their study did not allow to either indicate the genes and their variants involved in the disease or explain the mechanism if its inheritance.

Sequence - Based Genotyping (SBG) technique will allow to achieve an extensive amount of species-specific data from the whole genome. European bison specific markers will undergo genome wide association analysis (GWAS) to identify markers, regions of chromosomes and genes and their variants affecting susceptibility bison on posthitis. The results will enable to design simple genetic tests of the 20 - 30 most informative SNP markers detected. These tests will allow rapid and reliable

genotyping of bison susceptibility to posthitis and the carriers of unfavourable genetic variants.

The aims of the project are:

1. identification of the species specific SNPs (single nucleotide polymorphisms markers) associated with posthitis in the European bison
2. indication the genes and their variants, underlying the development of posthitis in the European bison,
3. developing the model of the disease inheritance,
4. verification of the potential role of the Y chromosome in the pathogenic process,
5. designing informative and cost-effective SNP -chip based genetic test that allows verification of susceptibility to posthitis as well as carriers of unfavorable variants

We provide:

1. participation in an interesting scientific project;
2. work in a friendly research team, in a well-equipped and organized biological laboratory with a support and supervision of competent colleagues;
3. the possibility of effective scientific development through cooperation with the best world research centres in the world;
4. possibility of extension the scholarship for subsequent 2 years;
5. possibility of additional funding through participation in other research projects;
6. the possibility to apply for a cheap accommodation in MRI PAS flats - at least temporal stay in BiaÅowieÅa during the project is required.

Candidates will be evaluated by a commission at the Mammal Research Institute Polish Academy of Sciences in BiaÅowieÅa. After a preliminary assessment of the submitted documents, the candidates will be invited for an interview.

Applications should be sent directly to the Project Leader by letter or electronically by August 30th 2017. The candidates will be invited to an interview and the decision will be announced by August 31th 2017.

Contact: - MaÅgorzata Tokarska PhD - posthitis project leader

Mammal Research Institute Polish Academy of Sciences
ul. Waszkiewiczza 1

17-230 BiaÅowieÅa, Poland

e-mail: tokarska@ibs.bialowieza.pl; phone +48 85 682-

77-61

tokarska <tokarska@ibs.bialowieza.pl>

Budapest Evolutionary Genomics

Budapest.EvolutionaryGenomics

Fully funded PhD position in evolutionary genomics is available to join the ERC 'GENECLOCKS' project (http://cordis.europa.eu/project/rcn/207593_en.html) headed by Gergely Szollosi (<http://solo.web.elte.hu>). The position is offered for 3 years with the possibility of extension of one year. The position comes with a salary of EUR 15,000 per year, as well as a travel and research funds.

We are looking for an individual who is highly motivated and is excited by the possibility of pursuing a PhD in Evolutionary Biology with a strong quantitative focus. A M.Sc. providing a strong quantitative background, such as physics, mathematics or computer science, is essential as well as experience with data analysis (e.g. in R) and/or computer programming.

A central theme of GENECLOCKS is disclosing new sources of information for dating the first three-quarters of Earth's evolutionary history that are independent from both fossils and molecular clocks. Life's early history has remained terra incognita until now, because the fossils needed to calibrate standard evolutionary timescales are simply not available for microbial life. Microbial fossils are scarce and difficult to interpret in a phylogenetic context with confidence. In previous work we have shown that patterns of lateral gene transfer inferred from modern genomes encode a record of co-existing lineages throughout the history of life, and that we can use this record to reconstruct the relative ages of microbial groups from the three domains of life in deep time.

This discovery is a game changer for anyone interested in the history of life, from either a geological or genomic perspective. It demonstrates the existence of a new and abundant source of dating information that is inscribed in the genome of any organism, provided a gene transfer occurred in its ancestry. This constitutes the overwhelming majority of the diversity of life.

The PhD student will develop with, and undertake a project under the supervision of Dr. Gergely Szollosi and will have the possibility to work together with and visit international collaborators (in Lyon, Bristol and

the KTH in Stockholm).

To be considered, please send a single merged PDF to ssolo@elte.hu that contains your CV including, academic transcripts, a statement of research interests (3 pages or less) as well as three academic references. Please include 'GENECLOCKS_PHD' in the subject of your email.

The GENECLOCKS research group is lead by Dr. Gergely Szollosi (<https://scholar.google.hu/citations?user=3DsPrYT-oAAAAJ>) and is hosted at Eotvos Universities Institute of Physics in Budapest. The Institute of Physics has been included in the Excellence Group of European Universities, and has achieved top placement in the number of citations, the number of ERC grants, the time available for PhD research and the gender balance of master's students in the CHE Excellence Ranking. Budapest is a vibrant capital city with exciting cultural life, a unique atmosphere and affordable living costs (cf. <https://goo.gl/86II3s>).

Please direct any enquiries to Dr. Gergely Szollosi (ssolo@elte.hu, <http://ssolo.web.elte.hu>).

sszolo@gmail.com

CIBIO Portugal Biodiversity

Master Fellowship

Reference: ICETA 2017-31

Link to the call <http://www.eracareers.pt/-opportunities/index.aspx?task=global&jobId=92692>

A Master Fellowship (BI) (Reference ICETA 2017-31) in the exploratory project IF/00641/2014/CP1256/CT0008 "EVOLVING BIODIVERSITY - USING EVOLUTIONARY THEORY TO UNDERSTAND WHAT MAKES THE MEDITERRANEAN ONE OF THE WORLD'S RICHEST HOTSPOTS" is available at CIBIO/ICETA, Instituto de Ciencias, Tecnologias e Agroambiente da Universidade do Porto, funded by the Fundacao para a Ciencia e a Tecnologia, I.P., (FCT/MCTES).

Eligibility Requirements:

Candidates must hold an MSc degree, but not a degree higher than MSc, in areas compatible with the work plan, i.e. Biological Sciences, and have experience in analyses of phylogenetic inference. We seek candidates with i) a solid background in procedures for

phylogenetic inference and related software, including e.g. accessing public databases to download sequence data, sequence handling and alignment, evolutionary model comparison, phylogenetic inference in a ML and Bayesian framework, phylogeny dating; ii) experience with the model organisms, i.e. mainly reptiles, but also amphibians, preferably from the Mediterranean region; iii) good verbal and written communication skills in English; vi) good communication and teamwork skills. The candidate's Curriculum Vitae must be compatible with the work plan. Candidates at the first stages of their academic career, with motivation for possibly following up on the research of the project in the future will be preferred.

Work plan:

The project investigates the ecological and evolutionary processes involved in shaping the Mediterranean Basin as one of the world's richest biodiversity hotspots, using amphibians and reptiles as a model system. This will be done by combining phenotypic data to phylogenetic hypotheses about each group of interest to test hypotheses on the evolutionary processes driving diversification of circum-Mediterranean herp taxa. The work of the fellowship holder will be to infer phylogenies for various groups of amphibians and reptiles based on published sequence data. For this purpose, the grant holder will need to conduct a bibliographic search on available publications, access public databases to download the necessary data, and conduct all analyses of phylogenetic inference. The grant-holder must be available for travelling to the MNCN, Madrid, Spain, in order to discuss the analyses with a member of the project team (Dr. Martane-Solano).

Applicable Legislation:

A bolsa e atribuada ao abrigo da Lei no40/2004, de 18 de Agosto (Estatuto do Bolseiro de Investigacao Cientfica) e Regulamento de Bolsas e Investigacao da Fundacao para a Ciencia e a Tecnologia em vigor <http://www.fct.pt/apoios/bolsas/docs/-RegulamentoBolsasFCT2015.pdf> .

Workplace:

The work will be conducted at CIBIOInBIO, UP - Centro de Investigacao em Biodiversidade e Recursos Geneticos, Universidade do Porto, Campus de Vairao, Rua Padre Armando Quintas, 7, 4485-661 Vairao.

Duration of the fellowship:

The fellowship will have a duration of 3 months, potentially renewable for an additional period of 3 months, starting on October 1st 2017.

Monthly stipend:

Monthly stipend is euro980 according to the stipends established by FCT, I.P. in Portugal (<http://alfa.fct.mctes.pt/apoios/bolsas/valores>). Payment will be made by bank transfer on a monthly basis. The successful candidate will also be entitled to the reimbursement of Social Security payments (Seguro Social Voluntario) and work insurance.

Selection criteria:

Evaluation of applications will be done according to the required competences and will be based on: a) specific past experience in tasks described in the work plan (40%); b) the quality of the scientific and academic curriculum vitae (30%); c) motivation letter, including motivation for following up on the project (30%). The jury may not award the fellowship if the quality of the candidates is less than desired.

Jury composition:

Antigoni Kaliontzopoulou (Chair), Fernando MartÃ­nez-FreirÃ­a (vowel), Inigo MartÃ­nez-Solano (vowel) and Ana Perera (substitute vowel).

Publicity and communication of results:

The ranking of applications will be published at a visible and public area of ICETA facilities, and all candidates will be informed by email about the result of their application.

Application:

The call for applications is open between 17 August 2017 and 3 September 2017 (24:00 GMT).

Applications should be submitted in Portuguese or English by email to bolsas@iceta.up.pt with the fellowship reference in the subject area, and the following documents attached: a) Curriculum vitae (including academic training and professional

— / —

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>

FUBerlin EcoEvoInsectImmunity

Freie Universitat Berlin, Institute of Biology

2 PhD positions: eco-evo-immunology of *Drosophila* bacteria interactions

Application deadline: 18th September 2017

Applications are invited for 2 PhD positions at the Freie Universitat (FU) Berlin, Institute of Biology. The positions are funded by the German Research Foundation (DFG). The principle investigator is Dr. Sophie Armitage (<https://www.uni-muenster.de/Evolution/-animalevolecol/armitage.shtml>), who will start a DFG Heisenberg Fellowship at the FU on the 1st October 2017. The PhD positions will start on the 1st December 2017, or as soon as possible thereafter. The group will collaborate with the evolutionary biology group of Prof. Jens Rolff (http://www.bcp.fu-berlin.de/en/biologie/-arbeitsgruppen/zoologie/ag_rolff/index.html). The projects are for three years each and the salary is according to the scale for public servants (TV-L E13/65%). The working language of the group is English.

Project background: Our research lies in the field of eco-evo-immunology, with a focus on host resistance and tolerance. Pathogens can have substantial negative fitness effects on their hosts. This creates a strong selection pressure on a host to have efficient immune defences. A host can counteract an infection by directly reducing its pathogen load, i.e., resistance, or by reducing the harm that the infection does to its fitness, i.e., tolerance. Given that resistance can be costly and involve autoimmune damage, a more resistant host is not always the fittest. Tolerance is therefore an interesting concept because it describes how well hosts are able to ameliorate the fitness costs of a given pathogen load. Resistance and tolerance are predicted to give contrasting perspectives on host-pathogen evolution and infectious diseases, therefore it is important to understand infection in the light of these two concepts.

The first PhD project will utilise experimental evolution to understand more about the evolution of resistance and tolerance strategies. Previous pathogen experience, so-called priming in invertebrates, can increase host survival when it is subsequently infected with the same pathogen, and is likely to be a significant route to immune defence. The second PhD project will thereby ask how previous pathogen experience affects tolerance and resistance.

Drosophila melanogaster will be used as the host, and different bacterial species will be used as pathogens. The projects will include fitness and resistance assays as well as molecular work (depending upon the project).

Requirements: Master's degree in biology, evolutionary biology or related fields.

Desirable: We would like applications from enthusiastic and highly motivated students with a background / interest in evolutionary ecology. The candidates should

have good communication skills and be happy to work independently as well as in a team, and be able to write proficiently in English. Knowledge of statistics would be a plus.

How to apply: Applications should be written in English, emailed as a single PDF file and include: (1) a cover letter with a short statement of motivation, (2) a CV including details of your research experience and any publications, and (3) the names of 2-3 potential referees. Please indicate in your cover letter whether you have a particular preference for one of the two projects, or whether both are potentially interesting. Please email your application no later than 18th September 2017 to sophie.armitage@uni-muenster.de, with the header “eco-evo PhD”.

For further information, please don't hesitate to email Sophie Armitage.

“sophie.armitage@uni-muenster.de”
<sophie.armitage@uni-muenster.de>

ICETA Portugal Conservation Genetics

Research Fellowship MSc

Reference: ICETA 2017-27

Link to the call <http://www.eracareers.pt/-opportunities/index.aspx?task=global&jobId=92490>
Scientific Area: Biological sciences

A Research Fellowship (BI) (Reference ICETA 2017-27) is now available in the area of conservation genetics, framed within the project PTDC/AAG-REC/6480/2014/ “ECOLIVES - Fostering sustainable management in Mediterranean olive farms: pest control services provided by wild species as incentives for biodiversity conservation” at ICETA-Instituto de Ciências e Tecnologias Agrárias e Agro-Alimentares, financed by national funds by FCT / MCTES and co-financed by Fundo Europeu de Desenvolvimento Regional (FEDER) throughout COMPETE - Programa Operacional Factores de Competitividade (POFC), in institution ICETA.

Admission requirements:

Candidates should hold a MSc. degree in Biology or related fields and should have a solid experience in molecular biology and metabarcoding analysis.

The candidates should demonstrate experience in: (i) molecular biology techniques, including DNA extraction from non-invasive DNA samples and DNA sequencing (with both Sanger and Next Generation Sequencing techniques); (ii) metabarcoding analysis; and (iii) management of databases and biological collections. High motivation, communication and team work skills, as well as fluency in English (spoken and written) will be highly valued.

Work plan:

The work plan is included in a project which investigates the value of natural biological control of the Olive fruit fly (*Bactrocera oleae*) and the Olive fruit moth (*Prays oleae*) ?the two major pests in olive farms worldwide ?, in farms following distinct pest management strategies. The project will particularly focus on the role of flying vertebrates (including both bats and insectivorous birds) biocontrol agents and will be carried out throughout the region of Alentejo, one of the main olive production region in Europe.

The candidate will be involved in several tasks: (i) DNA extraction of tissue and non-invasive DNA samples; (ii) amplification and sequencing of several molecular markers using both Sanger sequencing and Next Generation Sequencing techniques; (iii) barcoding of parasitoids and other organism of small size; (v) screening of larvae for the presence of parasitoids (vi) management of databases and biological collections. The successful candidate is expected to collaborate in writing technical reports and scientific publications.

Legislation and regulations:

The fellowship stipend will be euro980/month, according to the regulations of the FCT Postdoctoral Fellowships in Portugal (<http://alfa.fct.mctes.pt/apoios/-bolsas/valores>), the payment will be do monthly by bank transfer.

Workplace:

The work will be carried out at CIBIO - Research Centre for Biodiversity and Genetic Resources, Vairao, Portugal, under the scientific supervision of Doutor Pedro Beja.

Grant duration:

The fellowship will be awarded for a period of 12 months, potentially renewable for an additional period, up to a maximum duration of 24 months; expected to start in the 15th of September 2017.

Selection methods:

The ranking of candidates will be performed by a global evaluation based on the CV (40%), previous experience

of the applicant relevant to the project and work-plan (40%) and motivation letter (20%). If necessary, an interview with a shortlist of candidates may be performed. The jury may not award the fellowship if the expected quality and requirements of candidates are not fulfilled.

Composition of the Selection Panel:

Dr. Pedro Beja (Chair), Dr. Simon Jarman (Vowel), Dr. Bastian Egeter (Vowel), Dr. Mafalda Galhardo (Substitute Vowel).

Form of advertising/notification of results:

The final evaluation results will be published and the winning candidate will be notified by e-mail or telephone.

Deadline for application and presentation of applications:

The application period will be from the 8th August to 22th August 2017. Applications must be formalized by email to bolsas@iceta.up.pt together with the following documents:

- i. Curriculum vitae;
- ii. A motivation letter, including a brief description of the research experience and why the candidate is suitable for the position;
- iii. Degree certificates and other documents considered relevant to the application.

Applications must be submitted via email to bolsas@iceta.up.pt, containing in the subject the reference to which the candidate is applying (Reference ICETA 2017-27), under penalty of exclusion of the candidature.

Sem vÃrus. www.avast.com CIBIO-InBIO Divulgaçã

IGB Berlin FunctionalGenomics

PhD position in Functional genomics for aquaculture - growth, sex determination and disease resistance

at the Leibniz-Institute of Freshwater Ecology and Inland Fisheries (www.igb-berlin.de)

Since 1996, the IGB has been committed to research on sturgeon aquaculture, remediation and restoration, including several national and international projects and programmes.

Within EU ERA-Net, the COFASP project STURGEONOMICS involves France, Romania, and Germany (here subject to final approval of the Federal Office for Agri-

culture and Food, BLE).

At the IGB, the Research Group Applied Fish Physiology and Aquaculture, led by Dr. Sven Wurtz, is looking for a hard-working, enthusiastic

PhD student: Functional genomics for aquaculture - growth, sex determination and disease resistance, from now on for a 3 year period

Within STURGEONOMICS, whole genome-based approaches will be explored to improve sturgeon aquaculture, working on two species of sturgeon. The PhD candidate will experimentally extract candidate genes related to target traits (growth, disease resistance, sex determination) for an optimization of management strategies as well as breeding. During the project the candidate will be able to work collaboratively on high quality genome information and transcriptomics to determine the genetic basis of variability in disease resistance and growth during early development as well as sex determination and early sex differentiation. This work is an essential prerequisite for future selective breeding in order to improve rearing in aquaculture (aiming at maximized growth and disease resistance, as well as early determination of sex and subsequent selection of females for caviar production). The candidate will spend up to 6 months in the facilities of the other partners, which will enhance multidisciplinary training of the student, and give him/her important experience of both academic and non-academic sectors (sturgeon farming).

Applicants should have a 2.1 degree or equivalent in a relevant life science (bioinformatics, molecular biology, fisheries sciences, aquaculture). Excellent communication skills in English are required. Experience with molecular techniques (e.g. genome and transcriptome analysis, next generation sequencing) and fish rearing is highly preferred. Candidates with a background in aquaculture will be deemed highly competitive.

Salary will be according to TVoD (50%). In keeping with the IGB's policy regarding gender equity, female applicants are particularly encouraged. Among candidates of equal aptitude and qualifications, a person with disabilities will be given preference. This position is subject to approval of the responsible funding body (Federal Office for Agriculture and Food, BLE). Review of applications meeting the required standards will start immediately and continue until a candidate is appointed.

Please send your application and further inquiries to work leader Dr. Sven Wurtz (wurtz@igb-berlin.de), and project coordinator Dr. Matthias Stock (matthias.stoeck@igb-berlin.de).

Deadline 31. August 2017 Leibniz-Institut für

Gewässerökologie und Binnenfischerei im Forschungsverbund Berlin e.V., Muggelseedamm 301 D-12587 Berlin
The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (www.igb-berlin.de) is the largest research institute for freshwater research in Germany. It is member of the Leibniz Association and the Forschungsverbund Berlin e.V. IGB has close links to all three universities in the German capital and currently hosts about 50 doctoral students from approximately 15 different nations.

Matthias Stoeck <matthias.stoeck@igb-berlin.de>

JagiellonianU EvolutionaryPhysio

The Evolutionary Physiology Team
of the Institute of Environmental Sciences
of the Jagiellonian University
offers a PhD-student position and stipend

We are seeking for a highly motivated PhD student for a project entitled:

Experimental model of holobiont evolution: gut bacterial symbionts in bank voles selected for increased herbivorous capability

(a part of NCN OPUS project Experimental evolution of physiological and behavioral adaptations in the bank vole: molecular background and alimentary system bacterial symbionts).

Requirements

1. MSc in life science (biology, ecology, evolution, zoology or related);
2. interest in ecological physiology or microbiology and evolutionary biology;
3. an experience in working with terrestrial vertebrate animals (preferably rodents);
4. an experience in molecular or biochemical laboratory;
5. analytical thinking, creativity and high motivation in learning new methods;
6. good communication skills,
7. good level of spoken and written English,
8. admission in a PhD study program at the Institute of Environmental Sciences JU.

Task description

Symbiotic evolution played an important role at all stages of evolution of diverse life strategies. According to the “hologenome” concept, natural selection acts on the holobiont (host and associated microbes) rather than on animals alone. A unique opportunity to test the concept is offered by our artificial selection experiment on bank voles (*Myodes glareolus*). We observed that voles from lines selected for improved “herbivorous capability” had an altered composition of gut bacterial symbionts, even if the particular individuals had no contact with the special diet. We ask whether a) the difference in gut bacteria composition occurred in response to the short change of diet in parents, and was merely transmitted to offspring or b) the selected voles evolved genetically-based modifications allowing preferable hosting a modified bacterial community. The project consists of two main stages: 1) experiments on the voles (manipulation of diet, cross-fostering, measuring physiological traits and the size of internal organs, and collecting gut contents samples), and 2) molecular analyses of bacterial DNA in the samples, leading to description of the bacterial community and statistical analyses of its composition.

Deadline for application 31 August 2017, by e-mail

Conditions of employment: A scholarship for 36 months of 3000 PLN / month funded by the National Science Centre plus additional scholarships that can be obtained within the JU PhD programs.

The recruitment and enrollment consists of three steps:

1) The applicant should send CV (academic achievements included, 2 page maximum) and a cover letter in English (deadline: 31 August 2017). The letter should

- a) explain the applicant’s interest in the topic,
- b) provide the names and email addresses of two people with first-hand knowledge of the applicants skills and past research experience,

c) contain the following statement: “I hereby give consent for my personal data included in my offer to be processed for the purposes of recruitment, in accordance with the Personal Data Protection Act dated August, 29,1997 (uniform text: Journal of Laws of the Republic of Poland 2014 item 1182 with further amendments)”.

Send the complete application in a single pdf file to the principal investigator, Paweł Koteja: pawel.koteja@uj.edu.pl.

2) Enrollment for one of the PhD programs at the Institute of Environmental Sciences at Jagiellonian University:

- preferred: PhD Program in Biology in English (http://www.binoz.uj.edu.pl/studia/phd_biology/about-the-

studies; registration: https://www.erk.uj.edu.pl/-studia/karta/studia_id/4097/tryb_ubiegania/s/nr_naboru/1)

- acceptable: a standard PhD program (http://www.binoz.uj.edu.pl/dydaktyka/studia-doktoranckie-biologia/o-st_udiach); registration: <https://www.erk.uj.edu.pl/studia/3787/1/s>).

The registration through the OAS system ends at 6th September 2017 and the entrance exam will be between 13 and 20 September 2017.

3) From among the candidates accepted as PhD students at Institute of Environmental Sciences JU, the beneficiary will be chosen based on regulations about scientific scholarships for young researchers in research projects financed by the National Science Centre, Poland (<https://www.ncn.gov.pl/finansowanie-nauki/-koszty-w-projektach/stypendi>)

— / —

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>

LaurentianU Canada WolfCoyoteEvolution

M.Sc. opportunity-Evolution of wolf/coyote morphology throughout North America-contact Dr. Frank F. Mallory (fmallory@laurentian.ca)

Frank Mallory <fmallory@laurentian.ca>

MaxPlanck Germany 2 AvianCulturalEvolutionEcol

We are seeking two PhD students to join an exciting new research group studying the ecology and evolution of animal culture (supervisor: Dr Lucy Aplin), based at the Max Planck Institute for Ornithology, in Radolfzell, Germany. The PhD positions are 3.5 years fully funded with a competitive stipend, and open for applicants from any nationality.

Background:

Traditional views of Darwinian evolution focus on selection acting on genetically underpinned variation as a means of adaptation. However this may neglect the potential contribution of the over-generation transmission of information (cultural inheritance) as a source of locally adaptive behaviour - this might be particularly important in long-lived species and when facing novel or changing environments. For example, the capacity for innovation, social learning and cultural inheritance is thought to be vitally important in the success of humans as a species, facilitating our colonization of almost every terrestrial habitat on Earth. But has the cultural transmission and inheritance of behaviour been similarly important in the success of some other species? We investigate these questions using a combination of laboratory experiments and field studies in birds, utilizing state-of-the-art automated tracking technologies and analytical techniques.

Project 1: “Laboratory Experiments of Cultural Evolution”

How are the emergence, establishment and persistence of cultural behaviours influenced by social and environmental conditions? Can culture evolve over time, and if so, is this process ‘Darwinian’? We will test the link between cognition, social structure and emergent cultural phenomenon in large-scale laboratory experiments similar to ‘experimental evolution’ studies, with the longitudinal observation of groups of captive birds in a large aviary complex on site. The project will involve some local fieldwork with wild tits (*Parus major*), as well as captive work with small parrots.

Project 2: “Cultural Ecology in Urban Parrots”

Can social learning and the cultural inheritance of information be a source of behavioural flexibility to novel environments? This project will investigate this question in sulphur-crested cockatoos, *Cacatua galerita*. Sulphur-crested cockatoos have repeatedly colonized urban areas, both within their native range and as an invasive species. They are also highly social and relatively long-lived, with an extensive repertoire of vocalizations and foraging behaviours. In this project, our group will use a combination of citizen-science, GPS tracking technologies, field observations and experiments to a) describe the social ecology of this species, 2) test socio-cognitive mechanisms for urban adaptation, and 3) make within and between population comparisons in foraging and vocal behaviours to identify potential cases of ‘wild cultures’. This project will involve fieldwork in Australia, and is co-supervised by Dr. John Martin at the Royal Botanic Gardens, Sydney, Australia, in collaboration with the Australian Museum. Position Details: Suit-

able applicants should have a Masters Degree or 1st Class Honours Degree in Zoology, Ecology, or related subjects. Applicants with a background in computer science, physics, or engineering but who have demonstrated an interest in biology, are also encouraged to apply. Demonstrated experience of independent research is highly desirable. The working language in the group is English, and candidates should have proficiency in both written and spoken English. No German language skills are required. We are an inclusive and diverse group, and encourage applications from women and all under-represented minorities.

Location:

The lab is based at the world-leading Max Planck for Ornithology (MPIO), in Radolfzell, Germany: http://www.orn.mpg.de/3190/Location_Radolfzell. It is planned that the students will join the International Max Planck Research School (IMPRS) for Organismal Biology - a cooperative doctoral program between the Max Planck Institute for Ornithology and the University of Konstanz. As part of their degree, IMPRS fellows can attend a range of optional modules, e.g. programming and writing courses, and participate in a curriculum that involves more than 30 leading researchers from across 4 MPIO departments and the Department of Biology at Uni. Konstanz. The official teaching language is English. Website: http://www.orn.mpg.de/2453/Short_portrait. More broadly, the Bodensee area is fantastic place to live, with numerous outdoor activities including hiking, cycling and sailing, and with easy access to Zurich. The Institute and University have extensive facilities and support for new and international students and their families.

Application Process:

Interested applicants should send a short summary of their research

— / —

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>

MonashU
EvolutionaryEcologyDisease

Two fully-funded PhD position are available to work in the Hall group (see mattdhall.com) on themes broadly

related to evolutionary ecology, health, and fitness. Using species of *Daphnia* and their associated pathogens as a powerful experimental model, the successful candidates will work closely with Matt and his collaborators to develop projects that explore any one of the following eco-evolutionary processes.

1) Sexual antagonism and the evolution of health and fitness. Exploring how new mutations arise and influence different aspects of an organism's health. Can blend together both theory and empirical approaches to exploring genetic architecture as interests dictate (together with Tim Connallon at Monash, <http://timconnallon.com/>).

2) Energy flux and the spread of disease. The rate at which organisms use, transform, and expend energy defines not only an organism's "pace of life", but also how readily that can be exploited by a pathogen. Advances in high-throughput metabolic assays offer opportunities to incorporate energy flux into studies of host-pathogen co-evolution (together with Dustin Marshall and the Centre for Geometric Biology at Monash, <https://cgb.org.au/>).

3) Demography and host-pathogen interactions. Populations are rarely stable and different densities or growth trajectories can feed back into the spread of disease within and between patches. Experimental mesocosms offer opportunities to explore infectious disease in light of different demographic dynamics (Together with Ben Phillips at the University of Melbourne, <https://blphillipsresearch.wordpress.com/>).

A stipend (living-allowance) scholarship of ~\$26,288 per annum is provided tax free (the equivalent of approx. \$33,000 before tax) with no teaching requirements for 3.5 years (the length of a PhD in Australia). We also offer travel and establishment allowances to help in your move and our tuition scholarships cover the cost of tuition fees (normally \$38,900 per year). Guaranteed funding of project costs and research support, including the costs of attending at least one conference per year, is included.

Project start dates can be any time in late 2017 or early 2018 onwards.

To be eligible, applicants must have completed a 4 year degree with a research component or have post-graduate research experience in ecology, genetics, behaviour, or evolution (or will do so by the end of the year). Preference will be given to those with strong quantitative skills and publications in international journals. Interested students should send a CV and a brief statement of interests to Matt via matthew.hall@monash.edu.

Regards,

Matt

– Dr. Matthew D. Hall School of Biological Sciences,
G30D, 18 Innovation Walk Monash University, Clayton
Campus, Victoria, 3800, Australia

www.mattdhall.com Email: matthew.hall@monash.edu
Phone: +61 3 9905 5793 Mobile: +61 478 399 592
twitter: @mattd_hall

“matthew.hall@monash.edu”
<matthew.hall@monash.edu>

MPIO Seewiesen Evolution Cognition

Announcement

PARROT COGNITION (TENERIFE)

MASTER PROJECTS / VOLUNTEER RESEARCH
ASSISTANTS

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

The Max-Planck Comparative Cognition Research Group (CCRG) invites applications of Masters students and volunteer research assistants. The CCRG forms part of the collaboration between the Max-Planck Institute for Ornithology, Seewiesen, Germany, and the Loro Parque Fundación (LPF), Tenerife, Spain. We are currently running various comparative research projects on social and physical cognition in parrots. Interested candidates are encouraged to contact us to enquire about the ongoing projects. Successful applicants can expect to gain a solid insight in the field of Animal Cognition/Experimental Psychology and gain experience in working with psittacids in a dynamic, international research environment. The research is carried out on captive parrots of the LPF, which holds the largest parrot collection and gene reserve in the world (ca. 350 subspecies) for conservation and research purposes.

Logistics:

Voluntary research assistant position /Master Project start and end dates are flexible but preference will be given to students who can start in October/November 2017. The position requires a minimum of 4 months, but ideally 6 months, continuous commitment at the research station in Tenerife, Spain. Free accommodation in a shared student apartment can be provided.

Successful applicants will be responsible for their own transportation expenses to and from the research station (Puerto de la Cruz, Tenerife, Spain).

Important skills/qualifications:

Successful candidates will have:

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

To apply:

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

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

Museum Bonn Germany 2 Ricefish

There is an exciting opportunity for talented, motivated and independent applicants to join the Ricefish project at the Zoological Research Museum Koenig (ZFMK) in Bonn, Germany. The Project is associated with the Ichthyology section and the Centre for Molecular Biodiversity Research (zmb) of the ZFMK and funded by the Leibniz Association. The main focus is to connect state of the art morphological with genomic research to understand complex adaptive traits, here a unique breeding strategy in Sulawesi Ricefishes (Actinopterygii: Adrianchthyidae), called pelvic brooding. The study will integrate state-of-the-art morphological and genomic methods as well as fieldwork in Sulawesi (Indonesia) and will give applicants the possibility to participate in each part of the project and gain experience in a young team of researchers.

In Ricefishes from Sulawesi (Indonesia) a new mode of reproduction evolved at least twice in independent lineages. In pelvic brooding species, females carry the eggs in an abdominal concavity until they hatch. Studying pelvic brooding from different angles will help to gain a holistic understanding of the evolution of this adaptive

trait. Ricefishes are an ideal model to study adaptive genomics as phenotypic changes can be compared in parallel evolutionary lineages and as substantial genomic resources are available from the closely related model-organism *Oryzias latipes* (Medaka). Located at one of the large German natural history museums, the group will link the invaluable material of scientific collections with the new opportunities for advanced evolutionary biology studies in the age of genomics.

We are seeking highly motivated applicants, ideally trained in evolutionary biology, and preferably with a sound background in genetics and/or morphology. Experience in rearing fish, good laboratory and bioinformatics skills will be considered a plus. One PhD student will mainly focus on the morphological characterization of pelvic brooding based on state of the art morphological methods, like micro-computed tomography ($\frac{1}{4}$ -CT), Transmission Electron Microscopy (TEM) as well as histology. The second PhD student will mainly focus on the characterization of candidate genes for traits related to pelvic brooding via the analysis of tissue related gene expression and QTL mapping based on RNAseq, RADseq and whole genome resequencing. Field studies in Sulawesi (Indonesia) are planned as part of the first PhD project but can also be accomplished by the second PhD student or both. Projects should complement each other and tasks can be divided based on personal interest and expertise. The candidates should be able to work in a team and should have very good written and oral communication skills in English.

Salary and benefits are according to a public service position in Germany (TV-L E13, 50%), with payscale grouping depending on professional experience.

Please submit your application with the usual documents (letter of interest, CV, complete publication record, copies of relevant certificates and supporting documents) to Mrs. Heike Lenz: h.lenz@leibniz-zfmk.de until 15th September 2017. The positions will remain open until filled. Questions concerning the position may be directed to Dr. Julia Schwarzer: j.schwarzer@leibniz-zfmk.de

The ZFMK advocates gender equality and women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference.

The ZFMK is one of three natural history research museums in the Leibniz Association and a lead institute in the documentation, research, and interpretation of animal biodiversity. The combination of classical museum work and various cutting-edge approaches offers a highly motivating environment. For more information about the museum see <http://www.zfmk.de> . Julia Schwarzer

[<julia_schwarzer@hotmail.com>](mailto:julia_schwarzer@hotmail.com)

NewZealand FinfishGenomics

PhD Scholarship: Disease genomics of two New Zealand finfish species

Start date: Late 2017

We are seeking a highly motivated PhD student to be part of a group to investigate the disease genomics of the New Zealand snapper (*Chrysophrys auratus*) and trevally (*Pseudocaranx georgianus*).

Supervisors Dr. Maren Wellenreuther, Plant and Food Research (PFR), Nelson, New Zealand Dr. Steve Bird, Waikato University, New Zealand

Aquaculture is the fastest growing food-production sector and New Zealand has the potential to develop a range of locally grown finfish species to meet this increasing demand. New genomics-based selective breeding programs are needed to help develop recently domesticated fish species into premium products. Plant and Food Research (<http://www.plantandfood.co.nz>) is known worldwide for its innovative breeding and genomics research, and it is leading the development of New Zealand seafood genomics.

This PhD project will involve working alongside a group of experienced researchers to study the genomes of the New Zealand snapper and trevally to identify and characterize immune genes, screen for genome-wide disease markers using a pedigree from domesticated populations, evaluate the bacterial disease metacommunities and conduct gene expression analyses using transcriptomics and qPCR. This will involve using high-throughput sequencing approaches, coupled with automated and error-reduced phenotyping. The overall goal is to characterize the immune systems of both fish species to better understand disease resistance in domesticated populations, facilitating a rapid and efficient selective breeding programme.

PhD Project Aims 1. Use whole genome assemblies and transcriptomes to identify immune genes and pathways, 2. Use genomic information to improve detection of novel disease QTLs, 3. Assess stress and disease resistance of hatchery individuals, and understand their bacterial disease communities.

This PhD project will provide an excellent opportunity to learn the latest interdisciplinary technologies and

apply them to fish genomics. The PhD student will gain experience working in academic, government and private sector institutions. They will be a member of a highly active and collaborative group of researchers, and help develop new technological approaches and applied-genomic tools.

The successful candidate will be a highly motivated researcher, with a strong background and interest in genomics and molecular biology. Experience with a coding and/or scripting languages is a bonus. This position will be based primarily in Nelson (<http://www.nelsonnz.com>) and comes with a three-year scholarship that provides a stipend and university (domestic-level) fees. This project is supported by the MBIE grant 'Enhancing production of New Zealand's seafood sector using accelerated breeding techniques'.

Applicants should send a CV, a statement of their research interests and a cover letter to Maren Wellenreuther (Maren.Wellenreuther@plantandfood.co.nz) and Steve Bird (sbird@waikato.ac.nz). Candidates will be considered until the position is filled. The ideal starting date is 1 July 2017. International students with strong credentials are welcome and encouraged to apply. For more information about studying at Waikato University and the entry requirements for the PhD program please see <http://www.waikato.ac.nz/study/postgraduate-studies/higher-degrees/>. Maren Wellenreuther Senior Scientist

T: +64 3 989 7658 F: +64 3 546 7049
E: maren.wellenreuther@plantandfood.co.nz
www.plantandfood.co.nz The New Zealand Institute for Plant & Food Research Limited

Postal Address: Plant & Food Research Box 5114, Port Nelson, Nelson, 7043, New Zealand Physical Address: Plant & Food Research Seafood Research Unit, 293 Akersten St, Port Nelson, Nelson, 7010, New Zealand

Maren Wellenreuther <Maren.Wellenreuther@plantandfood.co.nz>

in botany, biodiversity, phylogenetics, or plant conservation in the Great Plains. Students will participate on a USDA Hatch project examining plant community assembly and phylogenetic biodiversity across plots with different land use histories, combining molecular phylogenetics, bioinformatics, and floristics. Research will be based at several SDSU Agricultural Experiment Field Stations in South Dakota, and on the SDSU campus. Successful applicants will have a degree in Biology, Botany, or related field and a strong background natural history and plant evolution. Experience with plant identification, phylogenetic analyses, and data manipulation/analysis using R is desired. A willingness to learn new techniques is required. The MS assistantships include a competitive stipend and tuition waiver.

The Department of Natural Resource Management at South Dakota State University combines Range, Wildlife, Fisheries, and Ecology within the College of Agriculture and Biological Sciences. The department is committed to quality mentoring and professional development opportunities for their students. SDSU is the Land Grant University for the state and has approximately 13,000 students. SDSU is located in Brookings, SD ca. one hour north of Sioux Falls and four hours east of the Twin Cities, and offers a low cost-of-living in a small college-town atmosphere.

To apply, send a single PDF with CV; unofficial transcripts; a letter describing your experience, research interests, and career goals; and contact information for three professional references to Maribeth Latvis (Maribeth.Latvis@sdstate.edu) by October 16, 2017.

Maribeth Latvis Assistant Professor South Dakota State University Natural Resource Management 1390 College Avenue Box 2140B Brookings, SD 57007

Maribeth.Latvis@sdstate.edu

TexasTechU RatEvolution

SouthDakotaStateU GrasslandCommunityPhylogenetics

Graduate Positions Available Grassland Community Phylogenetics South Dakota State University Department of Natural Resource Management

Two MS (or one PhD) research assistant positions are available (Jan 2018) in the Latvis Lab of the Department of Natural Resource Management for students interested

A graduate position in mammalogy with focus on evolution and conservation is available in Caleb Phillips' laboratory (<https://www.depts.ttu.edu/biology/people/-Faculty/phillipscaleb/>). The position will be supported by a Texas Parks and Wildlife State Wildlife Grant. Funding is secured to provide the student with experience as a Research Assistant as well as a Teaching Assistant, and part of tuition and fees costs will also be covered. The abstract from the funded grant proposal is provided below. During the course of research the

position will include a) field work in the Trans-Pecos Ecoregion of Texas, b) travel to museums in the United States for voucher specimen sampling and morphological measurements, c) DNA sequencing and phylogenetic analysis, d) niche modeling, e) presentation and f) publication of culminated work. Thus, a highly motivated person wishing to gain expertise in these areas will be successful. Given the scope of work, a PHD student is preferred, but a highly motivated person wishing to pursue a MS will also be considered.

The Phillips Laboratory approaches a variety of questions by integrating ecological and evolutionary theory with bioinformatic and cell and molecular biology. That said, the applicant will receive a diverse exposure to wet lab research, programming and statistics through their own work and through interaction with other lab members.

Interested persons should email caleb.phillips@ttu.edu to provide a CV and cover letter with a statement of interest. Be sure and put “fulviverter” in the subject line so it isn’t overlooked. Preferred start date is the January 2018 (Spring 2018 semester).

Abstract: The tawny-bellied cotton rat, *Sigmodon fulviverter dalquesti*, is a poorly understood Texas endemic that is listed as a Species of Greatest Conservation Need. *S. f. dalquesti* is only known from a single opportunistic sampling 26 years ago; 20 individuals were collected approximately 18 miles southwest of Fort Davis (Chihuahuan Desert Ecoregion; Stangl 1992a). The population was found to be viable, as the 20 individuals included juveniles as well as reproductively active males and females. Formal subspecific status of *S. f. dalquesti* was based on morphological comparisons to a New Mexican subspecies, *S. f. minimus*, in which *S. f. dalquesti* was found to be craniometrically larger and have distinct pelage characteristics (Stangl 1992b). Based on proximity of distribution, it was hypothesized that *S. f. dalquesti* is most closely related to *S. f. minimus*, yet the single known locality of *S. f. dalquesti* is about 200 km separated from the eastern edge of the *S. f. minimus* distribution. Subsequent phylogenetic work on the genus *Sigmodon* included comparison of *S. f. dalquesti* to a central Mexico subspecies, *S. f. fulviverter*, using the full mitochondrial Cytochrome b gene (Peppers et al. 2002). These subspecies were found to be a little more than 1% genetically divergent (i.e. 12 base pair differences across 1140 base pairs). Based on an accepted mammalian molecular clock, this level of genetic difference roughly equates to 100,000 years of divergence and at least 200,000 generations. Thus, limited existing data indicate that *S. f. dalquesti* is a genetically and morphologically distinct Texas endemic. However, Bradley and Schmidly (2016) remarked that

the range and population size of this subspecies remains unknown, and the above cited publication is the only known detection of *S. f. dalquesti*. This perspective, as well as its state abundance rank of S1, indicate the need to develop an improved understanding of *S. f. dalquesti* biology.

Proposed field work will help to clarify *S. f. dalquesti* occurrence and distribution, and will help inform best conservation plans for this population. In addition to field efforts to more accurately define *S. f. dalquesti* distribution, morphological and phylogenetic analyses will be used to establish evolutionary relationships among subspecies. This important missing information will confirm *S. f. dalquesti* morphological and genetic affinities, and will explain distinctness of *S. f. dalquesti* in comparison to all geographically proximate lineages. A clear understanding of *S. f. dalquesti* evolutionary distinctness is essential to conservation action. For example, the presumed rarity of *S. f. dalquesti*, along with its apparent genetic and morphological uniqueness, contrast sharply with the current Global Rank of G5 (i.e. secure- common; widespread and abundant). Work proposed herein will provide the data necessary to form an accurate conservation assessment.

“caleb.phillips@ttu.edu” <caleb.phillips@ttu.edu>

Toulouse Demographic Inference

Dear colleagues,

we are looking for an ambitious and independent PhD student to work with us (Olivier Mazet and Lounes Chikhi) on questions related to the demographic history of species in a context of genomic data and fragmented landscapes.

The PhD project is entitled “Global change, fragmentation and genomics : can we estimate the demographic history of populations from genomic data in a context of global environmental change”

The PhD candidate could have either of the following backgrounds: (i) training in maths/statistical stochastic modeling and programming, with an interest in questions related to population genetics, (ii) alternatively, training in population genetics/biology with a strong interest and demonstrated experience in scripting, programming or modeling. Potential candidates who are not sure to fit any of these two descriptions should contact us as we are more interested in independent-

thinking students than in specific backgrounds.

The PhD candidate will develop theoretical and computational work particularly (but not only) around the work on the IICR recently introduced by Mazet and collaborators (see references below). The aim will be to develop methods to infer complex demographic histories using genomic data from non model organisms.

The PhD student will be at the Institute of Mathematics of Toulouse, and based at INSA Toulouse, an engineer school where Olivier Mazet is a Assistant Professor. The PhD will be co-supervised by Lounes Chikhi, who works at the Evolution and Biological Diversity Lab in Toulouse and at the Instituto Gulbenkian de Ciência in Lisbon, Portugal. The candidate will work in close collaboration with Willy Rodríguez, a post-doc in Olivier Mazet's lab, and other members of the team working on the IICR (Simona Grusea and Didier Pinchon at INSA, and Simon Boitard, at INRA Toulouse).

Keywords: structured coalescent, Markov processes, simulation, estimation, inference, demography, fragmentation, spatial processes, genomics, non model organisms.

Due to funding constraints the PhD contract must start before the 31st December 2017.

Contacts: Olivier Mazet (omazet@insa-toulouse.fr) and Lounes Chikhi (lounes.chikhi@univ-tlse3.fr)

References:

Mazet O , Rodriguez VW and Chikhi L (2015). Demographic inference using genetic data from a single individual: separating population size variation from population structure. *Theoretical Population Biology*, 104:46-58.

Mazet O, Rodriguez WV, Grusea S, Boitard S, Chikhi L (2016). On the importance of being structured: instantaneous coalescence rates and human evolution - Lessons for inference of ancestral population size? *Heredity*, 116, 362-371. doi:10.1038/hdy.2015.104.

Chikhi L , Rodriguez WV, Grusea S, Santos P, Boitard S, Mazet O (submitted). The IICR (inverse instantaneous coalescence rate) as a summary of genomic diversity: insights into demographic inference and model choice. *Heredity*.

Chikhi, L., Sousa, V., Luisi, P., Goossens, B., Beaumont, M.A., (2010) The confounding effects of population structure, genetic diversity and the sampling scheme on the detection and quantification of population size changes. *Genetics*, 186: 983-995.

Quéméré, E., Amelot, X., Pierson, J., Crouau-Roy, B., Chikhi, L (2012). Genetic data suggest a natural pre-human origin of open habitats in northern Madagascar

and question the deforestation narrative in this region. *Proc. Natl. Acad. Sci, USA*, 109: 13028-33.

Heller, R., Chikhi, L., Sigismund H.R. (2013). The confounding effect of population structure on Bayesian skyline plot inferences of demographic history. *PLoS ONE* 8(5): e62992. doi:10.1371/journal.pone.0062992

Salmona, J, Heller, R, Quéméré E, Chikhi, L (in press) Climate change and human colonization triggered habitat loss and fragmentation in Madagascar. *Molecular Ecology*, 1365-294 UR - <http://dx.doi.org/10.1111/mec.14173> . "lounes.chikhi@univ-tlse3.fr" <lounes.chikhi@univ-tlse3.fr>

TrentoU FEM Italy MetagenomesEvolution

TrentoU_FEM.Italy.MetagenomesEvolution

A fully-funded 3-year PhD position is available to work on a project entitled: "Estimating microbial divergence times from METAgenomic data using molecular CLOCKS: setting up a new method for applied microbiology".

Student will use computational metagenomics and molecular clock theory to estimate for the first time divergence times of microbial organisms directly from metagenomic data. This will be accomplished by coupling newly developed strain-level shotgun metagenomic techniques with coalescent-aware relaxed clock methods, which will provide enough information to effectively estimate divergence times among closely related (unculturable) bacteria. Student will use human and insect pest as model environments to prove the success of this approach. The ideal candidate has strong willingness to explore a new field in biology, interest in Evolutionary Biology and Bioinformatics. Candidate ideally has some knowledge in one or more of this topics: metagenomics, molecular evolution, programming. Training will be given when needed.

The student will spend approximately half their time in the two collaborating research groups, those of Nicola Segata (Center for Integrative Biology, University of Trento, Italy), and Omar Rota-Stabelli (Sustainable Agroecosystems, Fondazione Edmund Mach, Italy).

Student will be enrolled at the University of Trento as part of the PhD Programme in Biomolecular Sciences. Deadline for application is 23 August 2017. Call and on line application at <http://www.unitn.it/en/ateneo/>

1961/announcement-of-selection The campus of the Center for Integrative Biology is located in Trento, and that of Fondazione Mach in the nearby San Michele all'Adige, both in the Province of Trento in the eastern Italian Dolomites, a World Heritage Site. The Province of Trento is rated as one of the best places in Italy for outdoor recreation and overall quality of life. Both University of Trento and Fondazione Mach are top ranking institutes for research and teaching. See also: <https://www.visittrentino.info/en> . Informal inquiries for further details should be sent to omar.rota@fmach.it

– Omar Rota-Stabelli PhD Researcher at the Agrarian Entomology unit, Department of Sustainable Agroecosystems and Bioresources, IASMA Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige, (TN), Italy. Phone:+39 0461 615393 Mobile:+39 389 8375091 Fax:+39 0461 615500

Councillor of the Italian Society for Evolutionary Biology www.sibe-iseb.it Society for Molecular Biology and Evolution www.smbe.org Scholar <http://scholar.google.it/citations?user=of14yMwAAAAJ>
Omar Rota-Stabelli <omar.rota@fmach.it>

TrentoU MosquitoEvolution

FEM_TrentoU_Italy.MosquitoVirusMicrobePhyloGenomics

A fully-funded 3-year PhD position is available to work on a project entitled “Genome evolution and molecular divergence of mosquitoes of biomedical importance and their microbiome: understanding the biology to ameliorate control”.

Project aims at reconstructing the evolutionary history of mosquitoes of the Aedes group (eg: tiger and yellow fever mosquitoes), insects of biomedical importance and vectors of viruses. The student will reconstruct the phylogeny, the divergences, and the evolution of key genes by coupling genomic (including metagenomic) data with molecular evolution and molecular clock techniques. Analysis will be carried out in mosquitoes and their microbiome (including zika, dengue, and other viruses) with the aim of better understanding the biology of mosquitoes, their epidemiology, and thier evolutionary dynamics to improve modeling and define new forms of biological control. Strong interest in evolution, genomics, epidemiology is required. Candidate ideally have some knowledge in one or more of this topics: genomics, bioinformatics, molecular evolution, programming; full training will be given where needed.

Student will be enrolled at the University of Trento as part of the PhD Progamme in Biomolecular Sciences of the Center for Integrative Biology of Univeristy of Trento. Student will be supervised by Omar Rota-Stabelli (a molecular evolutionists) and Annapoala Rizoli (an epidemiologist) and will carrie most of their research at the Department of Sustainable Agroecosystems of Fondazione Edmund Mach, Italy.

The campus of the Center for Integrative Biology is located in Trento, and that of Fondazione Mach in the nearby San Michele all'Adige, both in the province of Trento in the eastern Italian Dolomites, a World Heritage Site. The Province of Trento is rated as one of the best places in Italy for outdoor recreation and overall quality of life. Both University of Trento and Fondazione are top ranking institutes for research and teaching. See also: <https://www.visittrentino.info/en> . Deadline for application is 23 August 2017. Call and on line application at <http://www.unitn.it/en/ateneo/1961/announcement-of-selection>. Informal enquiries for further details should be sent to omar.rota@fmach.it

Omar Rota-Stabelli PhD Researcher at the Agrarian Entomology unit, Department of Sustainable Agroecosystems and Bioresources, IASMA Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige, (TN), Italy. Phone:+39 0461 615393 Mobile:+39 389 8375091 Fax:+39 0461 615500

Councillor of the Italian Society for Evolutionary Biology www.sibe-iseb.it Society for Molecular Biology and Evolution www.smbe.org Scholar <http://scholar.google.it/citations?user=of14yMwAAAAJ>
Omar Rota-Stabelli <omar.rota@fmach.it>

TU Braunschweig AmphibianSpeciesDelimitation

TU Braunschweig (Brunswick University of Technology), Zoological Institute

PhD - Genomic approaches to species delimitation in amphibians Application deadline: 25.09.2017

We are seeking a highly motivated PhD student at the TU Braunschweig, Zoological Institute (Evolutionary Biology), for a collaborative research project with the University of Potsdam, Institute for Biochemistry and Biology (Evolutionary Adaptive Genomics). The student will apply genomic approaches to species delimitation in amphibians, in a project funded by the German

Research Foundation (DFG) within the Priority Program TaxonOmics.

The project will generate multiple Next-Generation Sequencing data sets (e.g., RNAseq, RADseq, and others) for species complexes of European amphibians, such as newts and salamanders (*Triturus*, *Salamandra*) and frogs (*Rana*, *Discoglossus*), and comparatively test the performance coalescence-based approaches of species delimitation on this variety of markers. Eventually, the favored analysis pipeline will be applied to taxonomically poorly studied species complexes of amphibians from Madagascar, with the goal of achieving comprehensive taxonomic revisions including the description of new species.

The prospective PhD student ideally will combine a real interest in zoological taxonomy with previous experience in NGS approaches and bioinformatic analysis pipelines. Programming skills (e.g. python, R) will be of advantage, as will be basic knowledge of amphibian systematics. Good skills in English communication (written and oral) are necessary, as is a MSc degree (or equivalent) in biology or bioinformatics.

The successful candidate will be based at the Zoological Institute, TU Braunschweig (M. Vences lab). Part of the labwork will be carried out at the University of Potsdam (M. Hofreiter lab). Further information: <http://www.zoologie.tu-bs.de/index.php/en/evolutionsbiologie> <http://www.mvences.de> <https://www.uni-potsdam.de/ibb-genomics/group/hofreiter.html> The position is limited to 36 months with a presumed starting date of November 01, 2017. Salary scale: E13 (65%).

Applications of women are strongly encouraged. Severely challenged persons will be given preference in case of otherwise equal qualifications.

Please send your application (CV, transcript of records, letter of motivation, names of two references) to m.vences@tu-braunschweig.de before September 25, 2017.

Prof. Dr. Miguel Vences Division of Evolutionary Biology Zoological Institute Technical University of Braunschweig Mendelssohnstr. 4 38106 Braunschweig Germany Phone: +49 - 531 391 3237 Fax: +49 - 531 391 8198 E-mail: m.vences@tu-braunschweig.de <http://www.mvences.de/> Miguel Vences <m.vences@tu-braunschweig.de>

U Eastern Finland Human Evolutionary Biology

The University of Eastern Finland, UEF, is one of the largest multidisciplinary universities in Finland. We offer education in nearly one hundred major subjects, and are home to approximately 15,000 students and 2,500 members of staff. We operate on three campuses in Joensuu, Kuopio and Savonlinna. In international rankings, we are ranked among the leading universities in the world.

The Faculty of Science and Forestry operates on the Kuopio and Joensuu campuses of the University of Eastern Finland. The mission of the faculty is to carry out internationally recognised scientific research and to offer research-education in the fields of natural sciences and forest sciences. The faculty invests in all of the strategic research areas of the university. The faculty's environments for research and learning are international, modern and multidisciplinary. The faculty has approximately 3,800 Bachelor's and Master's degree students and some 490 postgraduate students. The number of staff amounts to 560. <http://www.uef.fi/en/lumet/etusivu> We are now inviting applications for an Early Stage Researcher (PhD student) (evolutionary biology/biomedicine) position, Department of Environmental and Biological Sciences, Joensuu and Kuopio Campus

We are seeking motivated Early Stage Researcher (PhD student) for our project "Molecular and immunological basis of gamete compatibility in humans" (funded by Academy of Finland). The primary aim of the project is to clarify molecular and immunological mechanisms of female-induced sperm selection ('cryptic female choice') in humans and find new tools for the development of next generation fertility treatments, which are better tailored to individual couples. See short description of the project: http://webfocus.aka.fi/ibi_apps/WFServlet?IBIF_ex=x_HakKuvaus2&CLICKED_ON=&HAKNRO1=308485&UILANG=en&IBIAPP_app=aka_ext&TULOSTE=HTML . The primary duty of hired Early Stage Researcher is to write and defend a PhD thesis according to the formulated research plan. Main tasks include (but are not limited to) sperm motility and chemotaxis measurements and determination of female-induced physiological changes in sperm. The Early Stage Researcher also has a possibility to

participate in molecular and immunological analyses of sperm selection mechanisms. His/her tasks also include data analysis and reporting of the results in scientific journals.

A person to be appointed as an Early Stage Researcher shall be qualified to pursue postgraduate studies, i.e. he/she is required to have completed a suitable higher university degree or an equivalent education, which in the country in question would qualify the person for similar academic studies (UEF University Regulations, Section 31). Suitable degrees for the filled position include e.g. various biological, biomedical and medical degrees.

The applicant is expected to have good written and spoken English. Earlier experience in laboratory work, flow cytometry, other relevant methods in cell biology (e.g. sperm motility or viability analyses, ELISA assays), immunology or molecular biology (e.g. RNA seq and bioinformatics) are viewed as a benefit for the applicant. If you have any of these skills, please indicate it in attached CV and/or motivation letter (see below).

English may be used as the language of instruction and supervision in this position.

The position is filled initially for a fixed term from 1 January 2018 to 31 August 2020. Potential continuation of the position (up to 31 December 2021) will be agreed later. A probationary period is applied to all new members of the staff.

Positions of early stage researchers shall always be filled for a fixed term (UEF University Regulations, Section 31).

The salary of the position is determined in accordance with the salary system of Finnish universities and is based on levels 2-4 of the job requirement level chart for teaching and research staff (euro 1,985.85 - 2,475.31/month). In addition to the job requirement component, the salary includes a personal performance component, which may be a maximum of 46.3% of the job requirement component.

The electronic application should contain the following appendices:

- A résumé or CV, including publications, if applicable (please follow the template: <http://www.tenk.fi/en/content/template-researchers-curriculum-vitae> < <http://www.tenk.fi> >, where applicable) - Copies of the applicant's academic degree certificates / diplomas, and copies of certificates / diplomas relating to the applicant's language proficiency, if not indicated in the academic degree certificates/diplomas

— / —

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

UHaifa CircadianClockMolEvol

Scholarships for graduate students are now available at the Tauber research laboratory for *Biological Clocks* at the University of Haifa, Israel. Research in the lab focuses on molecular evolution of genes of the circadian clock: a fascinating system that drives daily rhythms in physiology, metabolism and behaviour, and is evolutionary conserved. We study *Drosophila*, whose clock genes are well conserved in humans. We employ a broad range of techniques, including molecular cloning, transgenics and imaging, as well as quantitative genetics, behavioural analysis, and bioinformatics.

In the last few decades, the molecular basis of the clock has been elucidated. The fruit-fly *Drosophila* has been a major model system for identifying circadian clock genes, which are well conserved in human. By inducing mutagenesis and screening for *Drosophila* mutants that show aberrant light response, various proteins were identified to be involved in light transduction. Our research focuses on natural genetic variation related to clock function. We aim at identifying natural variants that have been evolved in wild populations, serving as molecular adaptations under different light and temperature conditions. We use broad range of techniques, including molecular cloning, transgenics and gene knockdown as well as quantitative genetics, behavioural analysis, and bioinformatics.

Potential Research Projects:

- 1) Study how natural genetic variations in clock genes modify the clock function in different environments.
- 2) Study the role of the circadian clock in deylength measurement (the photoperiodic clock), which is important for timing seasonal responses (for this area of research we are also using the Jewel wasp *Nasonia* as a model system).
- 3) Study the genetic basis that underlies preference for either diurnal or nocturnal activity in animals.

For more information visit our website: www.bit.ly/tauberLab Eran Tauber, Ph.D.

Associate Professor of Genetics Department of Evolutionary & Environmental Biology, The Faculty of Natu-

ral Sciences University of Haifa Haifa 3498838

Israel

Tel: +97248288784

New lab publications in BioRxiv

<http://dx.doi.org/10.1101/048736> <http://biorxiv.org/content/early/2017/05/07/135129> <http://bit.ly/tauberLab> Twitter: @TauberLab facebook: Tauber-Lab +972 52388 1360

eran.tauber@gmail.com

UIceland SpeciationEvolReprodBar

PhD position in biology, Institute of Life and Environmental Sciences, University of Iceland

A full PhD position in biology is open for applications, at the Institute of Life and Environmental Sciences for the project: Evolution of reproductive barriers in sympatric Arctic charr morphs.

How is phenotypic integrity maintained in the face of gene flow? What is the effect of hybridization on development and fitness? What are the molecular mechanisms behind hybrid incompatibilities? These and related questions will be addressed by a team of researchers, and a capable PhD student responding to this advertisement.

The project The Arctic charr (*Salvelinus alpinus*) of Lake Thingvallavatn is ideally suited to address these questions. The Lake was formed at the end of the last glacial epoch just 11-10 thousand years ago and despite its young age it now harbors four morphs of Arctic charr, whose distinct variation in life history characteristics, behavior and trophic morphology suggest rapid adaptive diversification, possibly followed by or causing build-up of reproductive barriers. The focus of this project will be on the two smaller Thingvallavatn morphs, planktivorous- (PL) and small benthic-charr (SB), which have diverged along the limnetic - benthic ecological axis, and inhabit different parts of the lake. Breeding populations of both morphs are large and their spawning overlaps spatially and temporally seemingly presenting ample opportunities for cross-mating. Yet, population genetic studies show that they constitute distinct populations, which suggests effective reproductive barrier(s). We intend to cast light on the nature of these barriers. The central hypothesis underlying our investigation is that reproductive isolation between SB and PL Arctic charr is partly due to strong negative

selection against hybrid offspring and/or differences in the exact timing of spawning (i.e. time of the day), precise spawning location and/or mating behavior. The Ph.D. project's aims are to: i) Assess hybrid survival and fitness during embryonic and early larval development ii) Study gene expression during development of hybrid and pure morph crosses iii) Study the spawning behavior of the two morphs and their interaction in the wild and in the lab. The applicant must have completed an M.Sc. degree in Biology or related fields from a University approved by the University of Iceland's Graduate School. Those with an advanced degree including at least a 60 ECTS credits thesis project will be given precedence. Diving experience is a plus.

We are seeking a student with dedication, drive and good theoretical background in evolution, developmental and molecular biology and an interest in animal behavior. The work involves planning and executing sampling in the field, acquisition and analysis of high-throughput sequencing data and numerical analyses, designing laboratory experiments. The position will be at the University of Iceland and the work will take place there. Experts at the University of Aberdeen, Scotland and the Holar University College, Iceland, will also participate in the project. Application deadline is 1st of August 2017. The PhD study should be completed within four years of full time study. The PhD student may be involved in teaching, for two semesters maximum. The selected candidate will have to formally apply for PhD studies at the University of Iceland in due time. Applications should be submitted here: <https://-ugla.hi.is/radningar/index.php?sid=2448&starf=192> accompanied by i) a letter of intent (maximum two pages) explaining interest in working on this project, the reason to pursue a PhD, hopes to gain and learn during the PhD studies and what makes them suitable for this project ii) CV, iii) transcripts of university diplomas, iv) courses taken at bachelor and masters level, v) degree project thesis and vi) names and contact information of two persons that could provide letters of references.

The student will join the Arctic charr group at the Institute of Life and Environmental Sciences, under the supervision of Sigurdur S. Snorrason, Arnar Pálsson and Zophonias O. Jonsson. The Arctic charr group consists of several PhD students and senior personnel, and has collaborators in Iceland, Denmark, Scotland and Canada. The combined expertise covers population ecology and genetics, molecular biology and bioinformatics. At the institute we have well equipped molecular biology labs, and instruments and computer pipelines for high throughput sequencing, are accessible there or at collaborating centers. For further information contact: Kalina H. Kapralova (kalina@hi.is)

or Sigurdur S. Snorrason (sigsnor@hi.is) Further information on Arctic charr group at the University of Iceland: <http://luvs.hi.is/en/arctic-charr-development-and-genomics>. The salary

— / —

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>

UJyväskylä 4 EvolutionaryBiology

Please note that the department of Biology at University of Jyväskylä in Finland has four open PhD positions. There are different projects that the candidates can apply to, including some in the field of evolutionary biology.

Please review the available projects and how to apply using the link below: <https://www.jyu.fi/bioenv/en/-study/doctoral-programme/phd-posts/2018/call> The deadline for applications is 31th of August.

Ilkka Kronholm

ilkka.i.kronholm@jyu.fi

UNewOrleans EvolutionaryPhysiology

UNIVERSITY OF NEW ORLEANS

A Ph.D. fellowship in evolutionary physiology is available in Simon Lailvaux's research group at the University of New Orleans (<http://fs.uno.edu/slailvau/index.html>). The fellowship is part of a new collaborative initiative between the Audubon Nature Institute and the University of New Orleans.

Candidates will apply for acceptance into the Integrative Biology doctoral program at UNO's Department of Biological Sciences, but will be able to take advantage of resources at the Audubon Nature Institute's facilities in New Orleans, including the Audubon Zoo, Audubon Insectarium, and the Audubon Center for Research of Endangered Species (ACRES) for research

purposes. The recently-established Alliance for Sustainable Wildlife, a partnership between the Audubon Nature Institute and the San Diego Zoo, also presents numerous possibilities for creative dissertation research on captive species from around the world housed at the 1,200 acre Freeport-McMoRan Audubon Species Survival Center in New Orleans. Opportunities for education and outreach exist through the many Audubon facilities.

The successful candidate will conduct high-quality research on topics within the broad purview of the Lailvaux lab (integrative evolutionary ecology), but ideally will also have interests in line with the Audubon Nature Institute's goals of species preservation and sustainability. Because the lab's research is question- rather than organism-driven, students could collaborate with ANI researchers and staff on a variety of study taxa.

Start dates can be anytime from early 2018 onwards. Interested students should send a CV and brief statement of interest to Simon via slailvaux@gmail.com

– Simon Lailvaux Virginia Kock/Audubon Nature Institute Chair in Species Preservation Department of Biological Sciences University of New Orleans 2000 Lakeshore Drive New Orleans, LA 70148

email: slailvaux@gmail.com phone: 504 280 6740

<http://www.fs.uno.edu/slailvau/index.html> Simon Lailvaux <slailvaux@gmail.com>

UNotreDame EvolutionEcology

Graduate Program in Ecology, Evolution, and the Environment at the University of Notre Dame

The Department of Biological Sciences at the University of Notre Dame offers a wide range of research opportunities and graduate coursework in ecology and evolutionary biology, allowing students to excel in field, laboratory, and mathematical biology. Strengths of the program include: studies on the dynamics and divergence of populations, evolutionary and ecological genomics, terrestrial and aquatic community and ecosystem ecology, epidemiology and disease ecology, experimental biology, and the impacts of global changes, including climate change, invasive species, and land use change. Our close-knit faculty provides interdisciplinary research opportunities and excellent research mentorship.

Our students take advantage of many resources at Notre

Dame, including excellent laboratory facilities in the Hank Family Center for Environmental Studies and state-of-the-art instrumentation in our Center for Environmental Science and Technology (CEST; <https://cest.nd.edu>), the Genomics & Bioinformatics Core Facility (<http://genomics.nd.edu>), and the Notre Dame Linked Experimental Ecosystem Facility (ND-LEEF). Other hubs of EEE research include the University of Notre Dame Environmental Research Center (UNDERC; <http://underc.nd.edu/>) with sites located in the Upper Peninsula of Michigan and western Montana and the Notre Dame Environmental Change Initiative (<http://environmentalchange.nd.edu/>). Numerous opportunities for interdisciplinary interactions among research areas are available, including our GLOBES graduate training program (<http://reilly.nd.edu/globes/>)

The following faculty members are currently training graduate students in diverse areas of ecology and evolution:

Beth Archie - behavioral ecology, disease ecology, and population biology

Gary Belovsky - terrestrial ecology and modeling, conservation biology

Sunny Boyd - behavioral ecology, neuroendocrinology and behavioral neuroscience

Jeff Feder - ecological and evolutionary genetics, speciation

Mike Ferdig - systems genetics of malaria parasite drug resistance

Hope Hollocher - population genetics, speciation, evolution, and landscape epidemiology

Stuart Jones - aquatic microbial and ecosystem ecology

Gary Lamberti - stream and wetland ecology, ecotoxicology, and plant-animal interactions

Jason McLachlan - ecology and evolution of plant populations, statistical modeling, paleoecology

David Medvigy - terrestrial ecosystem modeling, ecosystem-climate interactions

Alex Perkins - modeling, disease ecology, population biology of disease vectors

Mike Pfrender - ecological and evolutionary genomics, adaptation, phenotypic plasticity

Matt Ravosa - evolution and pathobiology of the mammalian skull and musculoskeletal system

Adrian Rocha - arctic terrestrial ecology

Jeanne Romero-Severson - genomics of adaptive variation in natural populations of forest trees

Jennifer Tank - stream ecosystem ecology and biogeochemistry

All graduate students are funded with competitive stipends. A variety of fellowship opportunities are open to top applicants. For more information regarding the Biology Graduate Program see <http://biology.nd.edu/> and <http://graduateschool.nd.edu/>. The deadline for receipt of all application materials for the Ph.D. program is December 1st, 2017, although earlier submission is encouraged to ensure full consideration for available fellowships. Please begin your application by directly contacting faculty of interest.

Elizabeth Archie <Elizabeth.A.Archie.2@nd.edu>

UPittsburgh EvolutionaryEcol

The Turcotte Lab at the University of Pittsburgh is looking for PhD students to experimentally test the dynamic interplay between rapid evolution and community ecology in the field. The goal is to disentangle and quantify how ecological and evolutionary processes reciprocally impact each other and understand their importance in nature using robust experiments.

The University of Pittsburgh is a leading research university and the Department of Biological Sciences is a dynamic and growing team of enthusiastic researchers and educators. The department also runs the Pymatuning Lab of Ecology, which is equipped with lab space and housing to facilitate field-based research in northwestern Pennsylvania. The City of Pittsburgh is a vibrant and beautiful place to live and is often voted the 'Most Livable city in the U.S.'.

If you are interested and you are attending ESA please contact me at turcotte@pitt.edu so can meet in person.

More details about the lab and applying here: www.martinturcotte.net Martin Turcotte, Ph.D. Assistant Professor, Department of Biological Sciences University of Pittsburgh

mart.turcotte@gmail.com

UQueensland UExeter EvolGenomicsNutritionAgeing

A unique joint institution graduate position is available in the labs of Steve Chenoweth (U Queensland) and Alastair Wilson (U Exeter). This Exeter-UQ collaborative research project seeks to address fundamental questions about the causes of ageing in a way that combines both mechanistic and evolutionary factors. It will take an experimental approach to understanding why individuals and genders differ in the speed with which they age.

Specifically, the project will dissect relationships between dietary intake, DNA sequence variation and ageing rates. To achieve this, the student will use a powerful experimental genomic system developed at the University of Queensland in the lab of Steve Chenoweth. A comprehensive set of genomic resources are now available for an model insect system that permits experimental investigations of ageing. These include panels of more than 100 sequenced living genomes, and a large panel of matched mutation accumulation lines. This will allow the student to investigate how new mutations shape individual ageing trajectories, and critically, determine whether harmful mutational effects can be offset through targeted dietary interventions. These genomic tools will be combined with an evolutionary approach, rooted in life-history models that give clear and general predictions about when, why and how senescence should occur. To test these predictions, genomic and genetic data will be investigated using modelling and analysis techniques developed in the group of Alastair Wilson at the University of Exeter.

This project offers students a rare opportunity to acquire a broad understanding of evolutionary biology and life-history theory, a well as specific skills in statistical genetics, bioinformatics and the experimental techniques used in nutritional research. The student will divide their time between experimental design, theoretical modelling and data analysis at the University of Exeter (Wilson), and experimental genomic work at the University of Queensland (Chenoweth).

The award includes a full living allowance, fee waivers, and a generous annual travel grant permitting frequent travel between the UK and Australia. The award has no specific nationality restrictions.

Applications close: 11 September 2017 for an anticipated start in January 2018

Further details and instructions on how to apply can be found at <https://global-engagement.uq.edu.au/node/-1628/3#3> and we suggest you get in touch with either of us in the first instance (s.chenoweth@uq.edu.au, A.Wilson@exeter.ac.uk).

Steve Chenoweth <s.chenoweth@uq.edu.au>

UTokyo PlantEvolutionaryEcol

The Shefferson lab at the University of Tokyo is recruiting graduate students at both the MS and PhD levels with interests in plant evolutionary ecology, for entry into the Graduate Program in Environmental Sciences (GPES, online at <http://gpes.c.u-tokyo.ac.jp/>) in Sept 2018. We specialize in evolutionary demography and plant/microbial evolution, with particular interests in rapid evolution and eco-evolutionary dynamics. We are particularly hoping to recruit students to work on the following funded research projects:

- 1) **Deep demography**: Demographic patterns are strongly influenced by both evolutionary history and geography, but a mechanistic understanding of these relationships is still lacking. We hope to unravel it using a number of large-scale projects focused on herbaceous perennial plant species.
- 2) **Evolutionary origins of plant-microbial symbiosis**: We seek to understand the first steps in the evolutionary process leading to the development of widespread symbioses, such as the mycorrhiza.
- 3) **Eco-evolutionary impacts of individual history**: We hope to understand how long-term experience influences evolutionary processes, particularly at the micro-evolutionary scale.

In addition to these projects, we seek students generally interested in the following topics:

- 1) Micro-evolutionary interactions between symbiosis and population dynamics, with a focus on the mycorrhiza.
- 2) The micro- and macro-evolution of senescence-related life history patterns and life history costs, with a focus on herbaceous plants and terrestrial fungi.
- 3) Interactions between community structure and phylogeny at differing timescales, with a focus on the myc-

orrhiza.

4) Eco-evolutionary impacts of conservation problems and associated management.

Students applying to work in the lab may focus on these topics, or choose other research themes in plant and microbial evolutionary ecology. Research methods typically involve *in situ* monitoring and experimentation, combined with modeling and analysis based in R and/or C++. We typically work with plants and their symbiotic microbes, and students should generally be interested in these study organisms. The Shefferson lab has active field sites in the Japan, USA, and Estonia, and also regularly conducts field work in China, Central America, and Western and Central Europe.

The Shefferson lab is located within the University of Tokyo, Komaba Campus. U Tokyo is home to some of the finest scientists in Japan, including ecologists and evolutionary biologists, and more Nobel laureates than you can shake a stick at. Komaba in particular has a particularly large community of ecologists and evolutionary biologists working on plants, animals, and fungi. The GPES program conducts all graduate education in English, although students have the opportunity to learn Japanese and take courses from throughout the U Tokyo curriculum. Our campus is only 15 minutes' walk from Shibuya, one of the most vibrant parts of Tokyo.

Applications to join the lab MUST be received by *24 November 2017*, and students MUST INCLUDE a current, official GRE transcript. Please note that GRE scores are only valid for 5 years, so students with transcripts older than this need to re-take the GRE. Applicants with high scores, high grades, and strong recommendations will be considered for a competitive, full-ride scholarship.

If interested, please contact me at, and please also explore the Shefferson lab website:

E-mail cdorm@g.ecc.u-tokyo.ac.jp

HTML: www.sheffersonlab.com – New book on the Evolution of Senescence in the Tree of Life <http://tinyurl.com/SenescenceBook> Dr. Richard P. Shefferson Associate Professor Organization for Programs on Environmental Sciences Graduate School of Arts and Sciences University of Tokyo 3-8-1 Komaba Meguro-ku, Tokyo 153-8902, Japan

E-mail: cdorm@g.ecc.u-tokyo.ac.jp Tel: +81-3-5465-7235
Fax: +81-3-5465-7236

Web: www.sheffersonlab.com Richard Shefferson
<dormancy@gmail.com>

UTulsa 2 EvolBiol

The Booth lab at The University of Tulsa is currently seeking graduate students starting in the fall of Spring or fall of 2018. Two projects are currently available at the M.Sc or Ph.D level:

1) Understanding the dynamics of rapid and pervasive mitochondrial heteroplasmy and recombination: Using a whole mitogenomic approach this project seeks to 1) assess the influence of mitogenomic divergence on the frequency of paternal leakage driven heteroplasmy; 2) to empirically and theoretically evaluate heteroplasmy decay; and 3) determine whether recombination hotspots can be detected within the mitochondrial genome.

2) Spatiotemporal metapopulation dynamics and host-species expansion of a disease-vectoring avian ectoparasite: Using both nuclear and mitochondrial markers, we aim to understand variation in the temporal and spatial structure of an avian ectoparasite undergoing both a population range expansion and a host-species expansion. This project has the potential to include both genomic and microbiomic aspects also.

Applicants for this position should have a interest in population and evolutionary genetics/genomics, molecular ecology, bioinformatics, or evolutionary biology, and meet the admission requirements for the Department of Biological Sciences graduate program. (<https://graduate.utulsa.edu/admission/-eligibility-requirements/>).

The students stipend, tuition, and medical insurance, is covered as part of the teaching assistantship (requires 20 hours per week teaching assistance).

Applications should include the following:

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

For more information about this opportunity, contact Dr. Booth (warren-booth@utulsa.edu).

Additional information regarding our research can be

found at our website: www.booth-lab.org —

Dr. Warren Booth

Associate Professor

Department of Biological Science The University of
Tulsa 315 Oliphant Hall

Tulsa, OK 74104

Tel.

(918) 631-3421 - Office

Lab website

“Booth, Warren” <warren-booth@utulsa.edu>

UValencia ViralEvolution

A PhD contract is available at the laboratory of Rafael Sanjuán (University of Valencia, Spain).

Starting date: end 2017.

Place: recently created Institute for Integrative Systems Biology (I2SysBio), Valencia, Spain.

Project title: Collective Infectious Units and the Social Evolution of Viruses.

Funding: ERC Consolidator Grant, 2017-2022.

Goal: understand how multi-virion infectious units determine social-like interactions in viruses (cooperation versus conflict). We will use baculoviruses as model systems.

Candidates should have a background in molecular/cell biology and virology (preferably with baculoviruses).

ERC project summary:

A widely accepted view in virology is that virions function as independent infectious units. However, recent work by us and others indicates that viruses are often transmitted as more complex structures, such as virion aggregates, lipid vesicles or protein matrices harbouring multiple infectious particles. This demonstrates that viruses can be transmitted as “collective infectious units”, in contrast with the current paradigm. Critically, these recent discoveries now set the stage for the evolution of social interactions, a previously unappreciated facet of viruses. We propose to investigate how collective infectious units drive virus social evolution using state-of-the-art tools from the fields of virology, genetics, structural biology, and nanotechnology. The effects of collective infectivity on viral fitness will be tested directly using experimental evolution and genetic

engineering, and confirmed in vivo. Three widely different viruses will be used to achieve generality: human enteroviruses, a vector-borne rhabdovirus, and a baculovirus. Furthermore, the implications of virus social interactions for the maintenance of genetic diversity, evolvability, virulence evolution, and the emergence of drug resistance will be investigated. New processes such as the putative extracellular fusion of viral particles will be also explored. We expect that infectious units constituted by viruses from different species will be uncovered as well, with far-reaching implications for epidemiology. It is becoming increasingly recognized that parasite sociality is a disease determinant, and our results may therefore inspire new antiviral strategies. Beyond their practical importance viruses will also provide a simple and tractable system that will help us to establish more general principles of social evolution.

Relevant literature: Sanjuán R. 2017. Collective Infectious Units in Viruses. *Trends Microbiol.*, in press. <https://www.ncbi.nlm.nih.gov/pubmed/28262512> Contact: rafael.sanjuan@uv.es; +34 96 354 32 70.

Rafael Sanjuan <rafael.sanjuan@uv.es>

UWestGeorgia EvolutionaryBiol

Graduate Assistantship positions at The University of West Georgia (UWG)

The Department of Biology at the University of West Georgia has openings starting in Spring 2018 for graduate students interested in pursuing thesis-based Master’s of Science degrees in Biology.

Faculty expertise in the department ranges from the sub-cellular to the landscape level. More information about particular areas of study is available from the faculty pages shown on this website: <https://www.westga.edu/~academics/cosm/biology/research-interests.php> Graduate students are eligible for Teaching Assistantships that provide tuition waiver and a stipend of \$8,000 for a 9-month contract, with the option for additional summer salary.

Applications are currently being accepted; admissions criteria are available at this website: https://www.westga.edu/academics/gradstudies/-program_page.php?program_id=3D80 UWG is located in Carrollton, GA, a growing city of ~25,000 people located in western region of the state ~ 45 west of Atlanta. The campus is within convenient driving

distance to national forests and three metropolitan areas. For more information about the M.S. degrees available through the Dept. of Biology, please contact Dr. Frank M. Fontanella (ffontane@westga.edu) or Dr. Melissa Cavallin Johnson (mcavalli@westga.edu)

– Dr. Frank M. Fontanella Assistant Professor Department of Biology University of West Georgia 1601 Maple Street Carrollton, GA, 30118

“ffontane@westga.edu” <ffontane@westga.edu>

UWollongong EvolutionFishSociality

We are seeking a highly motivated PhD student to join an on-going research project on the evolution of sociality in coral reef fishes, based at the University of Wollongong, NSW, Australia.

Overview: This is an exciting opportunity to join an interdisciplinary team of researchers to understand the causes and consequences of sociality in reef fishes. The project will combine field experimental investigations at multiple sites along the Great Barrier Reef with laboratory genetic analysis based at the University of Wollongong. Research funding for this project is secured, and we currently seek a motivated and talented student to undertake this project.

The project supervisors are: University of Wollongong: Dr. Marian Wong and Prof. Mark Downton University of Technology Sydney: Dr. Selma Klanten
 Outline: Sociality is a common and taxonomically widespread phenomenon in tropical marine fishes. In spite of this, comparative analyses of sociality to date have been focused on birds, mammals and insects. Coral-reef fishes are an ideal group with which to test the generality of hypotheses for social evolution because: i) they exhibit considerable inter-specific variation in social organization, ii) species-level phylogenetic relationships have already been resolved for some key groups of coral-reef fishes, and iii) they inhabit shallow coral reefs facilitating field observations, experiments and collections (for summary see: <https://academic.oup.com/bioscience/article/63/6/453/226119/Social-Systems-in-Habitat-Specialist-Reef>). As the ecology and life-history of fish differ in major respects to birds, mammals and insects, this comparative analysis of sociality will likely yield novel and transformative results that will significantly advance the field of social evolution (see: DOI: 10.3389/fevo.2017.00100). This PhD project will investigate the causes and

consequences of sociality in one particular group of coral-reef fishes known as “habitat-specialists”. These species reside permanently within discrete patches of reef habitat, including corals and anemones.

Mentorship: This project is supervised by Dr. Marian Wong, a behavioural ecologist and Senior Lecturer (<http://smah.uow.edu.au/biol/contacts/-UOW135217.html>; <http://marianwong.wixsite.com/-thefishlabuow>), Prof. Mark Downton, molecular ecologist and Head of Students at the University of Wollongong (<http://smah.uow.edu.au/biol/contacts/-UOW043319.html>) and Dr. Selma Klanten, a molecular biologist based at the University of Technology Sydney (<http://www.selmaklanten.com/>). The University of Wollongong offers excellent scholarship, career development and supervisory support for post-graduate students in a friendly and collegiate setting.

Applicant Requirements: The applicant is expected to have completed a recognised undergraduate degree in Biological Sciences with an Honours degree (or equivalent) in marine biology and/or ecology, and possess a demonstrated interest in animal behaviour. The successful applicant must also be SCUBA qualified. Boating skills are desirable but not essential. Domestic and international applicants are encouraged to apply - domestic students would need to apply for an AGRTP (<http://www.uow.edu.au/research/grs/prospective/-UOW070387.html>) and international students would need to apply for a UPA (<http://www.uow.edu.au/research/grs/prospective/UOW070389.html>) to cover stipend costs.

Applications: Please send a CV to Dr. Marian Wong (marianw@uow.edu.au) and Prof. Mark Downton (mdownton@uow.edu.au) no later than Friday 6th October.

Deadlines: 17th October (for scholarship applications for commencement of degree in February 2018).

O. Selma Klanten, PhD Research Scientist Fish Ecology Group School of Life Sciences Bldg 7 Level 6 University of Technology Sydney PO Box 123, Broadway NSW 2007, Australia Email: Oya.Klanten@uts.edu.au Alternate email: osklanten@me.com Fish Ecology Lab: <http://www.fishecologylab.com> selmaklanten.weebly.com Mob: +61-417341941 Secretary, Australian Coral Reef Society (ACRS) <http://www.australiancoralreefsociety.org/> Oya.Klanten@uts.edu.au

UWurzburg 2 EvolAmbrosiaBeetles

Two PhD positions - Evolutionary Ecology of Ambrosia Beetles

Research Group Insect-Fungus Symbiosis, Zoology 3, University of Würzburg, Germany

Application deadline: 30.9.2017

Two 3-year PhD positions in “Evolutionary Ecology of Sociality and Fungiculture in Ambrosia Beetles”

We seek highly motivated biologists with a keen interest in the ecology and evolution of insect social behaviour and/or fungiculture to join our newly established research group at the University in Wuerzburg, Germany (www.insect-fungus.com).

Description: Our main models are bark and ambrosia beetles (AB), which live in subsocial to eusocial societies within wood, where they cultivate fungi on walls of their tunnels. Both sociality and fungiculture evolved in several independent lineages under different ecological conditions, levels of relatedness and ploidy. They remained poorly studied although they are excellent models to test pending evolutionary questions.

Possible projects: - Is it possible to artificially select for/against sociality in AB? - How is division of labour regulated in AB societies? - How do AB suppress pathogens and promote cultivars in their fungus gardens? - How does AB social evolution affect the evolution of fungiculture and vice versa? - What are the factors that repeatedly selected for obligate fungiculture in AB? In our work we combine field studies with lab experiments and apply an interdisciplinary approach, combining selection experiments, experimental assays, and culturing methods with state-of-the-art molecular (e.g. qPCR, next-gen-sequencing) and biochemical (e.g. GC-MS) techniques.

We require: - MSc degree in (Forest) Entomology, Mycology, Evolutionary Biology, Chemical Ecology, Microbiology, Molecular Biology or Bioinformatics - Due to the interdisciplinary nature of the projects, successful candidates must be willing to become acquainted with methods from the fields above. - Experience working with insects or microbes. - Proficiency in English and a good team spirit are a must. - Knowledge on basic molecular methods, statistics (R skills), chemical ecology and bioinformatics are a plus.

We offer: - An exciting research project to build on a scientific career. - A cooperative and highly ambitious young research group, as part of a vivid department. - Opportunities to visit collaborating labs worldwide. - Salary according to public service positions in Germany (TVL E13: 65%) for three years. The University of Würzburg is an equal opportunity employer, i.e. female scientists are particularly encouraged to apply and disabled applicants will be preferentially considered in case of equivalent aptitude.

The Host: We are one of a few labs in the world to study AB. For details on our projects see www.insect-fungus.com or directly contact Dr. Peter Biedermann (peter.biedermann@uni-wuerzburg.de; +49(0)17699819095). The University of Würzburg offers tremendous expertise on social insect behaviour, evolution, chemical ecology and molecular ecology. Würzburg itself is a vivid student city in one of the most beautiful areas of Germany.

Application: Please submit the application (as a single pdf file including a letter of motivation, a short summary of research interests, a CV, certificates, and contacts of two potential referees) via e-mail to info@insect-fungus.com until September 30th 2017.

Dr. Peter H.W. Biedermann Emmy Noether Research Group Insect-Fungus Symbiosis Department of Animal Ecology and Tropical Biology Biocenter, University of Wuerzburg Am Hubland 97074 Wuerzburg, Germany phone: +49 176 99819095 email: peter.biedermann@uni-wuerzburg.de <http://www.insect-fungus.com>

Peter Biedermann <peter.biedermann@uni-wuerzburg.de>

UZurich SexChromosomeEvolution

Sex chromosome evolution in liverworts

Abstract: Evolution of sex chromosomes is well-studied in organisms in which sex is expressed in the diploid phase. In such organisms the lack of recombination and the asymmetry in haploidy are assumed to lead to the progressive decay of the Y chromosome. In organisms in which sex is expressed in the haploid phase both U and V chromosomes are equally devoid of recombination and show no asymmetry in recombination suppression. This provides a unique opportunity to tease apart the effect of this two factors on the evolutionary trajectory of sex chromosomes. We are using a combination of

classical genetic and comparative genomic approaches to test hypotheses concerning sex chromosome evolution in haploid dioecy using liverworts as a suitable model system (*Marchantia polymorpha*, *Preissia quadrata* and many more).

Job Description: The goal of this project is to (1) develop a new methodology for capturing and sequencing complete sex chromosomes in plant model systems and (2) to reconstruct their evolutionary history both at the gene and structural levels. Therefore, this position involves molecular laboratory work to develop and optimize capturing and sequencing protocols; bioinformatics work to analyze and interpret the generated next-generation sequencing data; and evolutionary and functional genetic analysis of the evolution of sex chromosomes in the model plant *Marchantia polymorpha* and other liverwort species. This project is aimed at addressing one of the fundamental questions of evolutionary biology, the genetic makeup of sex chromosomes in a haploid plant model organism, via developing a new cutting-edge method for third-generation sequencing.

The successful candidate will have a M.Sc. degree in plant molecular systematics, plant evolution, plant molecular biology/genetics as well as strong analytical skills and excellent skills in plant molecular biology. Experience in generating, handling, and analysing next-generation sequencing data including programming skills in R/Python/Perl is highly recommended. Proficient oral and written English skills are expected.

The successful candidate will be matriculated at University of Zurich and work 18 months at University of Zurich, Switzerland. The other 18 months at BaseClear, The Netherlands. Peter Szovenyi, University of Zurich; Prof. Elena Conti, University of Zurich, Prof. Michael Lenhard, University of Potsdam; Dr. Walter Pirovano, Dr. Adalberto Costessi and Dr. Daniël Duijsings, BaseClear BV, The Netherlands will jointly supervise the successful candidate. The fellowship period includes frequent periods of trans-national mobility. The complete 36 months will be under 100% working contracts.

Application documents: 1) Curriculum Vitae with list of publications (if applicable); 2) transcripts of University courses with grades and grading scale applied at the respective degree-granting University; 3) certificate of language proficiency in English (if available); 4) motiva-

tion letter explaining why the applicant is suitable for the position and indicating preferred starting date; maximum length: one page; 5) two letters of recommendation sent DIRECTLY to peter.szovenyi@uzh.ch by each referee. Send the application documents listed above (1-4) as ONE PDF DOCUMENT to peter.szovenyi@uzh.ch using "PlantHUB" in the subject line.

Review of applications will begin immediately and continue until the position is filled. Application deadline: 31st of September 2017.

This project is conducted in the framework of PlantHUB. PlantHUB is funded by the H2020 PROGRAMME Marie Curie Actions - People, Initial Training Networks (ITN). PlantHUB offers challenging and exciting research positions in an international, multidisciplinary research network. The employers are leading European universities and leading global companies. All PlantHUB ESR will follow a doctoral programme that is ground-breaking. The doctoral training is placed into an entrepreneurial environment of leading public and private organisations. It combines practical hands-on R&D and technology transfer in plant breeding and production with a PhD Program that concentrates on Responsible Research and Innovation training and practice.

Latest possible starting date of the working contract: 30.11.2017

Eligibility: Early stage researcher in the first 4 years (full-time equivalent) of their research careers, including the period of research training, starting at the date of obtaining the degree which would formally entitle them to embark on a doctorate either in the country in which the degree was obtained or in the country in which the initial training activities are provided. At the time of recruitment (=first day of the employment) by the host organisation, researchers must not have resided or carried out their main activity (work, studies, etc.) in the country of their host organisation for more than 12 months in the 3

— / —

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>

Jobs

ArizonaStateU DirectorLifeSciences	39	UCalifornia Berkeley QuantSystemsBiol	57
ArizonaStateU MechanismsOfEvolution	40	UCanterbury EvolutionaryBiology	58
AustNatInsectCollection ResProjOfficer	41	UCentralFlorida EvolutionaryGenomicsCompBiologist	59
BRCAS Taiwan EvolutionaryBiology	42	UGeorgia 2 EvolutionaryEcol	60
BRCAS Taiwan MicrobialDiversity	42	UGothenburg NextGenSequencing	61
ClaremontC EvolutionaryBiol	43	UIdaho LabManager EvolutionaryConservationGe-	61
ClaremontC EvolutionaryMicrobiol	43	nomics	61
ClarkU EvolutionaryEcol	44	ULouisiana Lafayette PopGenetics	62
EmoryU GenomeEvolution	45	UMassachusetts Lowell EvolutionZebrafish	63
Florida MNH AssistantCurator	45	UNAM Mexico CenterForGenomicScience	63
FWS NewMexico 2 FishEvolution	45	UNewHampshire ChairBiology	64
HalleU MolecularEvolEcol	46	UNewOrleans OrganismalBiol	64
InstitutPasteur 10 Bioinformatics	46	UOklahoma IchthyologyCurator	65
Lynker MarineConservation	48	UOregon EvolutionaryAnthropology	65
MichiganStateU BioStationDirector	48	UOtago BioinformaticsTech	66
MolEcoRes Journal EcolEvolution	49	UPittsburgh EvolutionaryBiology	67
Museum RichmondIndiana PartTime TeachingEvolu-	49	URhodeIsland ResAssist DiseaseVectorEvolution . .	67
tion	49	USouthernCalifornia LabTech CoralAquarist	67
NewCollege Florida EvolutionaryMicrobiol	51	UTulsa 2 EvolutionaryGeneticsMolBiol	68
NHM UOslo ResearchDirector	51	UVermont EvolutionaryGeneticsLecturer	69
PennsylvaniaStateU EvolutionaryGenomics	52	UWisconsinMadison 2 Genetics	70
PennsylvaniaStateU ResistanceEvolution	53	VanderbiltU EvolutionMicrobiome	70
RhodesC Memphis EvolutionaryBiol	54	WakeForestU EvolutionaryMicrobiologist	70
SanDiegoStateU ComputationalEvolutionaryBiology	54	YalePeabodyMuseum HeadBiodiversityInformaticsData	71
TexasAM ResAssist ParasitePopGenetics	55		
UBergen SystematicInvertebrateZoology	56		
UBritishColumbia TeachingEvolution	57		

ArizonaStateU DirectorLifeSciences

See also: https://sols.asu.edu/sites/default/files/sols-director-job-12081_0.pdf School Director (JOB#12081) Arizona State University School of Life Sciences

Arizona State University, rated first in the US for innovation (<https://about.asu.edu/rankings>), is a dynamic institution dedicated to interdisciplinary collaborations, rethinking university education, and integrating excellence in research, teaching, and service. To support this commitment, the School of Life Sciences (SOLS) in the College of Liberal Arts and Sciences at Arizona State University (ASU), Tempe Campus, invites applications for Director, with a concurrent appointment as Tenured

Professor. The anticipated start date is July 1, 2018, although some flexibility is negotiable.

SOLS is among ASU's largest and most distinguished units (<https://sols.asu.edu>). A vibrant community of scholars, teachers, and professionals, SOLS includes over 90 tenure-track faculty members within six Faculty Groups that serve 2,800 undergraduate majors and 280 PhD and MS students in ten graduate programs. A highly engaged and collaborative unit, SOLS is a leader in research and educational initiatives in biomedicine, molecular biology, genomics, bioinformatics, ecology, evolutionary biology, physiology, and sociobiology.

SOLS faculty are affiliated with a wide diversity of trans-disciplinary research groups, including the Biodesign Institute and the Julie Ann Wrigley Global Institute of Sustainability, and the Centers for Biodiversity Knowledge Integration, Biodiversity Outcomes, Bioenergy

and Photosynthesis, Biology and Society, Bio-mediated and Bioinspired Geotechnics, Evolution and Medicine, Global Drylands, Metabolic and Vascular Biology, Social Dynamics and Complexity, and the Arizona-Phoenix Long-Term Ecological Research program.

Additionally, SOLS has off-campus collaborations with Barrow Neurological Institute, Mayo Clinic, Translational Genomics Institute, the Phoenix Zoo, the Desert Botanical Garden, and the Smithsonian Institution, as well as with community partners in education, health care, and conservation.

The Director will develop and implement a comprehensive plan for SOLS and strategic initiatives related to the faculty, staff, and students, providing leadership, vision, and the capacity to engage faculty across a range of disciplines, while sustaining a culture of collaboration both within and beyond the School, strengthening links with other academic units at ASU, and with the wider community. The Director will promote the design principles of the “New American University” (<https://newamericanuniversity.asu.edu/about/design-aspirations>), fostering growth and innovation in the School’s research mission, working to attract, develop, and retain exceptional faculty members, promoting excellence in the undergraduate and graduate programs, developing interdisciplinary research and teaching initiatives, advancing entrepreneurial opportunities, and enhancing relations within and outside the university community.

Minimum Qualifications * A PhD or equivalent in Biology or a closely related field * A distinguished scholarly record commensurate with the rank of Tenured Professor * Relevant administrative experience

Desired Qualifications * Demonstrated appreciation for a breadth of research areas within Biology and interdisciplinary science * Demonstrated innovative and strategic leadership * Demonstrated experience serving a diverse student and/or faculty population

To apply, please submit to solsfacultysearch1@asu.edu: a letter of interest, a curriculum vitae, and contact information including emails for five references. References may be contacted at a later stage of the search and only with the candidate’s approval. Initial deadline for receipt of complete applications is October 13, 2017; if not filled, complete applications will be reviewed each week thereafter until the search is closed. A background check is required for employment. For additional information, please feel free to contact Professor Rajeev Misra (rajeev.misra@asu.edu).

Arizona State University is a VEVRAA Federal Contractor and an Equal Opportunity / Affirmative Action

Employer. All qualified applicants will be considered without regard to race, color, sex, religion, national origin, disability, protected veteran status, or any other basis protected by law. Women and minorities are encouraged to apply. Further information on ASU’s policies can be found at <https://www.asu.edu/aad/manuals/-acd/acd401.html> and its complete non-discrimination statement at <https://www.asu.edu/titleIX>.

— / —

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>

ArizonaStateU MechanismsOfEvolution

Assistant/Associate/Full Professor JOB #12075 School of Life Sciences and the Biodesign Center for Mechanisms of Evolution Arizona State University

The School of Life Sciences (SOLS) and the Biodesign Center for Mechanisms of Evolution (CME) at Arizona State University (ASU) invite applications for up to two full time, tenure-track, open rank faculty positions with an anticipated start date of August 2018. These are the first of six anticipated new Center faculty positions, focused on the mechanistic processes underlying evolutionary change. Members of the group will be housed in a new building in the Biodesign Institute (<https://biodesign.asu.edu/>), which itself supports a diversity of other interdisciplinary centers and is well-equipped with state-of-the-art facilities. The CME is part of a growing community of evolutionary biologists at ASU (<https://sols.asu.edu/evolutionary-biology-faculty> and <http://asupopgen.org/>).

The research focus of the Center will primarily be at the cellular level, with the group being populated by scientists from the areas of cell biology, microbiology, biophysics, biochemistry, and population genetics. The successful candidate will join a dynamic faculty working to advance innovative research and excellence in teaching through its work in the diverse and growing undergraduate and graduate student population at ASU. We invite you to learn more about the School of Life Sciences, the Biodesign Institute, and Arizona State University by visiting <https://sols.asu.edu>, <https://biodesign.asu.edu> and <https://newamericanuniversity.asu.edu/>, respec-

tively. Candidates can anticipate competitive salary and start-up packages.

Successful candidates will be expected to develop an innovative, extramurally-funded, independent research program; fulfill teaching requirements at both the undergraduate and graduate levels, including mentoring undergraduate and graduate students, and postdoctoral trainees; and have a commitment to outreach and service at levels within and outside the University community. Interaction and collaboration with faculty of SOLS and with other groups in the Biodesign Institute, the School of Molecular Sciences, and the recently announced Mayo Clinic and ASU Alliance for Health Care partnership is encouraged.

Minimum Qualifications: A doctoral degree or MD/PhD in the biological sciences or a related field, and two or more years of relevant postdoctoral experience at the time of appointment; demonstrated research and teaching/mentoring excellence; a significant commitment to evolutionary biology and to integrating theory with empirical work; a demonstrated record of significant publications; and potential to develop a strong research program on the mechanisms of evolution.

Desired Qualifications: Strong interest and training in understanding the mechanisms of evolution at the cellular and/or population-genetic levels; research areas that complement expertise of existing faculty and will expand our overall research and instructional capabilities. Examples of desired research foci include: the molecular mechanisms of evolution in experimental microbial populations; the evolution of protein structure and function; the evolution of bioenergetic and growth properties of cellular and subcellular features; the mechanisms underlying cell biological scaling laws; the evolution of intracellular communication systems such as transcription and signal transduction; and the development of high-throughput / nanotechnological approaches for addressing these issues. We are fully open to candidates whose research has strong applied implications. Demonstrated ability to work with diverse student populations and/or reaching out to diverse communities is desirable.

To apply, please submit the following materials in a single PDF document to solsfacultysearch3@asu.edu: (1) Cover letter that includes contact information (including email addresses) for three references who may be contacted a later stage of consideration, (2) a comprehensive curriculum vitae that includes a complete publication record, (3) three representative publications, (4) a statement of research vision and plans, (5) a statement of teaching philosophy/experience. All applications must be sent electronically. Specific scientific inquiries can be addressed to Michael Lynch, Director of the CME

(mlynch11@asu.edu). Initial deadline for review of complete applications is September 30, 2017; if not filled, review will continue every week thereafter until the search is closed. A background check is required for employment.

Arizona State University is a VEVRAA Federal Contractor and an Equal Opportunity/Affirmative Action Employer. All qualified applicants will be considered without regard to race, color, sex, religion, national origin,

— / —

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>

AustNatInsectCollection ResProjOfficer

Job: Res.Proj.Officer_Australian_National_Insect_Collection

The Australian National Insect Collection (ANIC) is the largest collection of Australian insects and related invertebrates in the world, with over 12 million specimens. The collection is an important component of CSIRO's National Research Collections Australia (NRCA), and critical to the future of insect biodiversity research in Australia. The collection has a staff of 20 including Research Scientists, Postdoctoral Fellows, PhD Students and technical officers who manage and improve the collection and conduct research in Australian insect taxonomy, systematics and related fields. Two Department of Agriculture and Water Resources staff are embedded in the collection and provide critical identifications and advice for biosecurity, in collaboration with ANIC research scientists.

The role of Research Projects staff in CSIRO is to collaborate in scientific activities with other research staff usually by assisting with detailed planning, undertaking or assisting with experimental and observational work, and in carrying out the more practical aspects of the work. This is one of several Technical Assistant positions in ANIC. Duties of this role include the curation and development of ANIC under the guidance of ANIC Director and ANIC Collection Manager. This will include, but will not be restricted to, specimen mounting, preparation, dispatch, identification and management upon return of specimen loans, molecular laboratory work

and support to ANIC staff, in particular to a Research Scientist.

To view the full position description and selection criteria for this role please go to http://www.csiro.au/~ /media/Positions/2017/NCMI/45781_Research_Projects_Officer_ANIC_CSOF4_PD.doc

Location: Black Mountain, ACT Salary: AU \$80K - AU \$91K plus up to 15.4% superannuation Tenure: Indefinite Ref No.: 45781

To be successful you will need:

* Relevant Bachelors/Master's Degree &/or equivalent experience in Biology, molecular biology and/or conservation. * Experience handling, identifying and curating biological specimens, especially insects, in a natural history museum setting. * Practical experience in the independent implementation and optimization of molecular laboratory protocols, including experience in DNA extraction, PCR, and Sanger Sequencing. * The ability to focus on complex tasks and attention to detail. * The ability to work effectively as part of a team, and carry out tasks autonomously in support of scientific research. * Ability to communicate basic facts in a courteous manner, also providing instruction and assisting other staff to complete allocated tasks and activities. * Willingness to accept personal responsibility for doing the job well and proven ability to demonstrate initiative and look for ways to make improvements. * Adaptability to accept the need for change to work routines or technology, and demonstrated ability & willingness to contribute novel ideas and approaches in support of scientific investigations

To apply for this position you will be required to submit your resume and cover letter, as one document, highlighting your experience as relevant to the role requirements.

Applications close: 11:59pm AEST on Tuesday 19th September 2017

Juanita.Rodriguez@csiro.au

BRCAS Taiwan EvolutionaryBiology

Tenure-Track Position in Evolutionary Biology - Effective 03 June 2017

The Biodiversity Research Center, Academia Sinica (BR-CAS; <http://biodiv.sinica.edu.tw/>), Taipei, Taiwan, invites applications for a tenure track position in Evo-

lutionary Biology. The rank is open, although junior scientists are preferred. Candidates with a research interest in evolutionary biology are encouraged to apply. Applicants who address evolutionary biology questions using molecular and genomic approaches are preferred. Applicants must have postdoctoral research experience and have a strong publication record.

BRCAS was officially established in 2005. The center consists of four divisions: Marine biodiversity and ecosystems, Terrestrial biodiversity and ecosystems, Molecular and genomic evolution, and Microbial biodiversity. BRCAS provides each PI with some internal support and a good start-up. It is in charge of a sequencing core with two HiSeq2500s, one MiSeq, and one PacBio Sequel. Academia Sinica is well-equipped with modern research facilities. The position will be open until filled; however, the first review will be conducted in mid-Sept 2017. Applicants should submit the names and e-mail addresses of three references along with CV (including a list of publications), 3-5 representative papers (pdf files), and a statement of past accomplishments and future research interests to Ms. Miao-Suey Lin (zomslin@gate.sinica.edu.tw). Please indicate the rank to which you want to apply: our "assistant research fellow" is equivalent to "assistant professor".

Tsai Isheng <ijtsai@gate.sinica.edu.tw>

BRCAS Taiwan MicrobialDiversity

Tenure-Track Position in Microbial Diversity

The Biodiversity Research Center, Academia Sinica (BR-CAS; <http://biodiv.sinica.edu.tw/>), Taipei, Taiwan, invites applications for one tenure-track position in Microbial diversity at the Assistant or Associate Research Fellow level, is equivalent to "assistant professor" or "associate professor". The applicant must possess a PhD, preferably with postdoctoral experience and a successful track record of scientific productivity.

We seek outstanding candidates in any area of microbiology who utilize various approaches (high throughput culturing, systematics, phylogenetics, molecular biology, ecology) to study microorganisms in fundamental and environmental contexts. We especially encourage candidates with research interest in areas of microbial ecology, diversity of microorganisms and microbial genomics.

BRCAS wishes to strengthen research in microbial diversity and systematics. The center provides each PI with

some internal support and good start-ups for new PIs. The center consists of four divisions: Marine biodiversity and ecosystems, Terrestrial biodiversity and ecosystems, Molecular and genomic evolution, and Microbial biodiversity. It is in charge of a sequencing core with one Pacbio Sequel, two HiSeq2500's and one MiSeq and Academia Sinica is well equipped with modern research facilities.

The position will be open until filled; however, the first review will be conducted in mid-September 2017. Applicants should submit the names and e-mail addresses of three references along with CV (including a list of publications), 3-5 representative papers (pdf files), and a statement of past achievements and future research interests to Ms. Miao-Suey Lin (zomslin@gate.sinica.edu.tw). Please indicate the rank to which you want to apply.

Tsai Isheng <ijtsai@gate.sinica.edu.tw> Tsai Isheng <ijtsai@gate.sinica.edu.tw>

ClaremontC EvolutionaryBiol

Description:

The W.M Keck Science Department of Claremont McKenna, Pitzer and Scripps Colleges invites applications for a tenure-track position in the ecology/evolutionary biology of disease at the Assistant Professor level, to begin July 2018. The department houses the biology, chemistry, physics and environmental science faculty for three of the five undergraduate Claremont Colleges, and offers innovative and interdisciplinary programs in both natural and physical sciences. Many of our faculty participate in collaborative research projects, both within the department and with research groups at nearby institutions. Candidates must be committed to excellence in teaching and development of a vibrant research program that engages undergraduate students. We especially seek candidates whose work on disease is cross-disciplinary within the sciences and speaks to students with diverse interests, including the environment and human health. Of particular interest are candidates who could offer courses on the mathematical modeling, ecology and/or evolution of infectious disease, disease and the environment, and/or emerging diseases. Teaching opportunities will include introductory courses in a core discipline (biology or environmental science), as well as courses in the candidate's area of expertise. A Ph.D., postdoctoral experience and a record of scholarly publication are required.

Procedures and Timetable:

Please apply online at <https://webapps.cmc.edu/jobs/-faculty/home.php>. Upload a cover letter, a curriculum vitae, a statement of your proposed approach to teaching science in a liberal arts setting, a statement (of no more than 1 page) describing your approach and experience in mentoring diverse student populations, a description of your proposed research, and the names and email addresses of three references. Inquiries regarding the position may be emailed to Professor Diane Thomson at dthomson@kecksci.claremont.edu. Additional information about the department may be found at www.kecksci.claremont.edu. Review of applications will begin October 1, 2017, and the position will remain open until filled.

The Keck Science Department of Claremont McKenna, Pitzer and Scripps Colleges is an equal opportunity employer. In a continuing effort to enrich its academic environment and provide equal educational and employment opportunities, the department actively encourages applications from women and members of historically under-represented social groups in higher education.

Thanks.

FFinseth@kecksci.claremont.edu

ClaremontC EvolutionaryMicrobiol

Description: The W.M. Keck Science Department of Claremont McKenna College, Pitzer College and Scripps College invites applications for a tenure-track appointment in Microbiology at the Assistant Professor level to begin July 2018. The department, which houses faculty in biology, neuroscience, chemistry, physics, and environmental analysis for three of the five undergraduate Claremont Colleges, offers innovative and interdisciplinary programs in the natural and physical sciences. Many faculty members participate in collaborative research projects, both within the department and with research groups at nearby colleges and universities.

We seek a broadly trained microbiologist who is committed to excellence in teaching and who will develop a vibrant research program using molecular and quantitative methods that fully engages undergraduate students. We are particularly interested in candidates with expertise in a range of experimental molecular microbiology subtopics including but not exclusive to bacterial physiology and metabolism; bacterial cell biology; gene

expression and regulation; cell-cell communication; and host-microbe interactions. The position offers opportunities to teach a combination of courses including microbiology with laboratory, introductory biology (cell and molecular focus), non-majors courses and advanced courses in the candidate's field. A Ph.D. degree, post-doctoral experience, and a record of scholarly publication are required.

Procedures and Timetable: Please apply online at <https://webapps.cmc.edu/jobs/faculty/home.php>. Please upload a cover letter, curriculum vitae, statement of teaching philosophy, a statement (of no more than 1 page) describing your approach and experience in mentoring diverse student populations, a description of your proposed research and including a brief description of important equipment and biosafety needs, and the names and e-mail addresses of three references. Enquiries may be addressed to Dr.

Patrick Ferree at pferree@kecksci.claremont.edu. Additional information about the department may be found at www.kecksci.claremont.edu. Review of applications will begin October 23, 2017, and the position will remain open until filled.

The Keck Science Department of Claremont McKenna, Pitzer, and Scripps Colleges is an equal opportunity employer. In a continuing effort to enrich its academic environment and provide equal educational and employment opportunities, the department actively encourage applications from members of historically under-represented social groups in higher education.

FFinseth@kecksci.claremont.edu

ClarkU EvolutionaryEcol

Biology Department Tenure Track Assistant Professor of Ecology (BIO18)

Founded in 1887, Clark is a teaching and research university located in Worcester, Massachusetts, and one of the oldest graduate institutions in the United States. The University's mission is to educate undergraduate and graduate students to be imaginative and contributing citizens of the world, and to advance the frontiers of knowledge and understanding through rigorous scholarship and creative effort.

Clark University's Department of Biology invites applicants for a tenure-track appointment at the rank of Assistant Professor to begin fall 2018. The successful

candidate will have research space in the Lasry Center for Biosciences and is expected to develop an externally-funded research program involving Ph.D., Masters, and undergraduate students. Any area of ecology will be considered; there will be opportunities to participate in interdisciplinary programs including Environmental Science, Mathematical Biology & Bioinformatics, and Public Health. Postdoctoral experience, evidence of external funding success, and promise of teaching excellence at undergraduate and graduate levels are desired. The successful candidate will teach Ecology, Biostatistics, and other courses in his or her area of expertise that serve the needs of the Biology Department.

Information about the department is available at www.clarku.edu/departments/biology/. We are especially interested in qualified candidates who can contribute, through their research, teaching, and/or service, to the diversity and excellence of the academic community.

Applicants should submit a curriculum vitae, statements of research and teaching interests, and three key publications in one pdf document. Three letters of reference should be submitted by the referees via email to the Ecology Search Committee (ecology@clarku.edu). Letters can also be mailed to the Chair of the Ecology Search Committee, Department of Biology, Clark University, 950 Main St, Worcester, MA 01610-1477. E-mail inquiries may be directed to Justin Thackeray (jthackeray@clarku.edu). Review of applications will begin September 15, 2017.

Clark University embraces equal opportunity as a core value. We believe that cultivating an environment that embraces and promotes diversity is fundamental to the success of our students, our employees, and our community. This commitment applies to every aspect of education, services, and employment policies and practices at Clark. Our commitment to diversity informs our efforts in recruitment, hiring and retention.

Clark University is an affirmative action/equal employment opportunity employer and strongly encourages members from historically underrepresented communities - inclusive of all women - to apply.

John G. Gibbons Assistant Professor of Biology
Clark University 950 Main Street Worcester, MA 01610
Email: jgibbons@clarku.edu Tel: 508.793.7129
<https://wordpress.clarku.edu/jgibbons/> John Gibbons
<JGibbons@clarku.edu>

EmoryU GenomeEvolution

We have a open search for a tenure-track position in the biology department at Emory University with a focus on genome evolution and epigenetics. The link can be found here <https://apply.interfolio.com/44127>. Meleah A. Hickman, Ph.D. Assistant Professor, Dept. of Biology Emory University Atlanta, GA 30322 Office: 1027 RRC, (404) 727-6491 Lab: 1083 RRC, (404) 727-6552 <https://scholarblogs.emory.edu/hickmanlab/> “Hickman, Meleah A.” <meleah.hickman@emory.edu>

Florida MNH AssistantCurator

The Florida Museum of Natural History, University of Florida, invites applications for an Assistant Curator (equivalent to Assistant Professor), a tenure-track position, who will serve as curator-in-charge of the Herbarium, including supervision of its staff. The successful candidate is expected to conduct a dynamic research program focused broadly on the evolutionary biology of plants.

Qualified candidates must have a Ph.D. in Biology, Botany, or a closely related field, and demonstrate a record of research and publication focused on the evolution of any group(s) of plants. Candidates should also be willing to collaborate actively, although not exclusively, with the University of Florida’s diverse botanical research programs in the Florida Museum of Natural History, Department of Biology (College of Liberal Arts and Sciences), and Institute for Food and Agricultural Sciences. Candidates must be capable of leading, promoting, and utilizing an internationally recognized Herbarium (FLAS) that includes >465,000 specimens of vascular plants, bryophytes, algae, and moss.

The appointee is expected to teach and mentor both undergraduate and graduate students at the University of Florida. Pursuit of external funding is expected. The anticipated start date is no later than August 15, 2018. Salary is competitive and commensurate with experience.

The search committee will begin reviewing applications on October 1, 2017. To be considered, all applica-

tions must be submitted on-line by October 1, 2017. To submit an application packet, please go to <http://explore.jobs.ufl.edu/cw/en-us/listing/> and search by Job# 503444. Applications received after this date may be considered at the discretion of the Committee and/or hiring authority. The application should include as a single PDF document: (1) cover letter, (2) curriculum vitae; (3) a statement of experience and philosophy for research, collections, teaching, and outreach (no more than 1 page for each); (4) PDFs of three representative publications; and (5) the names and email addresses of three colleagues who may be contacted for letters of recommendation.

Any questions regarding this position or nominations may be directed to search committee chair Dr. David C. Blackburn, Florida Museum of Natural History, University of Florida, Gainesville, Florida 32611 (dblackburn@flmnh.ufl.edu; +1-352-273-1943).

The University of Florida is an Equal Opportunity / Affirmative Action Employer. If an accommodation due to a disability is needed to apply for this position, please call (352) 392-2477 or the Florida Relay System at (800) 955-8771 (TDD). The selection process will be conducted under the provisions of Florida’s “Government in the Sunshine” and Public Records laws.

dblackburn@flmnh.ufl.edu

FWS NewMexico 2 FishEvolution

Could you please post the following two positons on EvolDir. Thank you. The following vacancy announcements are now open on USAJobs: Geneticist, GS-0440-09 (FPL 11), located at the Southwestern Native Aquatic Resources and Recovery Center, Dexter, New Mexico. This is a permanent, full-time, Geneticist (Fisheries) position, located at the Southwestern Native Aquatic Resources and Recovery Center in Dexter, New Mexico.

The Full Promotion Level for this position is GS-11. Duties - Extract and archive DNA. - Operate and maintain laboratory equipment, including automated sequencers (ABI 3130XL and 3500), centrifuges, and thermal cyclers. - Provide general advice and technical assistance to other professionals, agencies, tribal groups, and educational institutions on analytical techniques and applied research accomplishments. - Provide oral presentations at workshops, symposia, and other scientific meetings. - Provide overall technical coordination of complex molec-

ular genetics analyses for a variety of projects. R2-17-2001963-CL-DE R2-17-2002098-CL-MP Open 08.18.17 Close 08.31.17 and

The following vacancy announcement is now open on USAJobs: Interdisciplinary: Fish Biologist, GS-0482-09 (FPL 11), or Fish and Wildlife Biologist, GS-0401-09 (FPL 11) located at the Southwestern Native Aquatic Resources and Recovery Center, Dexter, New Mexico.

This is a full-time, TERM position, Not-to-Exceed 13 months, but MAY be extended up to 4 years at management's discretion.

The employee will serve as a Fish and Wildlife Biologist or Fish Biologist within the Research Unit of the Southwestern Native Aquatic Resources and Recovery Center in Dexter, New Mexico.

Duties

- Conducts applied research projects that include the application of advanced molecular tools to solve genetic management problems, using appropriate molecular techniques and knowledge of conservation biology to assist regional partners in endangered species management.
- Develops project proposals, scope of work, grants, and budgets for applied research investigations, which are submitted to internal (Service) and external funding sources.
- Implements, coordinates, and conducts monitoring of wild and captive populations, determines whether genetic changes have occurred and to what extent, and develops complex methodologies for monitoring genetic resource and life history patterns of wild populations with which captive individuals may interbreed.
- Prepares and delivers oral reports of findings at regional, national, and international professional conferences, workshops, seminars, program reviews, and public meetings.
- Prepares a wide variety of written materials including manuscripts for publication in peer-reviewed scientific journals, popular articles, technical bulletins, study proposals, and progress reports based on activities and findings.

R2-17-2002424-CL-DE Open 08.21.17 Close 09.01.17
For more information contact: Wade D. Wilson U.S. Fish and Wildlife Service Southwestern Native Aquatic Resources and Recovery Center P.O. Box 219 Dexter, NM 88230 Phone: (575) 734-5910 ext. 113 wade_wilson@fws.gov

“Wilson, Wade” <wade_wilson@fws.gov>

HalleU MolecularEvolEcol

Candidates pursuing a research program in 'evolution' will be very appreciated.

A full chair (tenured professorship) in Molecular Ecology is available from 01.04.2018 at Martin-Luther-University Halle-Wittenberg, Germany. We seek to appoint an internationally recognized scientist with a focus on the molecular ecology of insects. The successful candidate should hold a PhD and strengthen well-established research areas at the German Center for Integrative Biodiversity Research Halle-Jena-Leipzig (iDiv: <http://www.idiv.de>).

The candidate will have extensive experience both in conducting independent scientific research and in undergraduate and graduate education. Courses to be taught include all aspects of molecular ecology in the field of zoology. Requirements for application include 'habilitation' or an equivalent academic achievement (e.g. publication record as independent researcher after the PhD, PhD student supervision, and teaching experience), a proven track-record in internationally recognized research and appropriate teaching experience. Experience in the acquisition of third party funding is expected, as is knowledge of German, or a willingness to learn. Applications, including a cover letter, complete list of publications and academic teaching activities, evidence of successful acquisition of third party funding, and copies of certificates of the highest academic degree obtained, should be sent as a single pdf file via email (Dekanat.bnpn@natfak1.uni-halle.de) not later than 6th Sept 2017.

Robert Paxton <robert.paxton@zoologie.uni-halle.de>

Institut Pasteur 10 Bioinformatics

10 Permanent Positions in Bioinformatics and Biostatistics at Institut Pasteur (Paris)

Bioinformatics, biostatistics and integrative biology have emerged as strategic priorities for the Institut Pasteur. A new “Center for Bioinformatics, Biostatistics and Integrative Biology” (C3BI - <https://c3bi.pasteur.fr>)

has been created in 2015 on the Parisian campus. The objective of this center is to federate and strengthen capacities in bioinformatics and biostatistics in the different research areas developed within the institute around biology and health.

Within this framework and after 28 recruitments since 2014, Institut Pasteur proposes again ten permanent positions in bioinformatics and biostatistics for 2017. Successful applicants will be affiliated to the C3BI and to the Hub of Bioinformatics and Biostatistics and will be supervised by the director of the Center. They may be assigned for most of their time to other research units and/or technological platforms within Pasteur. Additionally, the positions also foresee teaching activities both at Paris and in the Institut Pasteur International Network.

TASKS AND RESPONSIBILITIES

The main objective is to provide support to research units and platforms at Institut Pasteur for the analysis of their data using bioinformatics and statistics approaches. This support will be provided in various ways:

- * advising and guiding in the use of existing methods and tools
- * maintaining an active bibliographical survey and evaluating existing tools and methods
- * developing new methods and tools when needed
- * collaborating with research units and platforms to analyze their data
- * helping, defining and implementing collaborative projects such as ANR, ERC, etc.
- * transferring knowledge and tools towards research units and platforms, and providing training in bioinformatics and biostatistics
- * supporting and maintaining methods and tools developed by research units, and ensuring their integration within open platforms such as Galaxy, ;
- * actively participating in the implementation of the web portal of the Pasteur Institute bioinformatics platform, to be open to the international community,
- * interacting with the Institut Pasteur International Network (IPIN, 33 institutes all around the world), mainly for setting up trainings and analyzing data

AVAILABLE POSITIONS

This year positions will mostly focus on the following domains:

- * Biological image analysis

- * Statistical genetics - Human genomics
- * New HTS data (single cell, long reads ;)
- * Epigenomics
- * Annotation of eukaryotic genomes and proteomes
- * evolution, phylogeny, population genetics
- * Development of software and bioinformatics pipelines
- * Metagenomics
- * Systems biology and modeling
- * Data management

EXPECTED PROFILES

In order to apply, you need to:

- * hold an engineering or master degree in (bio)informatics, (bio)statistics, applied mathematics or any other related domain, followed by at least 3 years of professional experience in bioinformatics and/or biostatistics in research or support to research activity,
- * or hold a PhD in bioinformatics, biostatistics, applied mathematics or any other related domain, followed by at least 2 years of professional experience in bioinformatics and/or biostatistics in research or support to research activity.

Strong experience in teaching bioinformatics/biostatistics will be a plus.

TO APPLY

Applications (cover letter, detailed CV and referees addresses) have to be filled on line at the following URL: <https://c3bi.pasteur.fr/careers/c3bi-2017-job-application/> The deadline for applications is September 5th, 2017. Candidate pre-selection will take place around October 2nd, 2017. Short-listed candidates will be called for an interview between October 10th and 12th, 2017 (dates to be reserved absolutely).

PLEASE DIFFUSE THIS ANNOUNCEMENT !!

Olivier GASCUEL <olivier.gascuel@pasteur.fr>

Lynker Marine Conservation

This is most definitely directed toward evolutionary biologists, with an emphasis on marine fisheries biology.

Marine Molecular Geneticist I

Lynker Technologies, LLC has an immediate opening for a qualified marine molecular geneticist to fill a position on a contract with the NOAA Fisheries service.

This role involves supporting Lynker's National Marine Fisheries Service (NMFS) operations at the Northwest Fisheries Science Center (NWFSC) within the Conservation Biology Division (CB), Genetics and Evolution Program.

In this role, the candidate will work with senior CB Genetics and Evolution Program staff members in supporting four general projects: 1. Genetic analysis of Chinook and Steelhead salmon populations for management purposes, 2. Genetic analysis of marine fish populations to assist population assessment and evaluation of life history parameters, 3. Genomic and physiological analyses related to the effects of ocean acidification on marine organisms, 4. Sequencing marine fish species for the Marine Forensic Voucher project.

Your work will contribute directly to NOAA's and the world's understanding of salmon and groundfish population and life cycles, which provide critical inputs to the management and conservation of these important commercial fishing species.

To be considered, you must meet the following minimum qualifications: * A Bachelor's degree from an accredited college or university with a major clearly in a related field of study with emphasis in molecular biology, population genetics, forensic science or a clearly related field and a minimum of three (3) years demonstrated field capability and related directly to the individual task order.

or * A Master's degree from an accredited college or university with a major clearly in a related field of study with emphasis in molecular biology, population genetics, evolutionary biology, forensic science or a clearly related field may be substituted for two (2) years of the required experience.

or * Three (3) years of progressively higher level graduate education leading to a Ph.D. or Ph.D. from an accredited college or university with a major clearly in

a related field of study with emphasis in molecular biology, population genetics, evolutionary biology, forensic science or a clearly related field may be substituted for the required experience.

and * Molecular genetics laboratory experience, including isolation of DNA and polymerase chain reaction * Experience with generation of genotype data, including single nucleotide polymorphism (SNP) data via TaqMan assays and next-generation sequencing of amplicons for GT-seq * Experience with spreadsheets and data entry * Demonstrated experience in the collection of biological samples, including the collection of tissues for the isolation of DNA. * Demonstrated experience with research on marine organisms (marine fish, mammals or invertebrates)

Please send your resume, list of references, and explanation of how you meet the requirements above to recruiting@lynkertech.com.

Thanks! Liz

Elizabeth J. Tarquin Director, Marine Sciences Division Lynker Technologies LLC (808) 747-3065 ltarquin@lynkertech.com www.lynkertech.com Lynker - a HubZone- and ISO-certified company

Liz Tarquin <ltarquin@lynkertech.com>

MichiganStateU BioStationDirector

Director and Professor W.K. Kellogg Biological Station at Michigan State University Michigan State University seeks a director for the W. K. Kellogg Biological Station (KBS) to provide leadership and promote a creative environment that fosters innovation and excellence in the Station's research, education, and outreach programs in ecology, evolution, agriculture, and conservation biology. This is an annual-year (12-month) full-time academic appointment based at KBS at the level of Full Professor, with a tenure appointment in a campus department appropriate to the candidate's expertise. The position is expected to be filled beginning August 2018.

Candidates should have a PhD and demonstrated potential to lead and manage a dynamic program of interdisciplinary research, education, and outreach, a record of research excellence in any area of ecology, evolution, agriculture, or conservation biology, and strong interpersonal skills. The position carries minimally a 60% administrative assignment; the remainder of the appointment can be split among research, teaching, and

outreach. Continuation of an active research program is encouraged and will be supported.

KBS is one of the world's leading biological field stations, and is located in southwest Michigan, 65 miles southwest of the MSU main campus in East Lansing. The Station includes 13 resident faculty, ~30 graduate students, postdoctoral scholars, and academic specialists. KBS programs are fully integrated into the academic and outreach programs of MSU. All faculty hold academic appointments in departments on the MSU campus, and they participate in campus teaching and departmental and interdepartmental graduate programs. KBS comprises over 1300 hectares of natural and managed, aquatic and terrestrial habitats, as well as modern research laboratories. In addition to the academic personnel, KBS includes the Kellogg Farm, Bird Sanctuary, and Conference Center. Additional information about KBS can be found at www.kbs.msu.edu. The KBS Director reports to the deans of the College of Agriculture and Natural Resources (lead college) and the College of Natural Science at MSU. The Director oversees the research and education programs at KBS and coordinates these programs with campus departments. The Director also leads major development efforts in support of KBS programs, and is responsible for promoting KBS to local, regional, national, and international organizations.

Applicants for the position of Director should submit 1) a CV and 2) a cover letter describing your interest in the position with an emphasis on your leadership experience and philosophical approaches to faculty development, student success, and achieving a culture of diversity and inclusion. At the end of the cover letter, please include names and contact information for three (3) references who are familiar with your work and leadership experience. Letters are not initially required, but these individuals may be approached for additional information only after obtaining the applicant's permission to do so. Applications should be submitted on line at <https://careers.msu.edu> (posting #453174). Review of applications will begin 15 September 2017, and will continue until a suitable candidate is identified. Questions regarding this position may be directed to the Search Committee Co-Chairs, Dr. Michael Jones (jonesm30@msu.edu) and Dr. Danny Schnell, (schnelld@msu.edu).

"Smith, Jennifer" <jlark@kbs.msu.edu> "Smith, Jennifer" <jlark@kbs.msu.edu>

MolEcoRes Journal EcolEvolution

We are hiring a PhD level "molecular ecologist or related" to work on the journal Ecology & Evolution.

The position is located in Oxford, UK.

Here is the job announcement:

https://www.linkedin.com/jobs/cap/view/379324763/-?pathWildcard=379324763&trk=job_capjs

and the journal website:

<http://onlinelibrary.wiley.com/journal/10.1002/-%28ISSN%292045-7758> Karen E. Chambers, Ph.D. Managing Editor Molecular Ecology - Molecular Ecology Resources John Wiley & Sons, 111 River Street, 8-02, Hoboken, New Jersey 07030

Phone: 201-748-7773

Manager.molecol@wiley.com molecol@wiley.com
www.wiley.com "Chambers, Karen - Hoboken"
 <kchamber@wiley.com> "Chambers, Karen - Hoboken"
 <kchamber@wiley.com>

Museum RichmondIndiana PartTime TeachingEvolution

We are searching for a passionate science communicator to coordinate our education and outreach program at the Joseph Moore Museum in Richmond, Indiana. Job ad below.

Position: Education and Outreach Coordinator

Department: Joseph Moore Museum

Status: Part-time Administrative Faculty (28 hours/week)

Salary: Commensurate with experience

The Joseph Moore Museum at Earlham College seeks a part-time (28 hours/week, 12 months) qualified and dynamic Community Engagement Specialist for immediate hire.

The JMM is a dynamic college museum focused on forging meaningful connections among community members

and supporting exploration and application of scholarly knowledge to topics of importance to society. Our museum is largely student-run, where faculty provide support, training, and mentorship for students who are learning to be tour leaders, researchers and collections specialists. We strive to create engaging community programs and exhibits that combine the strengths of our college natural history and ethnographic collections, planetarium, scholarly research of Earlham College faculty, and the passions of our three museum faculty and ~40 undergraduate student staff. First publicly opened in 1887, the JMM has long been known as the region's natural history museum and is located in Richmond, Indiana on the campus of Earlham College.

Responsibilities

- *Supervise, train and mentor Earlham College undergraduate student staff* in outreach (i.e. interacting with the public through tours, events, and museum hosting during open hours). The majority of the coordinator's work is supporting students who engage with the community.
- *Plan and implement community educational programs* for the Joseph Moore Museum in line with the museum's mission and vision, including designing, scheduling, staffing/leading, publicizing and promoting educational tours that meet state standards throughout the school year and in summer.
- *Plan and implement special events* to connect Earlham community members with each other and the broader Wayne County community around topics of importance to science and society. Must be available on evenings and weekends to oversee events.
- *Assist with exhibits*, including maintenance, refurbishment and design.
- *Prepare an annual report* documenting and critiquing community engagement at JMM. This includes keeping daily statistics on program attendance and student tour leader performance.
- *Assist with fundraising* for community engagement.
- *Assist with developing and implementing an Outreach and Education Plan* for JMM.

Minimum Qualifications

- Bachelor's degree, preferably in education with a scientific focus
- Previous experience in leading educational programming for children pre-k-12th grade.
- Previous experience as a supervisor
- Certified Interpretive Guide through NAI, or

available and willing to complete training <
https://www.interpnet.com/nai/nai/_events/-Event_Display.aspx?EventKey=3DCIG092017 >
 September 20th to 25th and have personal transportation during that time period.

Key Attributes

- Either a degree in a *scientific* field or substantial experience leading *science* or *nature* programs for children
- Ability to supervise, mentor, and organize college students
- Dedication to working enthusiastically as part of a team of faculty and students
- Ability to connect with people of diverse ages and backgrounds
- Excellent written and verbal communication skills
- Excellent attention to detail, logistics and daily planning
- Ability to work independently
- Strong commitment to community engagement
- Passion for communicating science
- Flexibility to work in a fast-paced environment

More information

Potential applicants are encouraged to contact JMM Director, Heather Lerner, at *765-983-1402* or *lernehe@earlham.edu*

Review of applications will begin immediately and continue until the position is filled. Position will begin as early as possible, preferably prior to September 25, 2017. Announcement posted August 17, 2017.

Application

Please send a cover letter detailing qualifications for the position, CV, a list of at least three professional references and a detailed sample plan for a science or nature-based elementary school tour as a single electronic file to: thistbe@earlham.edu.*

Earlham College continues to build a community that reflects the gender and racial diversity of the society at large, and, therefore, we are particularly interested in inviting and encouraging applications from African Americans, other ethnic minorities, and women. Earlham also is eager to solicit applications from members of the Religious Society of Friends (Quakers).

Earlham is an Equal Opportunity Employer.

Cheers,

Heather

Heather R. L. Lerner, Ph.D., M.S.

— / —

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>

NewCollege Florida EvolutionaryMicrobiol

Assistant Professor Position in Microbiology at New College of Florida

New College of Florida invites applications for a tenure-track Assistant Professor position in Microbiology starting in August, 2018. A Ph.D. in the biological sciences or a related field is required. Research interests incorporating environmental microbiology in marine or freshwater systems are preferred. The successful candidate must be committed to excellence in teaching and research, and postdoctoral research and teaching experience are strongly preferred. New College is committed to recruiting and retaining a diverse faculty. Women and candidates from underrepresented groups or whose knowledge or skills can support an inclusive culture and learning environment are especially encouraged to apply.

The teaching load is two courses per semester plus sponsoring individual and group tutorials. In addition to classes and tutorials, faculty members provide academic advising, supervise independent study projects, sponsor senior undergraduate theses/projects, and serve on baccalaureate committees. The successful candidate is expected to establish and maintain a program of research. We are particularly interested in candidates who have a demonstrated commitment to innovative undergraduate liberal arts teaching.

Situated on the Gulf Coast of Florida and Sarasota Bay, New College is a nationally recognized, highly-selective public honors college with an 11:1 student/faculty ratio. Students are intellectually independent and highly motivated. Undergraduate research has a central role in the curriculum, and a senior thesis/project is required of all students. Students receive narrative evaluations in lieu of grades. New College is committed to excellence in undergraduate teaching and research and encourages collaborative student-faculty scholarship. www.ncf.edu.

A description of the Division of Natural Sciences is at <https://www.ncf.edu/academics/undergraduate-program/division-of-natural-sciences/>. Facilities include a new wing of the science building and the Pritzker Marine Biology Research Center, which features circulating conditioned seawater and life support equipment suitable for culturing a wide variety of aquatic organisms.

A complete application will include a letter of application, curriculum vitae, the names of three references (including at least one who can address teaching), unofficial graduate transcripts, a statement of teaching philosophy (including course proposals), a statement regarding the candidate's contributions or approaches to supporting an inclusive culture and learning environment, and a description of proposed research that includes how undergraduates would be involved. Review of completed applications will begin Oct. 16 and continue until the position is filled. An online application: <https://ncf.simplehire.com/> should be completed. According to Florida law, applications and meetings regarding applications are open to the public upon request. New College of Florida is an EOE institution. — Katherine M. Walstrom, Ph.D. Associate Professor of Biochemistry and Chair, Division of Natural Sciences Div. Natural Sciences, HNS 111 5800 Bay Shore Rd. New College of Florida Sarasota, FL 34243-2109 phone 941-487-4493 FAX 941-487-4396

Katherine Walstrom <walstrom@ncf.edu>

NHM UOslo ResearchDirector

Research Director Natural History Museum University of Oslo, Norway

The Natural History Museum is looking for a new research director. The Natural History Museum's tasks include research, collection management, teaching and public outreach in the fields of botany, zoology, palaeontology and geology. The museum has about 150 employees, organized in 5 sections, and for 2017 had a total budget of 160 million NOK. Approx. 40 million NOK are related to research projects. The research section consists of 7 research groups.

The museum is in the middle of an exciting process where a new strategy is being developed, and action plans and sub-strategies will be prepared in the coming years. The research director shall have overall responsibility and the responsibility to follow-up the museum's research and education strategy. It is a stated goal

that a larger part of the research will be conducted in cooperation with external partners at home and abroad. Research in the museum today is focused specifically at systematic biology, palaeontology and geology. Once the strategy processes have been completed, there may be a need to adjust today's organization chart. The position is with a fixed-term of 6 years, with the possibility of a second term after public announcement and general competition.

Responsibilities: - Lead the research section and be responsible for initiating, coordinating and developing the museum's research efforts. - Motivate and ensure good cooperative relationships internally at the museum and at UiO elsewhere, nationally and internationally. - Encourage increased research efforts, increased acquisition of external funds, increased innovation, and strengthen the international profile of NHM. - Be a strategic driver of research at the museum and help develop the work in these areas. - Be the deputy director of the museum in matters that include the museum's scientific activities. - Ensure maintenance and strengthening of contacts with the museum's partners in the field of research.

We want a strong and clear leader who will contribute with leadership skills in a strong research environment. The research director reports to the museum director and is part of the museum's management team. The research director has financial and budgetary responsibility and daily staff responsibility for, among other things, the research group leaders.

Qualifications: - Has excellent leadership skills with experience from similar activities in the higher education sector and / or the research sector, which can document previous results. - Has solid experience in human resource management, and task and financial management. - Has skills in strategic and overall thinking. - Has a PhD or equivalent in a relevant subject. - Is result-oriented and skilled in implementation. - Can motivate and inspire its employees - Is a skilled team player and network developer - Has a good and relevant network of contacts with research environments at home and abroad, and broad knowledge of research policy - Has good communication skills in written and oral in English and a Scandinavian language.

Individual suitability for the position will be emphasized in the final recruitment.

We offer: A professionally stimulating working environment. Salary (position code 1111, Research director): NOK 769 100 - 938 700 per year, depending on qualifications.

Pension agreement with Norwegian Public Service Pension Fund (SPK) Attractive welfare benefits The ap-

plication must be sent via Jobbnorge and contain: - An application letter - CV with complete overview of education, experience and professional work. References should be given.

Application deadline Sept 17, 2017: <https://www.jobbnorge.no/en/available-jobs/job/139659/-research-director> Hugo de Boer

Natural History Museum University of Oslo P.O. Box 1172 Blindern 0318 Oslo, Norway Phone: +47 22851875

Leader of ForBio - the Scandinavian Research School in Biosystematics www.nhm.uio.no/english/about/organization/research-collections/people/-hugode/ www.forbio.uio.no/ Hugo de Boer <h.d.boer@nhm.uio.no>

PennsylvaniaStateU EvolutionaryGenomics

The Department of Biology in the Eberly College of Science (www.bio.psu.edu) and the Huck Institutes of the Life Sciences (<http://www.huck.psu.edu>) at The Pennsylvania State University seek enthusiastic, creative, and productive applicants for a tenure-track or tenured faculty position in Evolutionary Genomics. The evolutionary analysis of rapidly expanding genomic datasets requires development and implementation of sophisticated laboratory techniques and rigorous computational approaches. The successful applicant is expected to develop a strong, independent, externally funded research program leading to novel insights and paradigms in evolution from generating and/or analyses of complex genomic datasets. We are particularly interested in candidates working with vertebrate (including human and other mammalian) systems and in candidates developing the theoretical foundation of evolutionary genomics. The applicant must have a Ph.D. in biology, computer science, statistics, software engineering, or a related field. The successful applicant is expected to teach and perform research in a collaborative environment, with the opportunity to join one of the Centers in the Huck Institutes of the Life Sciences and to supervise students from interdisciplinary graduate programs.

This position features a competitive start-up package. Applications must be submitted electronically at <https://psu.jobs/job/73547> and must include a cover letter, curriculum vitae, research interests statement, teaching interests statement, and contact information for at least

three professional references. Review of applications will begin on September 15th and continue until the position has been filled.

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

Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to all qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national origin, disability or protected veteran status.

thanks, Kateryna

Kateryna Makova, Ph.D. Francis R. and Helen M. Pentz Professor Director, Center for Medical Genomics Department of Biology 310 Wartik Lab Penn State University University Park, PA 16802 Tel: 814-863-1619 Fax: 814-865-9131 E-mail: kmakova@bx.psu.edu Lab: http://www.bx.psu.edu/makova_lab/ Center: http://www.bx.psu.edu/ctr_med_genom/ Kateryna Makova <kmakova@bx.psu.edu>

PennsylvaniaStateU ResistanceEvolution

Faculty Cluster Hire in Resistance Evolution

Penn State is adding new open-rank faculty positions to build on existing excellence and intellectual leadership in evolutionary biology, infectious disease and genomics through a cluster hire. We seek outstanding scientists with broad interdisciplinary interests and a track record of applying theoretical and empirical approaches to gain insights on and mitigate against the growing threat of resistance evolution in pathogens (human, animal and plant), cancers and pest species including insects and weeds. Candidates with training in infectious diseases, cancer, evolutionary biology, chemistry, mathematics, physics, statistics, information sciences, and clinical or field studies, and an interest in developing programs that will provide novel insights on developing evolution-proof strategies to prevent the development of resistance are especially encouraged to apply. Successful candidates will have a Ph.D., M.D, or DVM or equivalent degree, along

with evidence of collaborative work across disciplines to identify novel insights and solutions to managing the risk of development and spread of resistance in microbial populations, cell lineages or pest populations. We particularly encourage candidates interested in research and teaching relating to resistance emergence and evolution, including theoretical and empirical approaches to understanding and mitigating the evolutionary impact of drugs, vaccines and pesticides on their targets and the role of ecological, evolutionary, medical and societal factors in the development, prevention, and control of resistance in major pathogens, cancers and pest species across scales. This global leadership initiative at Penn State is led by the Huck Institutes of the Life Sciences together with The Eberly College of Science (ECoS). New faculty will be offered an appointment and tenure home in one of many excellent Departments in ECoS. Successful candidates will become part of one of our centers of excellence such as The Center for Infectious Disease Dynamics (<http://www.cidd.psu.edu>) and The Center for Comparative Genomics (<http://www.bx.psu.edu> <<http://www.bx.psu.edu/>>), amongst others. This is a cluster hire with multiple offers at all ranks expected. Penn State offers access to an outstanding collaborative environment, world-class instrumentation and research facilities, as well as highly competitive salaries and startup packages. Please submit a cover letter as well as future research plans and teaching interests, a complete curriculum vitae and the contact information of three references at <https://psu.jobs/job/72415>. Referees will not be contacted without prior consultation with the candidates. Review of applications will start September 20, 2017 and continue until all positions are filled. We welcome informal inquiries regarding these positions to Andrew Read (a.read@psu.edu), Vivek Kapur (vkapur@psu.edu), or Peter Hudson (pjh18@psu.edu).

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

Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to all qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national origin, disability or protected veteran status.

– Andrew Read FRS, Director, Center for Infectious Disease Dynamics, Evan Pugh University Professor of Biology and Entomology, Eberly Professor in Biotechnology, Penn State

www.thereadgroup.net
<a.read@psu.edu>

Andrew Read

tee, at hill@rhodes.edu.

RhodesC Memphis EvolutionaryBiol

Evolutionary Biologist / Plant Biology

The Department of Biology at Rhodes College seeks qualified applicants for a tenure-track faculty position to begin in August of 2018. The Department invites candidates who can contribute to the goal of diversifying our faculty. Candidates must have a Ph.D. and must have a background and expertise in both evolutionary and plant biology. Applicants should have a commitment to teaching undergraduates as well as to maintaining an active research program that engages undergraduate students. Teaching responsibilities will include five lectures/labs per year (labs count as a full teaching involvement). Normal teaching responsibilities will include an upper-level Evolution course plus a role in the introductory biology course sequence. Other teaching opportunities include senior seminar, a course for non-science majors, or an additional course in the candidate's area of specialty. Of particular interest are courses in plant biology. We encourage applications from individuals whose interests go beyond traditional disciplinary boundaries.

Please apply online at jobs.rhodes.edu. Completed applications will include a letter of application, a statement of teaching philosophy, a research plan, a curriculum vitae, copies of graduate and undergraduate transcripts, and three letters of recommendation. Please address in your cover letter your interest in teaching at a liberal arts college and how your experiences with teaching, scholarship, and/or service might contribute to a college community that includes a commitment to diversity as one of its core values. Review of completed applications will begin September 22, 2017 and will continue until the position is filled. Candidates from backgrounds typically underrepresented in higher education are strongly encouraged to apply. The online application system will solicit letters of recommendation electronically from the candidate's recommenders once their contact information has been entered by the candidate and all other required application materials have been submitted. Background checks are required before candidates can be brought to campus for interviews.

For additional information regarding the position, please contact Dr. Terry W. Hill, Chair of the Search Commit-

tee, at hill@rhodes.edu.
Founded in 1848, Rhodes College is a highly selective, private, residential, undergraduate liberal arts college, located in Memphis, Tennessee. We aspire to graduate students with a lifelong passion for learning, a compassion for others, and the ability to translate academic study and personal concern into effective leadership and action in their communities and the world. We encourage applications from candidates interested in helping us achieve this vision.

Rhodes College values an inclusive and welcoming environment. We are an equal opportunity employer committed to diversity (<http://handbook.rhodes.edu/diversity>) in the workforce.

Memphis has a metropolitan population of over one million and provides multiple opportunities for research and for cultural and recreational activities. <http://www.rhodes.edu/content/our-city> .

Rachel Schmidt Jabaily <jabailyr@gmail.com>

SanDiegoStateU ComputationalEvolutionaryBiology

Assistant Professor: Computational Evolutionary Biology at San Diego State University: Sciences: Biology

Location: San Diego, CA

THE DEPARTMENT OF BIOLOGY AT SAN DIEGO STATE UNIVERSITY invites applications for a tenure-track faculty position in *COMPUTATIONAL EVOLUTIONARY BIOLOGY* at the Assistant Professor level. We are seeking a candidate whose research program centers around the use and development of modern computational methods to answer fundamental questions in evolutionary biology. Specific areas of research interest might include, but are not limited to: patterns/processes of species diversification, biogeography and macroecology, phenomics (large-scale phenotypic analysis), phylogenomics and population genomics, and comparative genomics or transcriptomics. We expect to hire a candidate who creatively bridges evolution and other fields of biology, with a demonstrated strength in organismal biology.

Candidates should have a Ph.D. in Evolutionary Biology or a related field, relevant post-doctoral experience, and a strong record of research accomplishments and

funding. The successful candidate should also display a commitment to undergraduate and graduate teaching. Teaching responsibilities will include participation in undergraduate biology courses, and additional graduate courses in the candidate's areas of expertise. The successful candidate will participate in the MS and Ph.D. programs in Evolutionary Biology and may also participate in the department's MS and Ph.D. programs in Cell and Molecular Biology, and Ecology. Preference will be given to candidates that can and wish to train graduate students in more than one graduate program.

SDSU is a large, diverse, urban university and Hispanic-Serving Institution with a commitment to diversity, equity, and inclusive excellence. Our campus community is diverse in many ways, including race, religion, color, sex, age, disability, marital status, sexual orientation, gender identity and expression, national origin, pregnancy, medical condition, and covered veteran status. We strive to build and sustain a welcoming environment for all. SDSU is seeking applicants with demonstrated experience in and/or commitment to teaching and working effectively with individuals from diverse backgrounds and members of underrepresented groups. The College of Sciences is host to a large number of federally-funded minority training programs (described at <http://www.sci.sdsu.edu/casa/>).

Application Instructions

Apply via Interfolio. Review of applications will begin *September 15, 2017*, and will continue until the position is filled. Incomplete applications are not guaranteed full consideration.

Apply Now < <https://dossier.interfolio.com/apply/-43326> >

Marshal Hedin <mhedin@mail.sdsu.edu>

TexasAM ResAssist ParasitePopGenetics

Texas A&M University in College Station: Research Assistant The lab of Charles Criscione (<http://www.bio.tamu.edu/index.php/faculty/criscione/>) is searching for a research assistant. The employee will participate in various population genetic studies of parasitic helminths including a NSF-funded study that will test the role parasite mating systems have in impacting the evolution of parasite life cycle complexity (example of previous work see Kasl et al. *Evolution* 69:3156). The

position is for up to 3 years, subject to annual renewal based on performance. The salary range is \$30,000-\$35,000 (depending on experience), with benefits.

Job duties: Under direction of the PI and graduate students, the research assistant will be involved in molecular lab work (e.g., DNA extractions, PCR) and extensive field work. Main duties will include obtaining microsatellite genotype data, dissecting host species (catfish, crayfish, leeches and other invertebrates) for helminth parasites, field-collection of host species (including backpack electrofishing, trapping, and netting), driving to remote field sites, and assisting in maintaining a stocked and organized laboratory. Occasional duties include assisting with animal husbandry, and interacting with private landowners and various state officials.

Education and Experience: Appropriate bachelor's degree in biology or related field or equivalent combination of education and experience. Preferred education is a master's degree in biology or related field. Experience in one or more of the following areas: molecular genetics research, parasitology, or aquatic field-based ecological research. Must have a valid driver's license. Must be able to conduct field work for extensive periods away from College Station, TX (e.g., up to a month at a time). Must be able to backpack or carry 50lbs of field gear while hiking distances of 1-3 miles. Previous experience in field-based ecological research on fishes or aquatic invertebrates, or working with helminth parasites will be heavily weighted. It is imperative that the research assistant have a strong attention to detail, the ability to collect data under strenuous field conditions, and the character to maintain a positive attitude after working long hours in hot, humid, and buggy conditions.

Applicants need to do an electronic application through <http://jobpath.tamu.edu/postings/112753>. In addition to filling out the information on the jobpath link, the application must include a single pdf file containing the following, in order 1) 1-page cover letter that includes summary of research experience and career goals, 2) C.V., and 3) List of three references with contact information (email, telephone, and mailing address). After identifying top candidates, we will request letters from these references. The position will begin as soon as possible. For questions about this position, please email ccriscione@bio.tamu.edu.

Charles D. Criscione, Associate Professor Department of Biology Texas A&M University 3258 TAMU College Station, TX 77843-3258

phone: (office: 979-845-0917, lab:979-845-0925, fax:979-845-2891) email: (ccriscione@bio.tamu.edu) faculty web page: <http://www.bio.tamu.edu/FACMENU/-FACULTY/CriscioneC.php> Charles Criscione

<ccriscione@bio.tamu.edu>

UBergen Systematic Invertebrate Zoology

Associate Prof in Systematic Invertebrate Zoology University Museum of Bergen University of Bergen, Norway

The Department of Natural History, University Museum of Bergen, has a vacancy for a permanent position as associate professor in biosystematics from 1.9.2017. The position is linked to the ForBio Research School in Biosystematics, externally funded by The Research Council of Norway and The Norwegian Biodiversity Information Centre

Work tasks and duties:

The successful candidate will dedicate 50% of his/her working time on research on systematic invertebrate zoology and 50% on continuing and developing the Nordic Research School in Biosystematics in collaboration with the ForBio leader in Oslo and coordinator colleagues in Trondheim and Tromsø. Tasks will include initiating, organizing and administrating research courses and other events, mostly aimed at PhD students affiliated with Nordic universities. The ForBio coordinator in Bergen will have an important role in shaping the University Museum's contribution towards the research school, as well as coordinating these activities with the educational activities at the Institute of Biology, University of Bergen. The museum retains the right to impose changes in the content of the required duties in case of future changes in the funding base for the position, for example including tasks related to curation of museum collections.

The University Museum of Bergen aims to strengthen its research on systematics of marine invertebrates. We are therefore looking for an active researcher with an interest in marine biodiversity and high competence in systematic zoology and taxonomic research. The invertebrate collections have several ongoing projects as well as national and international collaborations. The University Museum owns facilities for morphological (microscopy, SEM) and molecular studies (Sanger sequencing and IonTorrent), in addition to having access to shared infrastructure including the University of Bergen Genomics Core Facility (GFC), research vessels and field stations. The successful candidate will be expected to actively participate in the research group, as well as contribute

to securing additional external funds both for his/her own research as well as research school activities.

Required qualifications:

We are looking for an active researcher with excellent qualifications in systematic zoology, preferably with international research experience. The applicants must have obtained a doctoral degree on biosystematics of marine invertebrates or comparable qualifications. They should have a strong professional network in marine biology and systematics. Familiarity with taxonomic research, a good knowledge of marine faunistics, and experience from scientific cruises and museum work are desirable. Candidates will be evaluated based on their scientific competence, in particular pertaining to taxonomical research utilizing both molecular and morphological methods.

The applicants must have a genuine interest for teaching and doctoral education, a sound understanding of the Norwegian/Nordic higher education system, and knowledge on the relevant institutions involved in education, research and management. Prior experience in developing and organizing research courses or other similar activities will be useful. Within ForBio, the Bergen node is intended to have an emphasis on zoology and marine biology, and we hope to find a person with solid professional networks internationally and an overview of relevant higher education programs in the Nordic countries.

The successful candidate must have good collaboration and communication skills. Candidates should also have experience writing grant applications for external funding.

Basic pedagogical training is a requirement for the position. The successful applicant will be offered training if this requirement is not met prior to employment.

Working language at the department is Norwegian, but candidates must be fluent in both written and spoken English.

We can offer: - A good and professionally challenging working environment - Salary at pay grade 58 - 62 (code 1011, pay range 24) in the state salary scale. This currently amounts to an annual salary of NOK 494.800 - 537.700 before taxes. Further increase in salary will depend on seniority. A higher salary may be considered for a particularly well qualified applicant. - Enrolment in the Norwegian Public Service Pension Fund - A position in an inclusive workplace (IA enterprise) - Good welfare benefits

Your application must include: The application is to be written in English and must include: - CV - Diplomas

- References - Complete list of publications - List of academic work that the applicant believes should be taken into consideration in the assessment, maximum 10, including information about where this work was published - List with appendices that document your pedagogical qualifications

— / —

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>

UBritishColumbia TeachingEvolution

The Biology Program at the University of British Columbia (Vancouver) is enhancing its support for teaching and learning initiatives by creating two new positions for Science Education Specialists (SES) one of whom will be housed in the Department of Zoology and one in the Department of Botany.

These will be staff positions that work closely with teaching faculty to coordinate and support scholarship of teaching and learning projects, advise faculty on teaching and learning practices, and assist with course and curriculum revisions, pedagogical improvement projects, and assessment of teaching and learning effectiveness. Initial appointments will be for three years, with possibility of renewal.

We are seeking individuals with a background in any area of the Biological Sciences and experience in teaching and pedagogical development. A graduate degree in Life Sciences or equivalent experience is required.

Successful candidates will bring expertise in evidence-based education in the context of undergraduate life-science education. Experience in curriculum development and assessment of teaching effectiveness is considered an asset.

The SESs will join a vibrant educational community both within Biology and across the Faculty of Science, and will receive training and ongoing professional development from the Faculty of Science Centre for Learning and Teaching (Skylight) and the Biology Program.

We anticipate interviewing in mid-September, and start date is flexible.

For complete job requirements and to apply, visit the UBC Human Resources Careers site, and search for Science Education Specialist.

<http://www.hr.ubc.ca/careers-postings/staff.php> Best, Bridgette

Bridgette Clarkston, Ph.D.

Instructor, Botany Department

University of British Columbia Office: Copp 3205

Phone: 604.822.6495

Email: bridgette.clarkston@botany.ubc.ca

Mail to: 6270 University Boulevard Vancouver, BC V6T1Z4

“Clarkston, Bridgette” <bridgette.clarkston@botany.ubc.ca>

UCalifornia Berkeley QuantSystemsBiol

Hello, Department of Integrative Biology University of California, Berkeley

The Department of Integrative Biology at the University of California, Berkeley invites applications for a 100% time tenure-track position in quantitative systems biology at the rank of Assistant Professor. Potential start date is July 1, 2018.

We seek a colleague to join the department working in the area of computationally-oriented biology focused on the development and application of new methods to enable biological discovery from genomic, imaging and/or other large datasets. Areas of interest include, but are not limited to, computational methods for integrating data at different organismal levels to explore biological function and evolution, use of population genetic, ecological, evolutionary, and functional and comparative genomic data to explore the consequences of sequencing variation on phenotypes and pathologies in humans and other organisms, computational methods for analysis and mining of metagenomics or other community-associated data, use of Big Data, including geospatial data, to explore consequences of environmental and climatic factors and their interactions with functional and evolutionary aspects of organismal biology, and the application of genome sequencing to study genomic evolution, the molecular processes that drive it, and its link to organismal phenotypes and environments. Can-

didates who bridge the divide between molecular and organismal biology are strongly encouraged to apply, and we also welcome applications from candidates who combine wet lab or field approaches with theory and computation.

Candidates will also be expected to contribute to teaching in the undergraduate and graduate curriculum of the Department of Integrative Biology.

Required Minimum Basic Qualifications: Applicants with a Ph.D. or equivalent degree and an exceptional research record in any area of quantitative systems biology are encouraged to apply. The Department is interested in candidates who will contribute to diversity and equal opportunity in higher education through their teaching, research, and service. A Ph.D. or equivalent degree is required by date of application.

Additional Qualifications: Demonstrated excellence, originality, and productivity in research, and interest in undergraduate and graduate teaching as well as public outreach.

Applications must be received by September 29, 2017. To apply, please go to the following link: <http://apptrkr.com/1062237>. Please direct all questions to ib_ap_assist@berkeley.edu.

Applicants should include the following required documents: - Cover Letter - Curriculum Vitae - Your most recently updated CV - Brief Description of Research Accomplishments- Statement of Research Objectives - Statement of Teaching Interests - Statement of Contributions to Diversity - Statement addressing past and/or potential contributions to diversity through research, teaching, and/or service. - List of Publications - Significant Publication #1 - Significant Publication #2 - Significant Publication #3 - Large Publication File (Optional) In case file needs to be split - Large Publication File (Optional) In case file needs to be split - Large Publication File (Optional) In case file needs to be split

Applicants should arrange to have three letters of reference submitted online. All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are produced 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 Department of Integrative Biology is committed to addressing the family needs of faculty, including dual career couples and single parents. For information about potential relocation to Berkeley, or career needs of accompanying partners and spouses, please visit: <http://ofew.berkeley.edu/new-faculty>. The de-

partment seeks candidates whose research, teaching, or service has prepared them to contribute to our commitment to diversity and inclusion in higher education. The University of California is an Affirmative Action/Equal Opportunity 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>. Vanessa Phanouvong <vanessa@jolephant.com>

UCanterbury EvolutionaryBiology

Lecturer / Senior Lecturer in Biological Sciences (Evolutionary Biology) School of Biological Sciences University of Canterbury, New Zealand Job 5051 at <http://ucvacancies.canterbury.ac.nz/> Applications are invited for the continuing position of Lecturer/Senior Lecturer in Biological Sciences (Evolutionary Biology) in the School of Biological Sciences. [Lecturer is broadly equivalent to a (tenured) Assistant Professor in the US system; Senior Lecturer is broadly equivalent to a recently tenured Associate Professor in the US system].

We seek an ambitious colleague in evolutionary biology who will apply modern approaches and augment our existing strengths. The successful applicant will be capable of cutting-edge research and teaching, and be well versed in evolutionary biology at any scale of biological organisation. Applicants may adopt an empirical and/or theoretical approach to their research, and must be highly competent in genomic, bioinformatic, or computational approaches. All candidates must be motivated to address basic or applied evolutionary questions of fundamental importance to the field. It is expected that the successful candidate will establish an externally funded research programme, for which there are a variety of basic and applied contexts in New Zealand. They will also develop research linkages with research institutes, industry or charitable groups and/or civil society, and participate in undergraduate and postgraduate supervision and teaching.

Applicants should have a PhD or an appropriate equivalent qualification in biological sciences, an ability and willingness to deliver high quality teaching in evolutionary biology, and a commitment to do world-class research in an area complementary to current strengths

within the School of Biological Sciences. The successful applicant will demonstrate potential for academic excellence in teaching and research, be able to conduct innovative and effective lectures and laboratory classes from first year through postgraduate level, publish research at a high level as assessed by peer-reviewed publications, and, where appropriate, demonstrate impacts for community stakeholders. We are looking for an adaptable colleague who can work with others to embrace opportunities that contribute to our core mission.

The School of Biological Sciences has a high national and international profile and has an excellent teaching and research infrastructure, including multiple field stations in alpine, lowland and coastal habitats, and new research facilities. We have well-established research programmes from molecular to whole-organism and ecological scales, as exemplified in the Biomolecular Interaction Centre (<http://www.bic.canterbury.ac.nz/>) and the Centre for Integrative Ecology (<http://www.biol.canterbury.ac.nz/-cie/>). We also have strong linkages with other research institutes. For more information on the School of Biological Sciences see the webpage www.biol.canterbury.ac.nz. The University of Canterbury is committed to promoting a world-class learning environment through research and teaching excellence, and has a vision statement of Tangata Tu, Tangata Ora (“People Prepared to Make a Difference”). You will have the opportunity to work alongside members of a diverse academic community and enrich your own professional and personal development.

Equal opportunity in employment is University policy and the School is strongly committed to equality in the workplace. Applications from all suitably qualified persons are encouraged. The University of Canterbury offers generous leave provisions, including sabbatical and Erskine Fellowship leave. It also has excellent childcare, recreation and staff/graduates club facilities on campus.

For information about the range of benefits in joining UC please visit us online at: <http://www.canterbury.ac.nz/-joinus>. The closing date for this position is: 17 Sept, 2017.

Interviews for this vacancy are anticipated to take place in November, 2017.

The position will be available from 1 February, 2018, although the start date is flexible.

Applications for this position should include a completed University of Canterbury application form, a curriculum vitae, a summary of recent research achievements and a 1-2 page research proposal outlining intended research and research goals. Applicants are also expected to indicate their teaching experience and philosophy and

to indicate the ways they could contribute to courses within the School and to curriculum development in the future. They should also indicate the names and contact details of three referees. Applications should be combined into one document and

— / —

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>

UCentralFlorida EvolutionaryGenomicsCompBiologist

The University of Central Florida (UCF) recently established several interdisciplinary clusters to strengthen its academic and research missions. The Genomics and Bioinformatics Cluster (GBC) (<http://www.ucf.edu/-research/genomics>) is one of these clusters established with a goal to develop a nationally and internationally recognized program in the broad area of genomics and computation. As part of the GBC, we are currently seeking to hire two tenure-earning assistant professors. Candidates must have a strong research publication record and demonstrated independent research, with either existing research funding, or strong potential to initiate and obtain funding for their research program. The GBC emphasizes interdisciplinary research in genomics that covers at least two disciplines among biology, biomedical sciences, and computer science. In particular, the GBC is looking to expand research programs in genomics that are enabled by next-generation sequencing technologies and that address one or more areas among molecular evolution, biodiversity, microbiome research (environmental and plant/animal health), biological model systems, infectious diseases, translational applications for cancer, computational biology, systems biology, machine learning, and data mining. Strong candidates in other areas of genomics will also be considered.

The GBC members will be expected to strengthen their individual tenure homes as well as the cluster. The list of potential tenure home departments includes the Burnett School of Biomedical Sciences (College of Medicine), Biology (College of Sciences), and Computer Science (College of Engineering and Computer Science). Of the two assistant professor positions that we are seeking

to fill, one position is expected to have a tenure home in the Burnett School of Biomedical Sciences (College of Medicine) and conduct genomic research involving a combination of wet lab and dry lab techniques. For the second position, we are seeking candidates conducting computational research who will have a potential tenure home in one of the three departments listed above. A candidate may also be jointly appointed among these departments as appropriate to qualifications and interest. All GBC faculty members (and their students) will be co-located to facilitate collaboration.

Eric Hoffman Associate Professor and Undergraduate Program Coordinator UCF Department of Biology

Eric Hoffman <Eric.Hoffman@ucf.edu>

UGeorgia 2 EvolutionaryEcol

The Odum School of Ecology at the University of Georgia (<http://www.ecology.uga.edu/>) invites applications for a full-time Lecturer (non-tenure track) to contribute to instructional offerings in our B.S. and A.B. undergraduate degree programs in ecology and to provide support for administering these programs.

We seek candidates who are passionate about quality undergraduate education and who can contribute to advising and mentoring of students interested in either traditional ecological science careers (through the B.S. degree), or in careers focused on translation of ecological science into policy, management, and other applications (via the A.B. degree). Applicants must show evidence of excellence in teaching, an ability to collaboratively support a growing undergraduate academic program, and excellent organizational skills. To apply, candidates must have a PhD or terminal degree in ecology or a related field, such as sustainability, conservation biology or environmental policy.

This posting is for a 9-month academic position with 1-month of summer support provided (i.e., 10 months of salary) with responsibility for teaching 4 courses per year, including an introductory course in either ecology or environmental science, a service-learning course focused on environmental management or policy, a course in science communication, and other courses to be developed based on the expertise of the successful candidate. This position will contribute to administrative duties including advisement of undergraduate students for registration, facilitating undergraduate program assessment, coordinating undergraduate

internships, publicizing the degree programs, updating website materials, and participation in orientation and commencement activities. Lecturers at the University of Georgia are eligible for rank promotion as per UGA guidelines: <http://provost.uga.edu/index.php/policies/appointment-promotion-and-tenure/guidelines-for-appointment-and-promotion-of-lecturers>

To apply, candidates should electronically submit their application at <http://facultyjobs.uga.edu/postings/2594>. Applicants should submit, in PDF format, the following items: a) cover letter indicating career goals b) curriculum vitae c) 2-page statement of teaching philosophy and experiences regarding undergraduate instruction and mentoring d) name and contact information (address, email and phone) for three professional references who can address the candidate's qualifications.

A separate file with evidence in support of teaching excellence can also be uploaded, but should be limited to 10 pages (items included could be course syllabi, letters from students taught, peer teaching evaluations, or excerpts from student evaluations).

Applications should be received by 18 Sep 2017 to ensure full consideration.

Note that a second lecturer position (12-month appointment) in the Odum School of Ecology is being advertised, and applicants interested in both positions must apply separately. An application link for the 12-month position is available online: <http://facultyjobs.uga.edu/postings/2587>. Questions about both the 10-month and 12-month positions may be directed to Search Committee Chair Dr. John Wares (jpwares@uga.edu).

The University of Georgia is located in Athens, Georgia. Georgia is well known for its quality of life with both outdoor and urban activities (www.georgia.gov). UGA (www.uga.edu) is a land grant/sea grant institution located approximately 60 miles northeast of Atlanta. It is within an hour's driving distance from the North Georgia Mountains and four hours from the Atlantic coast. Athens enjoys a mild climate and yet still sees the benefits of the changing seasons. It is well known for its vibrant and evolving music scene, serving as the hometown of bands such as R.E.M., the B-52's, Widespread Panic, the Drive-By Truckers, of Montreal, and Futurebirds.

The University of Georgia is an Equal Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, gender identity, sexual orientation or protected veteran status.

Carolyn L Keogh, PhD Lecturer Odum School of Ecology University of Georgia ckeogh@uga.edu

Carolyn Lauren Keogh <ckeogh@uga.edu>

UGothenburg NextGenSequencing

A fully-funded, 23 month position is now available in the Antonelli research group for a Principal Research Engineer in Next Generation Sequencing. The position requires a PhD and NGS experience. Further details can be found in the job advertisement below. The application deadline is September 17.

We are looking for a highly motivated and skilled person, to support and further develop the research activities in evolutionary biology involving various kinds of next-generation sequencing (NGS) techniques to Professor Antonelli's Lab (<http://antonelli-lab.net>).

Job assignment includes:

- To provide practical, hands-on NGS guidance, support and supervision for students and researchers.
- To coordinate the physical development of our NGS labs, including the selection and acquisition of new equipment.
- To identify and test the latest emerging techniques and protocols for potential use in the group's research, including critical steps such as DNA extraction for genomics.
- To bridge the communication between lab engineers, students and researchers in the group.

In addition to these tasks, you will have the opportunity to carry out own research linked to NGS, at maximum 20% of your time. Moreover, in cases of substantial participation in projects led by students and researchers you will have the possibility of participating as co-author on eventual publications. Work division: Lab-related support 80%, own research up to 20%.

The applicant must have the following qualifications:

- PhD in molecular biology, chemistry, phylogenetic, or related field (the thesis must be awarded prior to the starting date).
- Documented experience with next-generation DNA techniques.
- Documented capacity to work in groups and independently.

-Excellent communication skills in English.

-Excellent social skills.

-Experience in mentoring or supervision.

-Interest in contributing to new and ongoing NGS projects in the lab.

Furthermore, the following qualifications are desirable:

-Experience with genomic projects.

-Skills in phylogenetics, parallelised computing, UNIX-environment.

-Experience with probe design for sequence capture.

-Wet lab experience with library preparations for at least Illumina and preferably for other methods as well, such as PacBio or Nanopore.

-Experience with reduced representation libraries (GBS, RAD, etc.).

-Experience with analytical pipelines related to phylogeography, population genetics, or selection.

-Experience and strong interest in overseeing students in the lab and pedagogic teaching of techniques.

The full advertisement is available at: http://www.gu.se/english/about_the_university/job-opportunities/vacancies-details/?id=1030 Best wishes, Allison

Allison Perrigo, PhD Coordinator Antonelli Lab < <http://antonelli-lab.net/> > & GGBC < <http://ggbc.gu.se/> > allison.perrigo@bioenv.gu.se Carl Skottsbergs gata 22 B 413 19 Goteborg
allison.perrigo@bioenv.gu.se

UIIdaho LabManager EvolutionaryConservationGenomics

Laboratory Manager in Evolutionary and Conservation Genomics Hohenlohe Lab, Institute for Bioinformatics and Evolutionary Studies University of Idaho

We are seeking a highly motivated lab manager to join our research group in evolutionary and conservation genomics at the University of Idaho. Current projects in the lab include the genetics of transmissible cancer in Tasmanian devils; population genomics in threatened island foxes, Columbia Basin pygmy rabbits, biocontrol beetles, and other taxa; and experimental evolutionary genomics in laboratory yeast populations. The lab man-

ager will help coordinate and facilitate these projects by:

- maintaining lab equipment, supplies, and protocols
- conducting genomics labwork, including RAD sequencing, whole-genome sequencing, and other techniques
- assisting with data management and bioinformatic analysis of genomic datasets
- training and assisting students and visiting researchers in molecular genomics techniques
- working with personnel in collaborating research labs at University of Idaho and Washington State University
- contributing to the intellectual environment of the lab and potentially conducting independent research projects

The successful applicant should have a bachelors or masters degree in biology, molecular biology, or a related field, and experience working as part of a team in a research laboratory. The position will begin as soon as possible. Initial appointment will be for one year, with the possibility to extend to future years.

Please submit application materials by Sep. 7, 2017, at: <https://uidaho.peopleadmin.com/postings/19055>
Lab website: <http://hohenlohelab.github.io/> For further information please contact Paul Hohenlohe (hohenlohe@uidaho.edu).

The University of Idaho is an equal opportunity employer and does not discriminate against any employee or applicant for employment because of race, color, religion, national origin, age, disability, sexual orientation, gender identity/expression or any other reason prohibited under Federal, State, or local laws. EOE AA/M/F/D/V

“hohenlohe@uidaho.edu” <hohenlohe@uidaho.edu>

ULouisiana Lafayette PopGenetics

University of Louisiana at Lafayette

Assistant Professor in Population Genetics

The Department of Biology (<http://biology.louisiana.edu>) at the University of Louisiana at Lafayette seeks to fill a tenure-track position at the Assistant Professor level. We are searching for an outstanding scientist who studies population genetics. Although we are especially interested in applicants that have a record of utilizing genome-scale datasets in animal or plant systems, researchers studying all aspects of population genetics are encouraged to apply.

Minimum qualifications are a Ph.D. in a relevant field, a significant publication record, and postdoctoral experience. Successful applicants will be expected to establish a vigorous, externally funded research program, provide instruction to undergraduates and graduate students (particularly courses in population genetics and genetics) and participate in our Ph.D. program in Environmental and Evolutionary Biology. Cover letter, curriculum vitae, statement of research interests, statement of teaching interests, and a list of three references (including postal and email addresses) should be emailed as a single pdf attachment to: Genetics.search@Louisiana.edu. To ensure full consideration, applications should be received by October 20, 2017.

The University of Louisiana at Lafayette is a public research university with High Research Activity and accreditation from the Southern Association of Colleges and Schools Commission on Colleges. With an enrollment of over 18,000 students and more than 800 full-time faculty members. UL Lafayette is the largest of nine universities in the University of Louisiana System. The University offers degree programs in 55 undergraduate disciplines, 15 post-bachelor certificates, seven graduate certificates, the master's degree in 28 disciplines, and the doctorate in 10 disciplines. UL Lafayette was ranked in the top 20% for total R&D expenditures in the biological sciences in the United States by the National Science Foundation (2015 Herd Data Report). The Brookings Institution recently ranked UL Lafayette 9th for promoting social mobility among four-year public universities in the United States. Further information about UL Lafayette is available on the University's webpage at <http://louisiana.edu>. The UL Lafayette Department of Biology is one of the largest biology programs on the Gulf Coast, with about 30 faculty members, 70 graduate students, and more than 900 undergraduate students. Support for research includes a mouse vivarium, aquatics labs, departmental vehicles, green houses, DNA sequencers and other shared instrumentation, the Ecology Center, Microscopy Center, and New Iberia Research Center (a primate facility), and Louisiana Universities Marine Consortium (LUMCON) marine lab. Opportunities for collaboration are available within the Department, and with personnel at university affiliated centers and two federal research centers (the USGS Wetland and Aquatic Research Center and the NOAA Estuarine Habitats and Coastal Fisheries Center) located in the University's Research Park.

The University of Louisiana at Lafayette is an EEO/AA employer and is dedicated to the goal of building a diverse faculty committed to teaching and working in a multicultural environment. Women, minorities, and individuals with disabilities are strongly encouraged to

apply.

–

Scott C. France france@louisiana.edu Professor & Graduate Admissions Chair Mr. Charles R. Godchaux/BORSF Professorship in Coastal Biodiversity Research Development Department of Biology University of Louisiana at Lafayette P.O. Box 43602 Lafayette, LA 70504 For more information about the graduate program please visit: <http://biology.louisiana.edu/programs/-graduate> Office: (337) 482-6320 Lab: (337) 482-6494 FAX: (337) 482-5834 For information on my research please visit: <http://www.ucslouisiana.edu/~scf4101/> “To learn and from time to time to apply what one has learned - isn’t that a pleasure?” - Confucius, 500 B.C.

– –

Scott C France <france@louisiana.edu>

UMassachusetts Lowell EvolutionZebrafish

General Summary of Position:

The University of Massachusetts Lowell Department of Biological Sciences invites applications to fill a full-time tenure-track faculty position, at the Assistant or Associate Professor level, to start September 2018. We have recently built a state-of-the-art aquatics facility and are interested in candidates using zebrafish or small aquatic animals as a model organism in their research.

The ideal candidate’s research focus should complement and leverage existing departmental and campus strengths. In addition to the broad range of research interests within the Biological Sciences Department, UMass Lowell has a diverse group of science and engineering faculty who use multiple model systems to evaluate new technologies (e.g. nanomedicine, biomaterials, robotics and tissue engineering) including an anticipated hire in the Chemistry department focusing on the biochemistry of muscle proteins. Candidates interested in establishing collaborations with faculty in these fields are therefore encouraged to apply.

The successful candidate will be expected to establish a vigorous, externally funded research program, and contribute to the department’s teaching mission. Teaching responsibilities may include the development of undergraduate courses, in addition to upper-level and graduate courses.

The University of Massachusetts Lowell is located in the heart of the life sciences supercluster of the northeast region of Massachusetts, which is home to more than 100 life science companies. Together with its proximity to the Boston/Cambridge biotechnology and biomedical hub, there are ample opportunities for scientific interaction, exchange, and collaboration.

Minimum Qualifications (Required): - Earned doctorate and postdoctoral experience (required at the time of application) - The ability to work effectively with diverse groups

Additional Considerations: - Demonstrated teaching ability at the undergraduate and/or graduate levels - Potential to establish a sustainable externally funded research program - Demonstrated publication record in scholarly journals - Excellent communication and interpersonal skills - Demonstrated ability to work with diverse student and faculty populations - The ability to work effectively with diverse groups

Special Instructions to Applicants:

Please submit a CV, cover letter, teaching philosophy and research statement. * Names and email addresses of three references will also be required during the application process. The references will be notified and should upload recommendation letters. Only recommendation letters that are uploaded to the system by the referee will be accepted. Emailed or hardcopy letters will not be accepted.

Review of applications will begin immediately and continue until the position is filled. However, the position may close once an adequate number of qualified applications are received

Nicolai Konow <Nicolai_konow@uml.edu>

UNAM Mexico CenterForGenomicScience

The Center for Genomic Sciences (CCG, <http://www.ccg.unam.mx>) of the National Autonomous University of Mexico (UNAM, located in Cuernavaca, Morelos) is looking for outstanding candidates to occupy three tenure-track faculty position at the level of Assistant Professor. Applicants must have a Ph.D and postdoctoral experience of at least two years. One position is in the area of bioinformatics and two positions are in the area of microbial genomics. The successful applicants must have an excellent scientific track record. Complete

postings can be found on the CCG webpage: <http://www.ccg.unam.mx/en/positions/available> El Centro de Ciencias Genómicas (CCG) de la UNAM (<http://www.ccg.unam.mx>), localizado en Cuernavaca, Morelos, esta buscando candidatos sobresalientes para ocupar tres posiciones como investigador, a nivel de Investigador Asociado C. Los solicitantes deberán tener un Doctorado y experiencia posdoctoral de al menos dos años. Dos plazas son para el área de Genómica Microbiana y una plaza es para el área de Bioinformática. Los solicitantes exitosos deberán poseer un historial con logros científicos de calidad. Las convocatorias completas se encuentran en la página del CCG. Convocatorias: <http://www.ccg.unam.mx/es/contrataciones/disponibles>; <<http://www.ccg.unam.mx/en/positions/available> >

For further details and inquiries please write to: Christian Sohlenkamp chsohlen@ccg.unam.mx

Diego Cortez <d.q.cortez@gmail.com>

<https://jobs.usnh.edu/>. Review of applications will begin on Nov. 1, 2017 and will continue until the positions are filled.

All applicants will be required to apply online at <http://jobs.usnh.edu/>. Please direct all inquiries to the Search Committee Chairs, Donald.Chandler@unh.edu.

The University seeks excellence through diversity among its administrators, faculty, staff, and students. The university prohibits discrimination on the basis of race, color, religion, sex, age, national origin, sexual orientation, gender identity or expression, disability, veteran status, or marital status. As a NSF ADVANCE grant recipient, the University of New Hampshire strives to enhance the recruitment, retention and advancement of women faculty and other underrepresented groups in STEM disciplines. Application by members of all underrepresented groups is encouraged.

Katherine Williams <KWilliams@graystoneadv.com>

UNewHampshire ChairBiology

Department of Biological Sciences Chair Position

The Department of Biological Sciences in the College of Life Sciences and Agriculture at the University of New Hampshire invites applications for the Chair position. Candidates must have a Ph.D. in a discipline of substantive relevance to each department's mission and focus.

We seek an individual to serve as an effective academic leader and vital member of the college's leadership team. Responsibilities include direction of department strategic planning processes; advancing and shaping multifaceted teaching and research programs; and providing professional, intellectual, and administrative leadership. The chair is responsible for evaluating faculty and staff, assigning workloads, allocating resources, and communicating between the department and the college. The chair is expected to teach one course per year, conduct research and serve the University and profession.

The successful candidate must have strong communication and interpersonal skills commensurate with the capacity to lead a diverse unit of faculty, students, and staff; be team-oriented; understand and appreciate the integrated teaching, research and service components of the land-grant mission; and have a compelling vision of the future of biological sciences in higher education.

Complete application information is available at:

UNewOrleans OrganismalBiol

EVOLUTIONARY BIOLOGISTS ARE ENCOURAGED TO APPLY FOR THE FOLLOWING POSITION:

The *Department of Biological Sciences, University of New Orleans *invites applications for a tenure-track position at the rank of ASSISTANT PROFESSOR.

We seek an *Organismal Biologist* with strong quantitative skills and broad interests in the areas of ecology and evolution. Successful candidates should have a research program that contributes to our Integrative Biology PhD program.

Applicants must have a Ph.D. and postdoctoral experience. Successful candidates will develop extramurally funded research programs, direct graduate students, and teach at the undergraduate and graduate levels. Applications from women and minorities are especially encouraged. For information about the department, see [*http://biology.uno.edu/](http://biology.uno.edu/) Applications will be accepted electronically as a single PDF file that combines: a curriculum vitae, statement of research interests and teaching methods/philosophy, and names and contact information of three references. Please apply here

<http://www.uno.edu/jobs/4169.aspx> *The University of New Orleans in an Equal Opportunity/Affirmative Action employer.*

– Simon Lailvaux Virginia Kock/Audubon Nature Institute Chair in Species Preservation Department of Biological Sciences University of New Orleans 2000 Lakeshore Drive New Orleans, LA 70148

email: slailvaux@gmail.com phone: 504 280 6740

<http://www.fs.uno.edu/slailvau/index.html> slailvaux@gmail.com

UOklahoma Ichthyology Curator

Assistant Professor/Curator - Genetic/Genomic Ichthyologist Department of Biology & Sam Noble Museum, University of Oklahoma

DESCRIPTION OF POSITION: We seek a creative, collaborative thinker with a collection-based research program involving molecular approaches to studying fish systems. We are especially interested in candidates who use genomic tools and data sets in combination with innovative computational, ecological, behavioral and/or comparative approaches to address important biological questions ranging from the origin and maintenance of organismal diversity, adaptation to changing environments, evolution, conservation, and human health and disease. Areas of research interests include, but are not limited to: comparative genomics, landscape/population genetics, geographical ecology, global change biology, evolutionary genetics, and mechanisms of evolution.

RESPONSIBILITIES: The successful candidate will be expected to: (1) develop and maintain an innovative, extramurally-funded research program in fish systems; (2) oversee care and obtain support for a collection of about 1 million specimens by maintaining records, identifying and cataloging specimens, supervising preparators and assistants, expanding and preserving the collections, and developing long-range plans for collection maintenance and development; (3) contribute to museum public exhibit development and support; (4) develop and contribute to museum-related outreach activities; and (5) contribute to undergraduate and graduate teaching, including instruction of one course per year (one-half the regular department teaching load) in ichthyology, animal behavior, biogeography, genetics, evolution, comparative anatomy, ecological modeling, or bioinformatics. A full-time Collection Manager is funded in this collection.

GENERAL INFORMATION: The Sam Noble Museum is an organized research unit of the University of Oklahoma and is one of the finest university museums in

the world. The museum has an outstanding curatorial, collections, education, exhibits, and support staff that serves the museum's mission from research to preservation to education at all levels. The Department of Biology is a leading academic department with a tradition of excellence in organismal biology. It is home to 20 of the 44 faculty in the University's graduate program in Ecology and Evolutionary Biology, and it is currently in the process of hiring several new faculty in the next two to three years to expand on its strengths in biology of behavior.

QUALIFICATIONS Preference will be given to biologists with a documented record of collections-based research in natural history, including field experience and a broad taxonomic understanding of fishes, who also clearly demonstrate cross-disciplinary research programs. A Ph.D., teaching experience, and field and museum research experience in ichthyology are required.

APPLICATION INSTRUCTIONS Submit a cover letter, curriculum vitae, summary of experience and goals (including teaching, research, and curation), representative pdf reprint examples, and three confidential letters of reference using at <http://apply.interfolio.com/43857>. Visit us at <http://snomnh.ou.edu> and <http://biology.ou.edu>.

Formal application review will begin 11 October 2017 and continue until the position is filled.

Lawrence J. Weider, Professor Department of Biology University of Oklahoma 730 Van Vleet Oval, Room 314 Norman, Oklahoma, U.S.A. 73019 phone: (00) 1-405-325-4766 FAX: (00) 1-405-325-6202 ljweider@ou.edu <http://www.ou.edu/content/cas-biology/people/faculty/lawrence-weider.html> "Weider, Lawrence J." <ljweider@ou.edu>

UOregon Evolutionary Anthropology

The Department of Anthropology at the University of Oregon seeks a tenure-track assistant professor in biological anthropology to begin on September 16, 2018. We seek an outstanding, broadly-trained evolutionary biological anthropologist who will complement, not duplicate, the existing strengths within the department. Examples of possible specialties include, but are not limited to, human evolutionary biology, evolutionary medicine, evolutionary anatomy, paleobiology, and paleogenomics. The successful candidate is expected to conduct a rigorous, fieldwork and/or laboratory based, externally-funded research program as well as teach at

both the undergraduate and graduate levels. A Ph.D. is required by September 15, 2018. Postdoctoral experience and an established publication record are preferred.

Applicants should submit a cover letter, a research statement, a teaching statement, a CV, and the names and contact information of three references. Submission is via Academic Jobs Online: <https://academicjobsonline.org/ajo/jobs/9455> (link is external). Questions regarding the position can be directed to the Search Committee Chair, Nelson Ting (nting@uoregon.edu) with "Bioanth Search" in the subject line. For full consideration, materials should be submitted by September 15, 2017. The position will remain open until filled.

The successful candidate will have the ability to work effectively with faculty, staff and students from a variety of diverse backgrounds.

Full job ad here: <http://careers.uoregon.edu/cw/en-us/job/520607/assistant-professor-of-anthropology> – Nelson Ting, Ph.D. Associate Professor Department of Anthropology Institute of Ecology and Evolution University of Oregon 308 Condon Hall Eugene, OR 97403 Office: (541) 346-5509 <http://molecular-anthro.uoregon.edu/-TingLab/> nelson ting <nting@uoregon.edu>

UOtago BioinformaticsTech

Bioinformatician

Department of Zoology, University of Otago, New Zealand

Job ID: 1701603

The Role

We are seeking a motivated person with advanced experience in bioinformatics to provide support for a range of research projects, including:

- * Understanding the genomic basis of flight loss in New Zealand's alpine stoneflies.
- * Inbreeding depression (hatching success and sperm abnormalities) in the Kakapo using whole genomes from all living birds.
- * How parental challenges (hypoxia, toxins, social isolation) affect DNA methylation and offspring gene expression patterns in zebrafish.
- * Using RNA-Seq to understand how gene expression corresponds to aggressive behaviour within and between

colonies of social wasps.

- * Community diversity metrics from amplicon sequencing data of bacterial nitrogenase genes (*nifH*) in different soil habitats.

This role will involve the use of existing bioinformatics software, analysis pipeline development, and training and supervising students and staff to promote bioinformatics capabilities within the departments of the Division of Sciences.

The person appointed to this position will be able to show initiative and have strong attention to detail whilst responding to a broad range of academic demands. The position requires a highly organised person who has a genuine interest in the application of bioinformatics to contemporary science and excellent communication and interpersonal skills, as well as being a team player and a problem-solver. Otago employs bioinformaticians in several departments, thus the successful candidate will also be expected to maintain relationships with bioinformaticians outside of the Division of Sciences departments.

Your Skills and Experience

- * MSc degree minimum in Bioinformatics or a related discipline.
- * Significant bioinformatic experience and a strong interest in Biological Sciences.
- * Familiarity with Linux shell scripting and analysis pipeline development.

Further Details

This is a full-time, fixed term position for three years and is available from 1 October 2017.

For further information about the position, the Department, and to apply, see:

<https://otago.taleo.net/careersection/2/-jobdetail.ftl?lang=en&job=1701603> ??

Specific enquiries may be directed to Associate Professor Bruce Robertson, Department of Zoology, bruce.robertson@otago.ac.nz

Applications quoting reference number 1701603 will close on Sunday, 24 September 2017.

sheri.johnson@otago.ac.nz

UPittsburgh EvolutionaryBiology

FACULTY POSITION IN EVOLUTIONARY BIOLOGY

The Department of Biological Sciences at the University of Pittsburgh invites applications for a tenure-track faculty position in the area of Evolutionary Biology. The position is anticipated at the ASSISTANT PROFESSOR level. We seek an outstanding scientist who will enhance and complement existing strengths in ecology and evolution in our broad-based, interactive biology department. We invite applications from all candidates working on cutting edge questions in evolutionary biology using animal, plant or microbial systems. Candidates working in the following areas are especially encouraged to apply:

- * Population, functional, evolutionary, or phylogenomics
- * Microbial evolution; evolution of the microbiome
- * Evolutionary dynamics of host-pathogen or mutualistic interactions
- * Experimental evolution, evolutionary development of plants

Further information about the Department of Biological Sciences and our field station is available at: <http://www.biology.pitt.edu>. Highly competitive start-up, compensation and benefits packages are offered. Successful candidates will have a Ph.D. and postdoctoral research experience and will be expected to establish an extramurally funded research program, train graduate students, and actively participate in undergraduate science education. To ensure full consideration, applications and reference letters should be received by 16 September 2017. Applicants can apply online at: <https://facultysearch.as.pitt.edu/apply/index/MTg3>. Candidates should submit (a) a letter of application, (b) a CV, (c) a 2-3-page statement of research accomplishments and future plans, (d) a brief description of teaching interests, (e) a description of how your research, teaching or service demonstrates a commitment to diversity and inclusion, and (f) at least three letters of reference. For each reference, you will have the opportunity to input a personal email address or an email address generated through Interfolio's Online Application Delivery. In both cases, an email notification will be sent to the designated address with instructions about uploading

letters of recommendation into our system. The position is pending budgetary approval. The University of Pittsburgh is an Affirmative Action/Equal Opportunity Employer and values equality of opportunity, human dignity and diversity. EEO/AA/M/F/Vets/Disabled

Dr. Tia-Lynn Ashman Distinguished Professor of Ecology & Evolution Department of Biological Sciences University of Pittsburgh Pittsburgh, PA 15260-3929 412-624-0984 <http://www.pitt.edu/~tia1/> "Ashman, Tia-Lynn" <tia1@pitt.edu>

URhodeIsland ResAssist DiseaseVectorEvolution

Research assistant position available in vector and vector-borne disease ecology and evolution at University of Rhode Island working in the Couret lab in the Department of Biological Sciences (<http://web.uri.edu/bio/couret-jannelle/>) Instagram @CouretLab - Twitter: @VectorEcology

Position is full time and posted at www.jobs.uri.edu/postings/2652 - applications submitted through the URI jobs portal. For additional questions about the position send emails with subject line "RA Position" to ncouret@uri.edu

Duties include both field and laboratory work on the ecology/biology of mosquitoes and ticks that transmit human pathogens. Required qualifications include a bachelor's in Biology and one year work experience in biology research. Preferred qualifications include experience with DNA extraction/PCR, experience with ArcGIS.

Nelle Couret <ncouret@uri.edu>

USouthernCalifornia LabTech CoralAquarist

Aquarist/Laboratory Technician

University of Southern California, Los Angeles

The Kenkel lab is looking for an Aquarist/Lab Technician to join our growing research group. The primary role of this position will be working to get our new

aquarium system for coral husbandry and manipulative experiments running, and being responsible for subsequent maintenance of life support systems and coral collections. Day to day responsibilities will include feeding, water quality testing, maintenance of tanks and life support systems and appropriate record keeping. The ideal candidate will have maintained aquaria in a public aquarium or research laboratory, with proven experience of running successful tropical coral systems, with a knowledge of coral propagation and husbandry and water chemistry management.

Secondary responsibilities will include basic laboratory management, such as ordering and inventory of lab consumables, and overseeing EH&S compliance of all lab spaces. The candidate will also have the opportunity to participate in field and laboratory experiments related to the focus of the lab - for more information on potential projects, please see our website at <http://dornsife.usc.edu/labs/carlslab>. Though an open water diver certification is desirable, support will be provided to the candidate to obtain necessary training and qualifications. Additional opportunities for career development include training in molecular genetic techniques, such as DNA/RNA extractions and PCR, and methods in coral ecophysiology.

This is a full-time/fixed-term position and includes benefits. The initial appointment will be for a 6-month probationary period, after which yearly reappointments are possible for successful and productive candidates. Desired start date is 1 October 2017.

Apply at: https://usc.wd5.myworkdayjobs.com/ExternalUSCCareers/job/Los-Angeles-CA—University-Park-Campus/Research-Lab-Technician-II_REQ20048316-1 Dr. Carly D. Kenkel Department of Biological Sciences University of Southern California 3616 Trousdale Parkway, AHF 231 Los Angeles, CA 90089-0371 Office: +1 (213) 821-1705 Email: ckenkel@usc.edu Twitter: @DrCarlsHorn <http://dornsife.usc.edu/labs/carlslab> Carly Danielle Kenkel <ckenkel@usc.edu>

UTulsa 2 EvolutionaryGeneticsMolBiol

Tenure-Track Positions in Molecular/Cellular Biology and Genetics/Genomics

The Department of Biological Science at The University of Tulsa invites applications for two tenure-track assistant professor positions with demonstrated interests and expertise in the areas of molecular/cellular biology and genetics/genomics. We seek creative and interactive individuals working on fundamental problems in any area of cellular/molecular biology or genetics/genomics, as they relate to basic biomedical and biological sciences. We anticipate a fall 2018 start date for these positions. The successful applicants are expected to have a Ph.D. and post-doctoral experience, to establish a vigorous extramurally funded research program involving both undergraduate and graduate students, and to participate in undergraduate and graduate teaching in his or her area of expertise.

Because two positions are available we will consider the recruitment of faculty members with overlapping or synergistic research programs in these areas.

Genetics/Genomics Position Responsibilities include teaching general genetics and appropriate upper-level/graduate courses in genetics/genomics.

Interested parties should submit a cover letter, current curriculum vitae, statements of research and teaching interests (max. two pages each), and names and complete contact information for three references. Applications should be submitted electronically to Genetics Search Committee Chair, Dr. Ron Bonett (ronbonett@utulsa.edu). For full consideration applications should be received by 30 September 2017.

Molecular/Cellular Biology Position Responsibilities include undergraduate and graduate level courses in molecular and/or cellular biology Interested parties should submit a cover letter, current curriculum vitae, statements of research and teaching interests (max. two pages each), and names and complete contact information for three references. Applications should be submitted electronically to Molecular Search Committee Chair, Dr. Mark Buchheim (mark-buchheim@utulsa.edu). For full consideration applications should be received by 30 September 2017.

The University of Tulsa The Faculty of Biological Science

is in the College of Engineering and Natural Sciences of The University of Tulsa (www.utulsa.edu) and offers BS, MS and PhD degrees (<https://engineering.utulsa.edu/academics/biological-science/>). At present, there are 13 full-time faculty members, 22 MS/PhD students, and approximately 135 undergraduate Biology majors. The department houses a complete genomics core facility including an Illumina MiSeq, Covaris sonicator, ABI capillary sequencer, StepOnePlus real-time PCR system, Agilent Bioanalyzer, and both Nanodrop and Qubit fluorometric quantifiers.

The University of Tulsa is a Carnegie National-Doctoral institution ranked in the top 50 private schools in the United States by US News and World Report. The fall 2016 enrollment for the university was 4,563 students in its four academic colleges (3,406 undergraduates and 1,157 graduate or law students).

The city of Tulsa, located in the rolling Osage Hills of northeastern Oklahoma, is one of the most livable and affordable cities in the United States with a lively arts and cultural scene, a metropolitan population of over 930,000 and a cost of living index of 85% of the national average.

The University of Tulsa is an Equal Opportunity Employer and is especially interested in candidates who can contribute to the diversity and excellence of the academic community through their research, teaching and/or service.

Ronald M. Bonett, Ph.D.

Associate Professor Department of Biological Science
800 S. Tucker Drive University of Tulsa Tulsa, OK
74104 Email: ron-bonett@utulsa.edu Office: (918)
631-3328 Lab: (918) 631-3327 Bonett Lab: <http://ronbonett.weebly.com/index.html> Ronald Bonett <ronbonett@utulsa.edu>

U**Vermont** Evolutionary**Genetics**Lecturer

Although not explicitly stated in the ad, someone doing evolutionary genetics could be appropriate for this position.

Lecturer in Genetics and Forensic Biology

The Department of Biology at the University of Vermont invites applications for a non-tenure track full-time Lecturer position in Genetics and Forensic Biology to

begin January 1, 2018 continuing through the Spring 2018 semester and Academic Year 2018-19 with the possibility of renewal. The successful candidate will be expected to teach a sophomore level majors course in genetics and coordinate and mentor teaching assistants running associated recitation sections. We are particularly interested in candidates who have expertise in forensic analysis and/or human genetics and would like to take a leadership role in a newly-developed minor in Forensic Biology. Additional teaching responsibilities include lecture or laboratory courses for non-majors and majors from the introductory to advanced level in the candidate's area of expertise.

Applicants are expected to have a PhD in Biology, Genetics, or a related field. Experience in university teaching, particularly courses for life-science majors, is strongly preferred. Submit cover letter, curriculum vita, statement of teaching philosophy, evidence of teaching effectiveness (including course syllabi and student feedback if available) and the names and contact information of three references online at www.uvmjobs.com. Search for the position using department name (Biology) only. The reference providers will be e-mailed information to upload their letters.

Review of applications will begin on September 21, 2017 and will continue until the position is filled. Questions may be directed to: Sara.Cahan@uvm.edu. The University is especially interested in candidates who can contribute to the diversity and excellence of the academic community through their research, teaching, and/or service. Applicants are requested to include in their cover letter information about how they will further this goal.

The University of Vermont is an Equal Opportunity/Affirmative Action Employer. Applications from women, veterans and individuals with disabilities, and people from diverse racial, ethnic, and cultural backgrounds are encouraged.

Burlington, Vermont is located in the beautiful Lake Champlain region, surrounded by the Green and Adirondack Mountains. It is a great place for families, with excellent public schools and year-round recreational opportunities. It is home to the University of Vermont and three independent colleges that provide an academically stimulating and culturally rich environment. Montreal, Canada and Boston are within easy driving distances.

Don Stratton <Don.Stratton@uvm.edu>

UWisconsinMadison 2 Genetics

Two faculty positions are available with the University of Wisconsin - Madison's Laboratory of Genetics. Please see the application links below for further details and search contact information.

Position 1 - Genetics and Genomics <http://jobs.hr.wisc.edu/cw/en-us/job/495897/tenuretrack-faculty-in-genetics> Position 2 - Human Genetics and Genomics <http://jobs.hr.wisc.edu/cw/en-us/job/495844/tenuretrack-faculty-in-human-genetics-and-genomics> "jpool@wisc.edu" <jpool@wisc.edu>

VanderbiltU EvolutionMicrobiome

Tenure-track Assistant Professor, Vanderbilt, Host-Microbiome Interactions

Vanderbilt University's Department of Biological Sciences and the Vanderbilt Institute for Infection, Immunology and Inflammation invite applications for a tenure-track, faculty position in host-microbiome interactions at the Assistant Professor rank. The individual will be expected to develop her or his own independent laboratory research program and contribute to departmental strengths in evolution, chemical biology, neuroscience, and cell and molecular biology (<https://as.vanderbilt.edu/biosci/>). The faculty member will play an integral role within the new trans-institutional Vanderbilt Microbiome Initiative and may benefit from collaborations with internationally recognized programs including the Vanderbilt Genetics Institute, the Vanderbilt Institute of Chemical Biology, or the Vanderbilt Institute for Global Health. The selection criteria are excellence in research and the ability to teach undergraduate and graduate students with a high level of effectiveness. Applicants should submit a letter of interest, full curriculum vitae, statement of current and future research interests, and statement of teaching philosophy and competency directly to <https://apply.interfolio.com/43974>. Applicants will arrange for four letters of recommendation to be sent to the same address. Completed applications must be received no later than October 27, 2017. Vanderbilt University has a strong institutional

commitment to recruiting and retaining an academically and culturally diverse community of faculty. Minorities, women, individuals with disabilities, and members of other underrepresented groups, in particular, are encouraged to apply. Vanderbilt is an Equal Opportunity/Affirmative Action employer. Vanderbilt University is a National Arboretum located in the heart of Nashville, TN and consistently ranks in the top 15 US Best Colleges.

Please direct any inquiries to Seth Bordenstein, s.bordenstein@vanderbilt.edu

—
Seth Bordenstein Departments of Biological Sciences and Pathology, Microbiology, and Immunology Director, Vanderbilt Microbiome Initiative Vanderbilt Institute of Infection, Immunology, and Inflammation Vanderbilt Genetics Institute Vanderbilt University VU Station B Box 35-1634 Nashville, TN 37235

Phone: 615.322.9087 Lab: <http://bordensteinlab.vanderbilt.edu> Twitter: @Symbioticism < <https://twitter.com/Symbioticism> > Science Education: Discover the Microbes Within! The Wolbachia Project < <https://my.vanderbilt.edu/discover/> >

s.bordenstein@Vanderbilt.Edu

WakeForestU EvolutionaryMicrobiologist

Ecologists and evolutionary biologists working on microbial interactions with other species, whether in natural or lab settings, are highly encouraged to apply for this position.

The Department of Biology at Wake Forest University invites applicants for a tenure-track faculty position at the Assistant Professor level who are broadly trained in microbiology and who will complement our existing strengths with a thriving, extramurally-funded research program on Bacteria, Archaea, or microbial eukaryotes and their interactions with other species or with their environments. Those whose research is driven largely by questions drawn from an applied medical perspective are less likely to be a good match for this position. We seek a teacher-scholar with a strong commitment to engaging students both in the classroom and through research mentorship at the undergraduate, MS, and PhD levels. The successful candidate will teach an upper-level course in microbiology, with opportunities to develop

additional courses in their area of interest. For more information and to apply see: <http://college.wfu.edu/biology/> . Founded in 1834, Wake Forest University (WFU) is a private university located in Winston-Salem, North Carolina that combines a small (approximately 5000 undergraduates) liberal arts collegiate university with 2,200 graduate students in schools of arts and science, medicine, law, business, and divinity. The Department of Biology awards both Masters and Ph.D. degrees. The quality of the undergraduate and graduate teaching environments is outstanding, and our faculty combine commitment to that mission with nationally and internationally recognized leadership in research. The Biology department spans both WFU campuses (Reynolda Campus and Wake Downtown), and offers many shared facilities in support of research, including a fully staffed, state-of-the art microscopy facility. Comprehensive Next Generation DNA sequencing (NGS) capabilities are located in the Cancer Genomics Shared Resource laboratory located at the Wake Forest Baptist Comprehensive Cancer Center Medical School campus, including sample processing, library preparation, automated high throughput sample handling, and sequencing on multiple Illumina NGS platforms (MiSeq and NextSeq 500). Comprehensive bioinformatics and bio-statistical analysis is available from the Bioinformatics Shared Resource and the Biostatistics Shared Resource located in the Wake Forest Baptist Comprehensive Cancer Center.

Teaching loads are consistent with our high expectations for research, and Wake Forest typically ranks in the top 30 of all U.S. universities in U.S. News & World Report's Guide to America's Best Colleges and Universities and the top 10 of undergraduate Biology majors by College Factual. We offer undergraduate degrees in Biology (BA and BS) and a degree in Biochemistry and Molecular Biology (BS, joint with Chemistry). Opportunities exist for collaboration with researchers from the Biology and Chemistry departments, the WFU Center for Molecular Signaling (<http://molecularsignaling.wfu.edu/>), the WFU Center for Energy, Environment and Sustainability (<http://cees.wfu.edu/>), and the Wake Forest School of Medicine (<http://www.wakehealth.edu/school/>). The University has a deep institutional commitment to public service and engagement with the world, as indicated by the motto "Pro Humanitate." For quick facts about the University, go to <http://www.wfu.edu/visitors/quickfacts.html> . Winston-Salem is part of the beautiful Piedmont Triad metropolitan region, which has a population of more than 1.5 million and is listed among the 35 best places to live in North America by Cities Ranked and Rated. Known as the "City of Art and Innovation," Winston-Salem

offers a vast array of arts experiences ranging from music venues to galleries to theatre and film festivals and active biomedical and environmental research communities. The city is ranked among the top 50 US cities for affordability on national surveys. Winston-Salem is 70 minutes from the Blue Ridge of the Appalachian Mountains and 4 hours from the Atlantic Ocean. Other prominent universities are approximately 90 minutes away in the Research Triangle area.

Review of applications will begin on October 1, 2017 until the position is filled. Applicants should apply online with a cover letter, curriculum vitae, and separate statements of research interest and teaching philosophy with each statement no more than 5 pages. Please note that materials should be in either Word or PDF format and there is a limit of 5 file uploads per applicant. At least three signed confidential letters of recommendation must be sent via email to letters@wfu.edu. The submission of an online

— / —

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>

YalePeabodyMuseum HeadBiodiversityInformaticsData

The Yale Peabody Museum of Natural History (YPM) and Yale University invite applications for a data scientist to help develop and advance the innovative use of informatics tools for the synthesis and utilization of biodiversity information in research and education. The YPM is among the oldest, largest, and most active university natural history museums in the world. The museum has a strong track record in specimen digitization and database efforts and in contributing to national biodiversity informatics initiatives. The university hosts a range of activities in biodiversity data science and global change, including the Max Planck Yale Center of Biodiversity Movement and Global Change and digital infrastructure projects addressing global phylogenies, remote sensing, and species distributions (Map of Life).

The Head of Biodiversity Informatics and Data Science is expected to support the development of an expanded vision for biodiversity- and specimen-based informatics that links the YPM scientific divisions and other university activities with the goal of developing national

and international leadership roles in this arena. Responsibilities include: advancing the innovative use of informatics tools for the synthesis and utilization of biodiversity information in research and education; setting priorities and developing plans and initiatives related to Biodiversity Informatics and Data Science; partnering in the development of grant proposals for funding of informatics and data science projects; facilitating interdisciplinary collaborations and research programs at the museum, University, and national and international levels; serving as a liaison and/or representative of YPM and its partner projects.

We seek an outstanding applicant working in any area of ecology, evolution, or paleobiology, and with demonstrated informatics expertise and a passion for contributing to this vision. A record of outstanding achievement and a promising research program are more important than the specific scientific area. While developer skills (below) are required, we seek candidates with active research programs and a strong record in obtaining funding in this area.

We expect candidates to bring a range of skills spanning software and database development, and to specifically have the following qualifications: - Experience in taxonomic integration, such as familiarity with concepts and tools addressing taxonomic harmonization. - Familiarity with taxonomic naming concept management and formal knowledge representation addressing ontologies and semantics. - Experience with Web GIS development. - Experience in relational database management and SQL, with Postgres/PostGIS experience particularly welcome. - Experience with API development. - Programming skills in Python and R required; JavaScript and Java a plus. - Experience in R package development. - Background in cloud architecture, cloud data flows and pipelines.

Preferred Education, Experience and Skills: Ph.D. in the natural sciences or computer sciences. Experience in planning, development, and implementation of biodiversity informatics projects or equivalent combination of education and experience. Competency in innovative approaches for data integration and data fusion. Previous experience with highly technical and collaborative projects.

Application: To apply, please go to <http://bit.ly/2fGpt34>. The review of applications will begin 2 October 2017; the search will remain open until the position is filled.

Yale University offers exciting opportunities for achievement and growth in New Haven, Connecticut. Conveniently located between Boston and New York, New Haven is the creative capital of Connecticut with cultural resources that include three major museums, a critically-acclaimed repertory theater, state-of-the-art concert hall, and world-renowned schools of Architecture, Art, Drama, Forestry & Environmental Studies and Music. We invite you to discover the excitement, diversity, rewards and excellence of a career at Yale University. One of the country's great workplaces, Yale University offers exciting opportunities for meaningful accomplishment and true growth. Our benefits package is among the best anywhere, with a wide variety of insurance choices, liberal paid time off, fantastic family and educational benefits, a variety of retirement benefits, extensive recreational facilities, and much more.

Yale University considers applicants for employment without regard to, and does not discriminate on the basis of an individual's sex, race, color, religion, age, disability, status as a veteran, or national or ethnic origin; nor does Yale discriminate on the basis of sexual orientation or gender identity or expression.

walter.jetz@yale.edu

Bee lab suggestions	73	GBS-RADSeq services answers	75
Caatinga Brazil FieldAssist MarmosetCommunication		Groningen VolFieldAssit ChilianBirds	76
73		GSA ProgramInMentoredPeerReview	76
Conservation Management Survey	74	QUBES TeachingEvolution	77
Drosophila equipment	74		
GBS-RADSeq services	74		

Bee lab suggestions

EvoDir community,

A strong undergraduate student working with me on a plant phylogenomics project will be applying to PhD labs this fall (starting fall 2018) and she's looking for lab recommendations. She's interested in honey bee evolution, including colony collapse disorder and interactions with pests/pathogens/pesticides generally.

Please let me know of any labs that are working on honey bee (or even native bee) questions. We're really casting the net wide, so don't hesitate to send me applied labs as well. Also feel free to forward this to your entomology colleagues.

Thanks!! James

James Beck Department of Biological Sciences Wichita State University www.becklaboratory.com/James
"James.Beck@wichita.edu" <James.Beck@wichita.edu>

Caatinga Brazil FieldAssist MarmosetCommunication

MSc student/ field assistant: common marmoset communication - Caatinga, Brazil

What:

Which roles did socio-ecological factors play during the evolution of human language? Which syntactic abilities are present in cooperatively breeding primates? Non-human primates are capable of combining calls into sequences but we don't know yet if this also results in combing call meanings. As marmosets and tamarins live in cooperatively breeding social systems, probably similar to ancestral humans, their communicative abilities are of prime interest. To investigate these questions this project will examine the complexity of call combinations

and their related contexts and potential functions in free-living common marmosets, a New World monkey species.

Work in the field will consist of focal individual observations recorded on audio and video, supplemented by opportunistic recordings, as well as pilot experiments. For another project on potential within-call variation linked to hormones we will also collect faecal samples. Working hours are mainly in the morning (starting early) and afternoon, with time for a break and computer work at midday. I am looking for someone to assist me in the field and to carry out part of the field work by him/herself under my supervision. This could either be a MSc student who would like to use this opportunity for an internship (including the preparation of a thesis) or a field assistant.

Where: Baracuh Biological Field Station, Caatinga area, Brazil (Paraiba)

When: Fieldwork October 2017 - January 2018 (4 months), for a MSc student: project start September 2017 (6-7 months in total)

Requirements:

- Motivated MSc student with an interest in vocal communication, primate behavior or syntax studies
- For an assistant: at least a BSc in a relevant field, ideally also a MSc or previous field experience with habituated animals
- Willingness to work in a semi-arid climate under field conditions and to adjust to a different culture and lifestyle
- Fluent in English, German or Dutch, ideally some basic understanding of Portuguese

Funding/support:

As I am a PhD student and have limited funds, I cannot offer a proper salary or cover travel costs to Brazil. However, I am happy to assist in applying for a student travel grant! I might be able to pay a small salary for a field assistant based on the rate of undergraduate research assistants in Brazil. Travel from Recife to the fieldsite and back might be covered depending on the travel dates. Lodging will be provided without any costs (incl gas/water/electricity/limited internet), meals will

be self-cooked, grocery shopping costs will be shared.

How to apply:

If you're interested, please send me a CV and a cover letter explaining if you're applying for a student or assistant position, your research interests and previous relevant experience. If you have any questions, don't hesitate to ask!

Contact: Meike Zemihn, meike.zemihn@gmail.com

More information: <https://www.universiteitleiden.nl/en/research/research-projects/science/ibl-combination-variation-and-reproductive-cues-in-vocalisations-of-the-common-marmoset-callithrix-jacchus> Meike Zemihn <meike.zemihn@gmail.com>

Conservation Management Survey

The Conservation Genetics Working Group within the Society for Conservation Biology is working to bring conservation managers and academic researchers closer together to help create and implement genetic assessments that can inform conservation management. To do this we need to know more about the current use of genetic assessments in conservation management and how geneticists can collaborate with managers to achieve their conservation goals.

If you are a conservation/resource manager we would appreciate you taking the time to complete the conservation manager survey (https://docs.google.com/forms/d/e/1FAIpQLSfv9auU2Op87u2gqXbp-4.yA37666FXcABGhU8pV56SihjgUA/viewform?usp=sf_link). Also please share the survey link with any conservation managers you know, we aim to distribute this as widely as possible.

If you have any questions please contact me, Dr. Heather Taft, at Heather.R.Taft@gmail.com.

Thank you for helping us out!

Joshua Miller <millerjm86@gmail.com>

Drosophila equipment

Drosophila rearing material available If you are in need of Drosophila rearing equipment, especially if setting up a new lab this fall, I might be able to help. I am cleaning out an old lab once designated to rearing and sorting flies. May have some university bureaucracy to overcome, but lots of bottles, vials, racks and miscellaneous materials that I would hate to throw out, especially if someone is in the Ohio region (i.e., transport will require assistance by the recipient).

To inquire, contact Bob Krebs r.krebs@csuohio.edu or krebs.r@gmail.com

Dr. Bob Krebs Dept. of BGES Cleveland State University 2121 Euclid Ave. Cleveland OH 44115

Robert Krebs <krebs.r@gmail.com>

GBS-RADSeq services

Hi

I am searching for the best possible option for genomic sequencing services, available for an academic research entity (Mexican University), thus it will be of great help to get different suggestions.

We need to obtain polymorphic SNPs, data that will be used for population and landscape genomics, annotation for loci under selection, and the sort.

The GBS or single/double RadSeq service we need includes library preparation; we will provide the appropriate DNA samples of different animal species (initially rodents). We wish to obtain the raw data (fasta files) from which to perform the Bioinformatics (no need the service companies to do it).

I have already contacted these companies: Data2Bio and Floragenex (they already gave me some quotes); Genewiz and HudsonAlpha (still waiting to hear from them); and GenScript and Edinburgh Genomics (do not provide such services).

Many thanks in advance Ella

Ella Vázquez Domínguez Instituto de Ecología,

UNAM Ap. Postal 70-275, Ciudad Universitaria México DF 04510 México Tel +52 55 5622 9015 Email: evazquez@ecologia.unam.mx <http://web.ecologia.unam.mx/laboratorios/evazquez>
evazquez@ecologia.unam.mx

GBS-RADSeq services answers

Hi

I truly thank so many people that provided suggestions and information regarding my inquire about 'GBS/RADSeq services companies' (which is at the bottom of this message), it was of enormous help!!!

I have compiled the information in some order, and included only those companies that I have checked already or that their web page indicate they perform such services. Some companies were mentioned that I do not include here because I know they do not provide GBS services anymore (Cornell), do only sequencing but not library construction (Macrogen) or do other kind of jobs, like Ultra conserved elements (UCEs) (e.g., Rapid Genomics).

Highly recommended and mentioned by several: a) The Elshire Group: <https://www.elshiregroup.co.nz/> (based in New Zealand). Rob Elshire invented GBS sensu stricto (<http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0019379>). He and Robyn Johnston are fantastic to work with, their offer high-quality services, and their prices are globally competitive.

b) Diversity Arrays Technology: <http://www.diversityarrays.com> (based on Australia but with partners in other parts). Service provider for the joint generation of thousands of polymorphic SNPs and dominant markers for non- model organisms. Their technique is called DArTSeq. We had very good experience with them and they can provide results from SNP tables till raw FASTQs if requested, including a BLAST/annotation of all markers against various genomes.

c) SNPSaurus: <http://snpsaurus.com> costs similar to Floragenex, on the high ranges

d) Novogene (www.novogene.com), Chinese company, indicated as cheaper than Floragenex

e) LGC ([http://www.lgcgroup.com/services/-dna-sequencing/genotyping-by-sequencing-\(gbs\)/#.WYVtSYHTXqA](http://www.lgcgroup.com/services/-dna-sequencing/genotyping-by-sequencing-(gbs)/#.WYVtSYHTXqA)); indicated as slow in

answering inquires and long project times

Others: f) GenoScreen (in France) <https://www.genoscreen.fr/en/> g) TexasAMU Genomics <http://www.txgen.tamu.edu>; <http://genomics.tamucc.edu> h) Genomix4life (in Italy) <http://www.genomix4life.com/en/> i) IGATech (in Italy) <http://igatechnology.com> j) Center for Anchored Phylogenomics at FSU run by Emily Moriarty Lemmon and Alan Lemmon (<http://anchoredphylogeny.com>). Partnership between researchers and the Center (from organization of the project to publication of the study).

k) Genohub: <https://genohub.com/> They don't do the work themselves but rather contact a number of companies which then place bids to do the work you want them to do. If you accept the low bid, then the company contacts you and you make arrangements to send of your DNA. I've used them 3x now and it's always been cheap, I've got good quality data, and the turn around was fast.

Ella Vázquez Domínguez Instituto de Ecología, UNAM Ap. Postal 70-275, Ciudad Universitaria México DF 04510 México Tel +52 55 5622 9015 Email: evazquez@ecologia.unam.mx <http://web.ecologia.unam.mx/laboratorios/evazquez> Original post:

Hi

I am searching for the best possible option for genomic sequencing services, available for an academic research entity (Mexican University), thus it will be of great help to get different suggestions. We need to obtain polymorphic SNPs, data that will be used for population and landscape genomics, annotation for loci under selection, and the sort. The GBS or single/double RadSeq service we need includes library preparation; we will provide the appropriate DNA samples of different animal species (initially rodents). We wish to obtain the raw data (fastq files) from which to perform the Bioinformatics (no need the service companies to do it).

I have already contacted these companies: Data2Bio and Floragenex (they already gave me some quotes); Genewiz and HudsonAlpha (still waiting to hear from them); and GenScript and Edinburgh Genomics (do not provide such services).

evazquez@ecologia.unam.mx

Groningen VolFieldAssit ChilianBirds

PhD research project of the department of Behavioural Ecology at GELIFES (Groningen Institute for Evolutionary Life Science) Field work close to Santiago de Chile, in collaboration with Universidad de Chile

I am looking for a field assistant with experience bird catching and handling. Due to an accident, I can not perform these activities by myself and need help on very short notice. In september, I will study the incubation behaviour of the small passerine thorn-tailed rayadito, *Aphrastura spinicauda*. This bird breeds in nest boxes which makes it convenient to study.

The field assistant would catch the birds with mist nets during the nest building stage (cautious to prevent abandoning), ring them with PIT tags, to follow the incubation behaviour later on. Another responsibility would be the measuring and bleeding of the nestlings (mass, wing length, skull length, etc.).

Travel and housing will be paid for. Successful candidates should have experience in the above mentioned tasks and should be independent workers. As daily working hours can be long, the candidate should be highly motivated and have a hard-working mentality. Free hours and days depend fully on the bird behaviour and will be scheduled spontaneously.

The candidate would work closely together with me, a newly started PhD researcher. I am a hard worker myself, however temporarily limited by my injury. I like to have a good atmosphere while working and having a good laugh. The working language in Chile is Spanish. Spanish skills would be a plus but no obligation.

Interested? Contact me through mlmbirker@gmail.com, so we can set a Skype meeting for further information.

Kind regards,

Martje Birker PhD candidate University of Groningen
mlmbirker@gmail.com +31 63 411 57 33

Martje Birker <mlmbirker@gmail.com>

GSA ProgramInMentoredPeerReview

Dear colleagues, We're now recruiting the first group of senior graduate students, postdoctoral fellows, and junior faculty to take part in a pilot peer review training program: <http://www.genetics-gsa.org/careers/-training-program.shtml> Peer-reviewers are vital to science. Yet early career scientists in genetics rarely receive formal training in how to be a good reviewer. This uneven training means we're often failing to prepare the next generation of reviewers. But it also means many students and postdocs miss the chance to develop skills central to their success in science: understanding the mindset and expectations of peer reviewers and editors, critical thinking, evaluating research, and providing constructive feedback on scientific projects not directly related to their own.

The GENETICS Editorial Board and the GSA Publications Committee are addressing this deficiency with a program that gives early career GSA members real-world peer review experience. Participants will receive training and one-on-one mentoring in peer review from GENETICS editors, while reviewing manuscripts submitted to GENETICS that are within their areas of interest and expertise.

To pilot this program, we invite applications from GSA members who are senior graduate students and those within seven years of receiving their PhD degree. Applicants from anywhere in the world are encouraged to apply. We particularly welcome applications from members who lack opportunities to receive peer review training in their home labs or departments. For this pilot, we are seeking applicants able to review manuscripts for any of the following journal sections: - Cellular Genetics - Developmental and Behavioral Genetics - Population and Evolutionary Genetics Applications are due August 14, 2017: <http://www.genetics-gsa.org/careers/training-program.shtml> To learn more about the development of the program please visit <http://genestogenomes.org/learning-to-peer-review/> Please help us develop this important program by spreading the word to your colleagues.

Yours sincerely,

Mark Johnston, Editor-in-Chief, GENETICS David Greenstein, Secretary and Publications Committee

Chair, Genetics Society of America, Senior Editor, GENETICS Aleeza Gerstein, Liaison, Publications Committee and Early Career Scientist Communications and Outreach Subcommittee Sonia Hall, Director, Engagement and Development, Genetics Society of America

Aleeza Gerstein <gerst035@umn.edu>

QUBES Teaching Evolution

The QUBES (Quantitative Undergraduate Biology Education and Synthesis) project is announcing two new opportunities for faculty to learn effective and fun approaches to teach math and modeling to biology students.

These opportunities are Faculty Mentoring Networks, in which small groups of faculty from around the country meet online to learn, share, implement, test, and refine new educational approaches. QUBES Faculty Mentoring Networks provide faculty with “extended duration, low intensity” mentoring and peer interactions during the challenging classroom implementation stage of instructional reform, not just beforehand in a summer workshop.

Erin Bodine from Rhodes College is hosting a faculty mentoring network on using student- friendly (non-calculus) models in biological applications ranging from population growth and species interactions to natural selection and population genetics. The focus will be on discrete difference equations and other approachable but useful mathematical model types. Learn more and apply here: https://qubeshub.org/groups/discretefinn_f2017 (Application Deadline September 30).

Second, Holly Gaff from Old Dominion University is hosting a faculty mentoring network on using manipulatives and physical models to help learners break through prior fears and develop an appreciation for how mathematical reasoning informs problem solving, inference, and precise communication in biology. The focus will be on hands-on, active learning approaches to introducing modeling. Learn more and apply here: <https://qubeshub.org/groups/beanbagbiology> (Application Deadline September 15).

In both cases, participants will earn recognition from a national educational initiative (i.e. a letter for your faculty annual report/ line for your CV), and have opportunities for professional products to result from their work (e.g., educational publications or presentations at biology education conferences). Both networks will feature lots of biological applications of modeling. Neither network requires or presumes mathematical or modeling expertise, and both will provide instructional approaches suitable for introductory biology or ecology/evolution courses. High school and community college instructors are encouraged to apply.

Check out these faculty mentoring opportunities and other quantitative biology education resources and ideas at <https://qubeshub.org> . Best,

Jeremy Wojdak

Radford University, Department of Biology

QUBES (Quantitative Undergraduate Biology Education and Synthesis)

jmwojdak@radford.edu

Kristin P. Jenkins, PhD Director

BioQUEST Curriculum Consortium bioquest.org (608) 622.9394

Kristin Jenkins <kristin.jenkins@bioquest.org>

ArizonaStateU CoalescentTheoryVirusEvolution ...	78	UCambridge 2 EvoMicrobialGenomics	101
ArizonaState UnivMontana PopulationGenomics ..	79	UChicago ComputationalGenomics	101
ArizonaStateU PrimateGenomics	79	UChicago PopulationGenetics	101
AubrunU 2 EvolutionaryPhysiology	79	UColorado Boulder DispersalEvolution	102
Budapest 2 EvolutionaryGenomics	80	UColorado Boulder MolecularEvolution	103
CaliforniaAcademyOfSciences CycadEvolution	81	UEastAnglia 2 BeeEvolution	104
Cambridge UK MolecularEvolution	82	UExeter ArcticConservation	104
CharlesU Prague SexChromosomeEvolution	83	UGothenburg TreeOfLife DeadlineEXTENDED ..	105
ColumbiaU ProtistGenomicData	84	UHelsinki SexConflictResolutionInSalmon	105
CornellU CropGenomics	84	UIllinois FunctionalGenomicsBumbleBeePathogens	107
CornellU HumanPopulationGenomics NutriGenomics	85	UKentucky EvolutionaryEpigeneticsGenomics	107
CSU MontereyBay DiversityOfTheIndoPacific	86	UKonstanz CichlidSpeciesDeliniation	108
GeorgeWashingtonU EvolutionCarbonCycling	87	UKonstanz GenomicsOfAggression	108
JagiellonianU AmphibianEvolutionaryGenomics ...	87	UMinnesota EvolutionAdaptationInSymbiosis	109
JagiellonianU EvolutionaryPhysiology	88	UMinnesota FungalAdaptiveEvolution	109
KunmingInstZoology Metabarcoding	89	UMontana BacterialEvolutionaryGenomics	110
MaxPlanck Germany AvianCulturalEvolutionEcol .	89	UNottingham EvolutionaryBiol	111
MaxPlanckInstitute EvolutionaryGenomics	90	UOklahoma ComparativePhylogeography	112
MichiganStateU ConsevationBiol PopGenomics	91	UOregon Bioinformatics EvolutionaryGenomics ..	112
MIT EvolutionaryPlantPhysiology	92	UOregon BiologyAging Biodemography	112
NortheasternU Genomics	92	UPerpignan France Metabarcoding	113
OklahomaStateU EvolutionaryBiology	93	UPittsburgh EvolutionaryEcology	114
Oregon ForestBioinformaticsGenomics	94	USouthernMississippi FinfishGenetics	114
PennStateU PlantEvolutionaryGenomics	94	USouthFlorida EvolutionaryGenomics	114
PurdueU Conservation	95	USouthFlorida SpartinaEvolutionaryEpigenomics	115
SantaFeInstitute Omidyar EvolutionaryBiol	96	UTexas-Houston InferringDemographicHistory ...	116
StellenboschU CamouflageEvolutionStonePlants ...	96	UWisconsin Madison EvolPopGenomics	116
StockholmU YeastExperimentalEvolution	97	UZurich LifeHistoryEvolution	117
TUMunich Museomics	98	Versailles France PlantVirologyBioinformatics	117
UArizona ProteinEvolutionBioinformatics	98	VirginiaTech Macroevolution	118
UCalifornia Davis AedesAegyptiPopulationGenomics	99	WSL Switzerland EnvironmentalGenomics	119
UCalifornia Davis MosquitoEvol	100		

ArizonaStateU CoalescentTheoryVirusEvolution

Postdoctoral position: Theoretical and Computational Population Genetics

The Jensen Lab (jjensenlab.org) at Arizona State University is searching for a postdoc to investigate the application of multiple merger coalescent models to the study of virus evolution. Projects will thus involve both theory and statistical method development, as well as the analysis of large-scale datasets from both human cytomegalovirus and influenza A virus. As such, the successful applicant is expected to be strong computationally, and have a background in population genetic

theory, experimental evolution, or virology. Funding is available for two years, with the possibility of a third year extension.

Being in the School of Life Sciences, as well as the Centers for Evolution & Medicine and Mechanisms of Evolution, the Jensen Lab is part of a large and diverse population genetics community at ASU spanning theory, computation, and analysis (ASUpopgen.org).

Interested applicants should send a CV, brief statement of research interests, and contact information for two references to jeffrey.d.jensen@asu.edu by September 15.

“Jeffrey D. Jensen” <jeffrey.jensen@epfl.ch>

ArizonaState UnivMontana PopulationGenomics

Postdoctoral position: Adaptation to Changing Environments

The Good Lab (University of Montana, thegoodlab.org) and Jensen Lab (Arizona State University, jjensenlab.org) are searching for a joint postdoc to investigate the population genetics of seasonally changing coat color in mammalian systems. This project has two years of funding, with one year being spent at UM focused upon data collection and generation, and one year being spent at ASU focused upon statistical method development and analysis. There is also potential for a third year extension. An important focal point of this work will be the development of improved methodology for the analysis of time-series data.

The Division of Biological Sciences at the University of Montana offers a large research community (hs.umt.edu/dbs), and the Good Lab is part of a suite of newly constructed space dedicated to evolutionary genomics research. The School of Life Sciences at Arizona State University additionally offers a diverse faculty, with multiple interacting labs particularly focused around empirical and theoretical population genetics (ASUpopgen.org).

Interested applicants should send a CV, brief statement of research interests, and contact information for two references to jeffrey.d.jensen@asu.edu. The application deadline is September 15, after which the position will remain open until filled.

“jeffrey.jensen@epfl.ch” <jeffrey.jensen@epfl.ch>

ArizonaStateU PrimateGenomics

The Pfeifer Lab (spfeiferlab.org) at Arizona State University is searching for a Postdoc to investigate the fine-scale changes in rates of mutation and recombination through evolutionary time within the primate clade. Projects will involve computational methods development as well as analyses of large-scale genomic data sets. Thus, the successful candidate is expected

to have a strong computational and statistical background (programming proficiency in R, Perl, or Python, and shell scripting is essential; experience with analyzing high throughput sequencing data is highly desired) along with a genuine interest in genetics and biology. Preference will be given to candidates with a strong publication record, evidence of research productivity, and ability to successfully communicate scientific information. Funding is available for three years, contingent on annual renewal based on progress. The start date is flexible.

The Pfeifer Lab offers a vibrant work environment with excellent opportunities for collaborative efforts as well as independent accomplishments. The Lab is integrated within a diverse bioinformatics, evolution, and population genetics research community at ASU (ASUpopgen.org), as well as the Centers for Evolution and Medicine (evmed.asu.edu) and Mechanisms of Evolution (biodesign.asu.edu/mechanisms-evolution). Additional information about the Lab and research can be found at: <http://spfeiferlab.org>. Interested applicants should send a short summary of research interests, CV, and contact information for two references to susanne.pfeifer@asu.edu. The evaluation of applications will begin on September 1st, 2017, and will continue until a suitable candidate has been found. Informal inquiries are welcome.

Susanne Pfeifer <spfeife1@asu.edu>

AubrunU 2 EvolutionaryPhysiology

2 Postdoctoral Fellows in Evolutionary Physiology at Auburn University

The Hood lab at Auburn University is hiring 2 postdoctoral scholars to 1) evaluate the role of oxidative stress and mitochondrial function in life history trade-offs and 2) evaluate the effects of genetic variation in the intracellular stress response on reproductive fitness and mitochondrial performance. Projects will be completed in wild-derived house mice and deer mice, respectively. Both projects are funded by the National Science Foundation. A strong background in ecology/evolutionary biology and physiology and excellent communication, organizational, and leadership skills are required. Applicants with strong lab skills will be given preference. Preferred skills include isolating mitochondria and measuring mitochondrial respiration, running western blots, and performing elisa's. Post-docs will be expected to

assist with training graduate students in the lab, develop synergistic projects, write grants, and produce first authored papers and contribute to co-authored papers. These are one-year positions with the possibility of renewal for a total of 2 or 4 years, pending satisfactory work.

Information about Hood lab and abstracts for funded projects can be found at: thehoodlaboratory.com. This work will be completed in collaboration with Dr. Andreas Kavazis, School of Kinesiology at Auburn (<http://www.education.auburn.edu/initiatives/-muscle-biochemistry-lab-dr-andreas-kavazis/>) and Dr. Hippokratis Kiaris, School of Pharmacy, University of South Carolina (<http://sccp.sc.edu/Hippokratis.kiaris>). Applicants must have a Ph.D. in an appropriate field. The candidate selected for this position must be able to meet eligibility requirements to work in the United States at the time the appointment is scheduled to begin and continue working legally for the proposed term of employment. Women and minorities are strongly encouraged to apply. This announcement is informal in nature and candidates of interest will be asked to submit a formal application for complete consideration after initial screening. If interested, please send a CV and a statement of interest with a list of relevant skills to Wendy Hood at wrhood@auburn.edu (please note our mail system is limited to 25Mb messages). Receipt of application will be confirmed within 3 days. Review of applications will begin August 7, 2017, and continue until a suitable applicant is found.

wrh0001@auburn.edu

Budapest 2 EvolutionaryGenomics

Budapest.2.EvolutionaryGenomics

Second call for postdocs in evolutionary genomics and phylogenomics are available to join the ERC 'GENECLOCKS' project (http://cordis.europa.eu/-project/rcn/207593_en.html) headed by Gergely Szollosi (<http://ssolo.web.elte.hu>). Two positions are offered for 2 years with the possibility of extension up until the 2022 end date of the GENECLOCKS project. The position comes with a salary of up to EUR 43,200 per year (approx. up to EUR 2,400-2,900 net per month after taxes), as well as a travel and research funds.

We are looking for an individual who received his or her PhD preferably within the last six years, who is highly self-motivated and can work independently on a

project that he or she will help develop in the context of GENECLOCKS.

A central theme of GENECLOCKS is disclosing new sources of information for dating the first three-quarters of Earth's evolutionary history that are independent from both fossils and molecular clocks. Life's early history has remained terra incognita until now, because the fossils needed to calibrate standard evolutionary timescales are simply not available for microbial life. Microbial fossils are scarce and difficult to interpret in a phylogenetic context with confidence. In previous work we have shown that patterns of lateral gene transfer inferred from modern genomes encode a record of co-existing lineages throughout the history of life, and that we can use this record to reconstruct the relative ages of microbial groups from the three domains of life in deep time.

This discovery is a game changer for anyone interested in the history of life, from either a geological or genomic perspective. It demonstrates the existence of a new and abundant source of dating information that is inscribed in the genome of any organism, provided a gene transfer occurred in its ancestry. This constitutes the overwhelming majority of the diversity of life.

Postdocs will undertake projects together with international collaborators with the goal of either i) developing new methods that systematically extract information on the pattern and timing of genomic evolution by explaining differences between gene trees, or ii) apply existing methods to resolve the timing of microbial evolution and its relationship to Earth history and answer long standing questions. Possible collaborations and associated projects include:

Reconstructing a dated phylogeny of Bacteria in collaboration with Vincent Daubin at the LBBE in Lyon.

Developing and implementing bayesian methods for the species tree aware reconstruction of gene trees with Nicolas Lartillot at the LBBE in Lyon.

Reconstructing a dated phylogeny of Eukaryotes including their position within Archaea in collaboration with Tom Williams at the University of Bristol.

Developing and implementing new methods for species tree reconstruction in the context of hierarchical gene tree-species tree methods with Jens Lagergren at the Science for Life Laboratory in Stockholm.

Implementing and applying methods to include transfer derived relative age constraints in molecular clock estimates with Bastien Boussau at the LBBE in Lyon.

Developing novel gene tree-species tree reconciliation methods that model correlated gene histories with Eric

Tannier at LBBE in Lyon.

Research visits of up to several months are foreseen as part of potential collaborations.

To be considered, please send a single merged PDF to ssolo@elte.hu that contains your CV including publication list, preferably with a link to your google scholar profile, academic transcripts, a statement of research interests (3 pages or less) as well as three academic references. Please include 'GENECLOCKS17' in the subject of your email. Applications will be considered until October 1st, 2017, or until the position is filled. The position is available from the fall or winter of 2017.

The research group is lead by Dr. Gergely Szollosi (<https://scholar.google.hu/citations?user=3DsPrYT-oAAAAJ>) and is hosted at Eotvos Universities Institute of Physics in Budapest. The Institute of Physics has been included in the Excellence Group of European Universities, and has achieved top placement in the number of citations, the number of ERC grants, the time available for PhD research and the gender balance of master's students in the CHE Excellence Ranking. Budapest is a vibrant capital city with exciting cultural life, a unique atmosphere and affordable living costs (cf. <https://goo.gl/86II3s>).

Please direct any enquiries to Dr. Gergely Szollosi (ssolo@elte.hu, <http://ssolo.web.elte.hu>).

sszolo@gmail.com

California Academy of Sciences Cycad Evolution

Rose Postdoctoral Fellow

POSITION SUMMARY: A postdoctoral research position is available to conduct research on cycads at the California Academy of Sciences. This position reports to the Associate Curator of Botany within the Institute of Biodiversity Science and Sustainability and the successful candidate is expected to work in this collaborative environment. This is a temporary one year position with the possibility of renewal for up to two years, contingent on research progress. The fellow will conduct research on the population genetics of Australian cycads to examine the roles of pollination and seed dispersal in gene flow to inform cycad conservation. However, applicants with expertise in any area of plant evolution will be given full consideration. The candidate will contribute to the development of herbarium and

genomic collections, and bioinformatic resources at the California Academy of Sciences. Additionally, public outreach through in-person and online interactions will be a component of the position.

ESSENTIAL DUTIES AND RESPONSIBILITIES: - Conduct original, scientific research with Dr. Nathalie Nagalingum on cycad population genomics, addressing questions such as maternal versus paternal gene flow and population demographics - Organize and participate in research expeditions, requiring international travel for 2-4 weeks per expedition, including securing appropriate research, export and import permits. - Publish and present results in scientific journals and at national and international meetings, and contribute to grant proposals - Contribute to and participate in educational, public, and development programs of the Academy - Follow all Academy regulations with respect to collections, safety and other institutional guidelines. - Other duties as assigned

QUALIFICATIONS: To perform this job successfully, an individual must be able to perform each essential duty satisfactorily. The requirements listed below are representative of the knowledge, skill, and/or ability required. Reasonable accommodations may be made to enable individuals with disabilities to perform the essential functions.

EDUCATION and/or EXPERIENCE: The ideal candidate will possess a combination of the following education and/or equivalent experience: - Doctoral degree (Ph.D.) in a relevant discipline, with all requirements completed by the starting date of fellowship. - Research expertise in plant evolutionary or population genomics combined with a strong publication record - Experience working in a laboratory environment with proper safety precautions - Field work experience

KNOWLEDGE, SKILLS AND ABILITIES: - Ability to conduct original and creative scientific research in collaboration with the Associate Curator of Botany - Strong academic record with peer-reviewed publications - Knowledge of and experience with molecular biology, next-generation sequence library preparation and sequencing, and related bioinformatics tools and programming - Understand and comply with all local, international (CITES), Australian, and US Federal regulations relating to export and importation of specimens and genetic material. - Interest in science communication/outreach including through social media - Must have or be able to obtain a valid passport; willingness to travel internationally

LANGUAGE SKILLS: Ability to read and interpret documents such as scientific papers, safety rules, operating and maintenance instructions, and procedure manuals.

Ability to write reports, correspondence, and scientific articles. Ability to speak effectively before groups or individuals.

PHYSICAL DEMANDS & WORK ENVIRONMENT: The physical demands and work environment described here are representative of those that must be met by an employee to successfully perform the essential functions of this job. Reasonable accommodations may be made to enable individuals with disabilities to perform the essential functions. While performing the duties of this job, the employee is frequently required to stand, sit, walk, and reach with hands and arms, and talk or hear. Must be able to perform repetitive motions 50% of the time and lift 30 lbs. The employee will be required to work in a laboratory, handle chemicals, and comply with safety regulations. Must be able to walk in steep terrain in hot and humid conditions $\frac{3}{4}$ ability to travel by plane.

APPLICATION INSTRUCTIONS: Please submit your cover letter and resume online at <http://calacademy.snaphire.com>. Note that the recruitment timeline for positions vary and depend on many factors, so it is impossible to accurately predict when a position will close. We appreciate your patience during this process. No phone calls please.

The California Academy of Sciences will consider for employment all qualified applicants with criminal histories in a manner consistent with the requirements of the San Francisco Fair Chance Ordinance (SF Police Code, Article 49).

— / —

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>

Cambridge UK Molecular Evolution

A position is available in Nick Goldman's group at the EMBL-European Bioinformatics Institute (near Cambridge, UK) for a Research Scientist (post-doctoral/senior post-doctoral level).

The position is available immediately, and is expected to be for 3 years in the first instance.

Full details are viewable at https://ig14.i-grasp.com/-/fe/tpl_embl01.asp?newms=jj&id=55969&aid=15470

<https://www.nature.com/naturejobs/science/jobs/-622287-scientist-in-molecular-evolution> and the job description is included below.

Nick Goldman

Nick Goldman <http://www.ebi.ac.uk/research/goldman>
European Molecular Biology Laboratory tel: +44-(0)1223-492530 European Bioinformatics Institute tel: +44-(0)1223-494522 Wellcome Genome Campus, Hinxton, Cambridge CB10 1SD, UK

//

Job Description

We are seeking to recruit a Scientist to join Nick Goldman's research group (<http://www.ebi.ac.uk/research/-goldman>) at the European Bioinformatics Institute (EMBL-EBI) located on the Wellcome Genome Campus near Cambridge in the UK.

The group researches the evolutionary analysis of DNA and protein sequences, genomic data analysis methods, modelling of molecular evolutionary processes and statistical inference based on these models. We are interested in applications of existing and novel sequence analyses in large-scale comparative genomics and Next Generation Sequencing, and have recently become involved in studies around the use of DNA for digital information storage.

You will work with Nick Goldman and other members of the group on both phylogenetic methodology and biological applications. You will be expected to participate in research projects already under way in the group and to develop your own projects in related areas.

In addition to pursuing research, you will take responsibility for various tasks maintaining and developing the efficient operation of the group. These may include management or leadership of research projects of your own and the group's devising; supervision of other staff (including post-graduate students and junior visitors); compilation of materials for reports and presentations; preparation of grant applications; teaching at training events (including abroad); liaison with colleagues and collaborators both within and outside of EMBL.

EMBL-EBI is part of the European Molecular Biology Laboratory (EMBL) and it is a world-leading bioinformatics centre providing biological data to the scientific community with expertise in data storage, analysis and representation. EMBL-EBI provides freely available data from life science experiments, performs basic research in computational biology and offers an extensive user training programme, supporting researchers in academic and industry. We have close ties with both the

University of Cambridge and the Wellcome Trust Sanger Institute.

Qualifications and Experience

You will have a PhD and further research experience and publications in computational biology. Necessary attributes include: understanding of and enthusiasm for the questions biologists ask of genome sequence data, experience of mathematical modelling and statistical data analysis, scientific computer programming.

A background in biology, mathematics/statistics, computer science or other technical disciplines, combined with subsequent cross-disciplinary experience, is the likely career path.

Past success in the leadership responsibilities described above will be advantageous.

Excellent communication and interpersonal skills are required.

Benefits

EMBL is an inclusive, equal opportunity employer offering attractive conditions and benefits appropriate to an international research organisation. The remuneration package comprises a competitive salary, a comprehensive pension scheme and health insurance, educational and other family related benefits where applicable, as well as financial support for relocation and installation.

We have an informal culture, international working environment and excellent professional development opportunities but one of the really amazing things about us is the concentration of technical and scientific expertise — something you probably won't find anywhere else.

If you've ever visited the campus you'll have experienced first-hand our friendly, collegial and supportive atmosphere, set in the beautiful Cambridgeshire countryside. Our staff also enjoy excellent sports facilities including a gym, a free shuttle bus, an on-site nursery, cafés and restaurant and a library.

Application Instructions

To apply please submit a covering letter and CV, with two

— / —

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>

CharlesU Prague SexChromosomeEvolution

CharlesU_Prague.Postdoc.SexChromosomeEvolution

Postdoc position in Evolution of sex chromosomes in squamate reptiles

One postdoc position is currently open in Department of Ecology, Charles University, Czech Republic. The successful candidate will join our current projects on the study of the evolution of sex chromosomes in squamate reptiles with molecular and cytogenetic methods.

Project description: The aim of the project is to examine the evolution of sex chromosomes and their homology based on gene content in selected lineages of squamate reptiles (eg. lizards and snakes). Squamate reptiles possess lineages with either XX/XY, ZZ/ZW or temperature-dependent sex determination. Despite the recent advances in the field, our knowledge about their sex determination systems and sex chromosome homology is limited only to few groups of reptiles (eg. iguanas, advanced snakes), while the majority of reptilian lineages remain unstudied. The successful candidate will collaborate with the other team members and will study the evolution of sex chromosomes in a multidirectional approach, involving cytogenetics (eg. FISH, chromosome painting), molecular genetics (eg. qPCR) and bioinformatics (eg. transcriptomics). More information about our current research activity can be found in the following publications: <https://www.ncbi.nlm.nih.gov/pubmed/27037610> <http://www.ncbi.nlm.nih.gov/pubmed/26702042> <http://www.ncbi.nlm.nih.gov/pubmed/24433436>

Qualifications: The ideal candidate would have a Ph.D. diploma and proven expertise in cytogenetics. Experience in phylogenetics, genomics and/or bioinformatics would be desirable. Previous experience in herpetology is not necessary. The applicant should be scientifically motivated, have good communication skills and demonstrate publication record in reputable journals. High standard of spoken and written English is required.

Application: The applicant should send a short letter explaining his/her background and motivation, full CV and contact information for two references to Dr. Michail Rovatsos (michail.rovatsos@natur.cuni.cz).

The position could be either short-term (3-6 months)

or long-term (2 years) with possibility to expand, as it is in the framework of two major 3-year long research grants. Suitable candidates will be interviewed immediately, and preferably the candidate should be able available to start in September-October 2017. For any additional information, do not hesitate to write an email (michail.rovatsos@natur.cuni.cz).

Michail Rovatsos

Researcher Department of Ecology Faculty of Science Charles University Vinicna 7, 128 43 Praha 2 Czech Republic

“Michail Rovatsos, Ph.D.”
<michail.rovatsos@natur.cuni.cz>

ColumbiaU ProtistGenomicData

Postdoctoral Research Scientist

Description: The Duhamel Lab for Marine Microbiology and Biogeochemistry at Lamont-Doherty Earth Observatory of Columbia University seeks a Postdoctoral Research Scientist to join the laboratory to participate in a research project on the molecular ecology of small-sized marine protists. This position is located in Rockland County, NY at the Lamont Campus of The Earth Institute at Columbia University.

The lab is located near the NYC metro area, offering many opportunities for interactions within Columbia University departments, and other area Universities.

This project is in collaboration with the Kim Lab at the American Museum of Natural History, where part of the experimental work will be done. Tools and approaches for this work include collection and analyses of next-generation molecular sequence data as well as physiological and chemical measurement data. The position will entail laboratory experiments (including continuous cultures), and data analysis (including bioinformatics tools) and may additionally necessitate time at sea on research cruise(s).

Qualifications: A PhD is required in microbiology, biological oceanography or a related field. Experience in microbiology, and/or biological oceanography, and computational biology/bioinformatics is preferred. Applicants with experience in microbial ecology and a strong bioinformatics background are encouraged to apply. Familiarity with the analysis of high throughput sequencing data including strong programming skills (e.g., R, Python, etc.) is preferred. Familiarity with

continuous culturing of plankton species would be a plus. Excellent command (verbal and written) of the English language, organization and meticulousness, and strong interpersonal skills desired. Applicants must be willing and capable of participating in oceanographic cruises.

The start date for this position is flexible but a start in the fall 2017 is preferred.

Appointment will be for 1 year, with continuation pending funding and progress.

Search will remain open for at least 30 days after the ad appears and will continue until the position is filled.

Application: Please visit our online application site at academicjobs.columbia.edu/applicants/Central?quickFinde093 for further information about this position and to submit your application, including a cover letter, which should detail past research experience and future interests, current CV, and the names, phone numbers and email addresses of three references.

Columbia University benefits offered with this Officer of Research appointment.

Columbia University is an Equal Opportunity/Affirmative Action employer – Race/Gender/Disability/Veteran.

We accept online applications only. – Helen Olivette Human Resources Coordinator

Lamont-Doherty Earth Observatory of Columbia University 61 Route 9W, Palisades, NY 10964 Phone: 845-365-8357 / Fax: 845-365-8142

Helen Olivette <olivette@admin.ldeo.columbia.edu>

CornellU CropGenomics

Postdoctoral Associate for Comparative Quantitative Genetics and Genomics in Sorghum and Maize

Position Function

A Postdoctoral Associate Position is available to work in the area of comparative quantitative genetics and genomics in the Plant Breeding and Genetics Section. The position will be part of the ARPAE-funded, project entitled “Transportation Energy Resource from Renewable AgricultureâEnergy-Crop Phenotyping Platform (TERRA-MEPP; <https://terra-mepp.illinois.edu/>”).” This position requires an experienced scientist to employ genomics and statistical tools in constructing a

comparative sorghum-maize haplotype map (HapMap). The intent is to develop an evolutionary model to better understand the levels and patterns of diversity between maize and sorghum, along with the application of these findings to enhance genome-wide association studies and whole-genome prediction of complex traits in sorghum. The ideal candidate will have expertise in quantitative genetics, genomics, programming and statistics. Responsibilities will include independent research in the analysis of large whole-genome resequencing data sets, developing evolutionary models, complex trait dissection, and training scientists and students. The position will involve close collaboration with a dynamic team of plant physiologists, geneticists, crop modelers, and robotics engineers.

Position requirements * Ph.D. with research experience in statistics, plant or animal breeding, genetics, bioinformatics, computational biology or related discipline. * Experiences in constructing and analyzing whole-genome resequencing, RNA-seq, or variome data sets with genomics software (GATK, BWA, PLINK, TASSEL, BEAGLE). * Extensive skills in programming (Python, Java, or C/C++) and statistical tools (R, ASReml, or SAS). * Proficiency in developing and implementing complex computational pipelines on Linux operating systems and high-performance computing clusters. * Excellent interpersonal and communication skills with a strong publication record.

Preferred qualifications * More than 3 years of experience in quantitative genetics, genomics or bioinformatics. * Extensive experience in integrating and analyzing whole-genome resequencing and comparative variome data sets. * Experience in implementing machine learning algorithm (random forest, artificial neural network, etc.) * A record of publication in the field of quantitative genetics and genomics. * Experience in population genetics or comparative genomics. * Knowledge of plant breeding and genetics approaches is a plus.

Supervision Exercised

The position will include some supervision of undergraduate and graduate students involved in research on the project.

How to Apply

A letter of interest in the position, C.V., and contact information for three references should be emailed together as a single PDF file to Michael Gore at: mag87@cornell.edu

Review of applications will begin immediately and continue until the position is filled.

Michael Gore

Associate Professor

Liberty Hyde Bailey Professor

Plant Breeding and Genetics Section

Cornell University

310 Bradfield Hall

Ithaca, NY 14853

E-mail: mag87@cornell.edu

Vox: (607) 255-5492

Fax: (607) 255-6683

<http://www.gorelab.us>

Michael Allen Gore

<mag87@cornell.edu>

CornellU HumanPopulationGenomics Nutrigenomics

Postdoctoral positions in human population genomics, nutrigenomics, & association studies

Two postdoctoral positions and one programmer/analyst position are available in the group of Alon Keinan at Cornell University (keinanlab.cb.bscc.cornell.edu). Current and past lab members came from backgrounds in computer science, statistics, genetics, nutritional genomics, physics, mathematics, and genetic anthropology, which facilitates the trans-disciplinary development and genomics application of methodologies, along with functional interpretation of discoveries. Listed in the full advertisement (link below) are representative publications from the lab of projects related to the fields of the new positions. The successful candidate can join one of the many ongoing projects in the group or start new projects, either from an array of planned projects or their own ideas. Thus, projects will be aligned with the interests of the successful candidate and her/his expertise, or expertise they desire to develop further. As the group also draws a large number of the strongest undergraduate students in computer science, computational biology, etc., postdoctoral fellows can aim to carry out a broader project or several projects by relying on their help, while potentially developing mentoring skills. Importantly, projects do not necessarily have to be associated with any of the existing funding sources of the PI.

The ideal candidate will have a strong track record in either population genomics, statistical genetics, nutritional genomics, or human genomics in general, as well as strong programming and statistical skills, with a Ph.D. in any of the fields mentioned above or a related field. The starting date is flexible and can be as early as September 2017. Applications will be accepted until the positions are filled. Competitive salaries commensurate with experience and skills, as well as a very generous benefits package will be offered. Funding will be guaranteed for at least 3 years, and the PI will also help the successful candidate secure fellowships/future funding. Former postdocs in the group went on to a tenure-track faculty position at University of Maryland College Park, a tenure-track faculty position at University of Minnesota Twin Cities, a Research Associate position at Cornell University, as well as research positions in industry: Associate Director of Think Team at Otsuka Pharmaceutical Companies (US), Investigator II at Novartis, Computational Biologist at NRGene, and Research Scientist at Embark.

Further details and application instructions can be found at <http://keinanlab.cb.bscb.cornell.edu/content/jobs> (or directly in the ad at http://keinanlab.cb.bscb.cornell.edu/sites/default/files/Keinan_lab_postdocs_programmer_ad_2017_2018.pdf)

Sincerely, Alon

Alon Keinan, PhD Associate Professor of Computational Biology, Cornell University Department of Biological Statistics & Computational Biology Center for Comparative and Population Genomics | Center for Vertebrate Genomics | Center for Enervating Neuroimmune Disease

102C Weill Hall | Cornell University | Ithaca, NY 14853
 alon.keinan@cornell.edu | 607-254-1328 phone | 607-255-2323 fax
<http://keinanlab.cb.bscb.cornell.edu/> | @AlonKeinan

“alon.keinan@cornell.edu” <alon.keinan@cornell.edu>

CSU Monterey Bay
DiversityOfTheIndoPacific

The Diversity of the Indo-Pacific Network (DIPnet; <http://diversityindopacific.net/>) seeks a full-time coordinator. DIPnet was founded in 2012 with the goal of increasing communication and collaboration among biodiversity researchers across the Indo-Pacific. In doing so

we have two primary goals 1) promote education and collaboration through workshops and 2) build a state of the art open-access database for metadata associated with DNA sequence data. To achieve these goals DIPnet has already hosted three workshops in Bali, the Philippines, and South Africa with one more workshop scheduled for 2018. We have also developed the Genomic Observatory Metadatabase (GeOME; <http://www.geome-db.org/>) an open access repository for geographic and ecological metadata associated with biosamples and genetic data.

The DIPnet Coordinator is a full-time position and responsibilities include: (1) continuing to develop GeOME and the DIPnet website (WordPress) and serve as its primary curator, (2) promoting research coordination among DIPnet participants and recruiting new participants, (3) developing original, collaborative research projects based on data stored in GeOME (currently >35,000 Sanger sequences from > 200 species) (4) organizing a data mobilization workshop in Fiji together with the annual 2018 workshop and transferring educational content to the website, and (5) assisting the steering committee in seeking funding to further sustain the network into the future.

This position is paid through University of Hawaii's Hawaii Institute of Marine Biology, but the Coordinator is located in Seaside CA at the California State University, Monterey Bay. Appointment will be 12 months with another year possible upon review by the DIPnet Steering Committee. Qualifications: We need someone who is highly organized. The Coordinator will curate new datasets submitted to GeOME, maintain the DIPnet website and membership lists, and be fluent in at least one of the following programming languages: R, python, java, or JavaScript. The Coordinator will be responsible for organizing a Data Mobilization workshop in Fiji in 2018 as well as the final DIPnet workshop likely to be held subsequently. A background in population genetics is preferred and an ability to talk with biologists from a diversity of fields that employ molecular methods (marine, terrestrial, metabarcoding, genomics, etc) is essential. The position will remain open until filled with a preferred start date of November 1st 2017.

Interested parties should contact Dr. Eric Crandall at ecrandall@csumb.edu with a CV and a letter of interest.

Eric Crandall <ecrandall@csumb.edu>

George Washington U Evolution Carbon Cycling

Postdoctoral position in tropical wood decay and carbon cycling at GWU

A postdoctoral position is available in the Zanne lab at George Washington University (GWU) in Washington, DC, USA. The postdoctoral scientist will work on joint NSF (with Steve Allison: UCI) and NERC (with Paul Eggleton: NHM London) funded field- and lab-based projects. The goal of these projects is to measure the relative roles of microbes and termites in deadwood carbon turnover in tropical Australia to better inform earth system models. The projects will be based at Lucas Cernusak's lab at James Cook University (JCU) in Cairns, QLD, Australia. The postdoc will move between the Zanne and Cernusak labs. Motivated applicants with experience working with saprotrophic microbes and/or termites monitoring wood decay and/or gas fluxes are especially encouraged to apply. Applicants should have a PhD in a relevant field, strong writing and quantitative skills, and a record of publishing in peer-reviewed journals. Applications will be reviewed as received and the position will be open until 17 September 2017. Applications should include a research statement, including relevant skills for the project and future goals (max: 1-2 pages), CV, and contact information for three references (including emails and phone numbers). Materials should be sent to Amy Zanne: aezanne@gmail.com. In addition, candidates should apply directly through GWU's recruitment website <http://www.gwu.jobs/postings/-45664>. The university is an Equal Employment Opportunity/Affirmative Action employer that does not unlawfully discriminate in any of its programs or activities on the basis of race, color, religion, sex, national origin, age, disability, veteran status, sexual orientation, gender identity or expression, or on any other basis prohibited by applicable law.

Dr. Amy Zanne Department of Biological Sciences
George Washington University
Science and Engineering Hall
800 22nd Street NW
Suite 6000
Washington, DC 20052

Office: 6690 SEH Office Phone: (202) 994-8751 Lab:
6420 SEH Lab Phone: (202) 994-9613 Fax: (202) 994-
6100 Website: <http://www.phylodiversity.net/azanne/>
Amy Zanne <aezanne@gmail.com>

Jagiellonian U Amphibian Evolutionary Genomics

Postdoc position in Amphibian Evolutionary Genomics (3 years)

A postdoctoral position in amphibian evolutionary genomics is available in the group of Wiesław Babik at the Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland (http://www.molecol.eko.uj.edu.pl/en_GB/zespol/pracownicy/-wieslaw-babik). The position is within the recently awarded National Science Centre (NCN) grant "Do antigen-processing genes coevolve with MHC class I genes in salamanders?"

Background. Understanding the mechanisms driving evolution of the genes underlying adaptive immunity is of major scientific importance and has implications for conservation. In this project we will test whether Antigen Processing Genes (APG) coevolve with Major Histocompatibility Complex (MHC) class I genes in salamanders. Coevolution has been suggested as the ancestral vertebrate condition, potentially limiting the efficiency and flexibility of adaptive immunity. Selection pressure to remove this constraint is therefore expected in multiple evolutionary lineages. Limited information available for salamanders reveals intriguing patterns of MHC I and APG variation, making this group ideal for testing the coevolution hypothesis and providing fundamental insights into the evolution of the adaptive immunity.

Job description. The postdoc will test predictions of the coevolution hypothesis. More specifically (s)he will: i) resequence the focal genes in multiple species from several families, ii) perform bioinformatics analysis of resequencing data, iii) test for correlation between APG and MHC variation iv) look for signatures of adaptive evolution. (S)he will work together with the PI and other team members, including a network of international collaborators.

Requirements. The suitable candidate will have a PhD degree obtained not earlier than in 2010 (extensions for parental leave apply), be fluent in English and have

strong interest in evolutionary genomics. The candidate should have Linux/scripting language skills, experience in bioinformatics analysis of DNA sequence data and background in population genetics; background in molecular evolution will be an advantage. Employment: full time research-only for three years. Salary: ca. 6500 PLN gross (before tax, includes benefits).

How to apply. For informal enquiries email wieslaw.babik@uj.edu.pl. The application (a single pdf file) should include: statement of research interests, CV with the list of publications, contact information for two referees and scan of the PhD certificate. Please send the application by email to: wieslaw.babik@uj.edu.pl no later than August 31st 2017. Selected candidates will be invited for live or Skype interviews. Preferred start date November-December 2017.

– Wiesław Babik Institute of Environmental Sciences Jagiellonian University Gronostajowa 7 30-387 Kraków Poland tel. +48 12 664 51 71 fax. +48 12 664 69 12 www.molecol.eko.uj.edu.pl/en_GB/zespol/-pracownicy/wieslaw-babik w.babik76@gmail.com

JagiellonianU EvolutionaryPhysiology

The Evolutionary Physiology Team

of the Institute of Environmental Sciences

is hiring a postdoctoral fellow (a research assistant) in physiological genomics

Research tasks:

The post-doc will perform the “molecular” part of a project entitled

Experimental evolution of physiological and behavioral adaptations in the bank vole: molecular background and alimentary system bacterial symbionts

funded by the Polish National Science Centre. The project is based on a long-term experimental evolution program, with lines of bank voles selected in three distinct directions. The specific objective is to investigate molecular basis of the evolution of increased aerobic exercise metabolism and propensity towards predatory behavior in the selected lines, through a) identification of genes with modified frequency of Single Nucleotide Polymorphism (SNP) alleles, and b) analyses of the correlation between SPN genotypes and pheno-

typic values of the selected traits. The specific tasks performed by the post-doc will include laboratory molecular analyzes, bioinformatic and statistical analyzes of high-throughput sequencing data, and participation in physiological measurements on laboratory rodents. This project is a continuation of the research presented in Konczal et al. 2015 (doi:10.1093/molbev/msv038) and 2016 (doi:10.1093/molbev/msw121). Additional information can be obtained from the principal investigator, Dr. Paweł Koteja (pawel.koteja@uj.edu.pl).

Key words: animal physiology, behavior, evolution, genomics, high-throughput sequencing, locomotor performance, metabolism, neurophysiology, predation, selection experiment, SNP

The main requirements:

- PhD degree in biology or related sciences obtained not earlier than 7 years prior to employment in the project (note: this period does not include periods of maternity or parental leave, or other circumstances described in the Polish National Science Centre OPUS project regulations),

- or a statement that the PhD dissertation has been submitted and the candidate is expected to obtain the degree before commencing the employment;

- Experience in analyzing data from high-throughput sequencing and working in a Unix/Linux environment.

Conditions of employment:

- full-time contract for 24 months, about 7000 PLN/month (gross),

- benefits of a full-time employee according to the Polish law (health insurance, retirement benefits, etc.)

- all social benefits of the University staff (www.en.uj.edu.pl/en/staff/staff-benefits/office),

- beginning of the employment: between 1.11.2017 and 1.03.2018 (negotiable).

Deadline for applications: 10 Sept. 2017-09-10; Interviews: 18-22 Sept. 2017; Decision: 30 Sept. 2017

If no candidate meets the requirements, the recruitment period will be extended. If you are interested in this position but cannot apply before the deadline, let us know and we will inform you about the extension.

For details of the requirements and the recruitment procedure see:

<http://www.eko.uj.edu.pl/index.php/en/institute/-announcements/470-an-op-en-postdoctoral-a-research-assistant-position-in-physiological-genomics>

Contact person:

Dr. Paweł Koteja (pawel.koteja@uj.edu.pl)
 Institute of Environmental Sciences
 Jagiellonian University
 7 Gronostajowa Street, 30-387 Krakow, Poland
 office phone: +48 12 664 5209
 mobile phone: +48 606 240 746
 skype: pkoteja
 fax: +48 12 664 6912
 Paweł³ Koteja <pawel.koteja@uj.edu.pl>

Douglas Yu

– Prof. Douglas W. Yu School of Biological Sciences,
 University of East Anglia, Norwich, Norfolk NR4 7TJ
 UK, mob +44-7510-308-272

Kunming Institute of Zoology, 21 Qingsong Lu, Kun-
 ming, Yunnan 650201 China ofc +86-871-519 9178, mob
 1860-871-7369

www.uea.ac.uk/bio/People/Academic/Douglas+Yu,
eastanglia.academia.edu/DouglasYu/Papers for pdfs

Douglas Yu <dougwyu@gmail.com> Douglas Yu
 <dougwyu@gmail.com>

KunmingInstZoology Metabarcoding

The Chinese Academy of Sciences offers 1-to-2-year post-doctoral fellowships and 2-to-9-month visiting fellowships for faculty, under its PIFI program (Presidential International Fellowship Initiative).

All fellowships come with an internationally competitive salary and round-trip airfare.

<http://international-talent.cas.cn/front/index.html#/-bicsite/pifiIntroduce/pifi> My lab at the Kunming Institute of Zoology welcomes environmental scientists from anywhere in the world who are working with environmental-DNA, metabarcoding, and/or mito/metagenomic data for biodiversity conservation. This includes scientists working in statistical ecology, who would like to start using these new data sources. My lab is fully funded for coffee and sequencing.

We are particularly interested in collaborations in these areas: The biodiversity impact of the One Belt One Road Initiative and of climate change. The integration of remote-sensing data, joint species distribution modelling, and high-throughput data for monitoring biodiversity and ecosystem functions and services. See this article for more detail: <https://www.nature.com/articles/s41559-017-0176> The Kunming Institute of Zoology is very active in evolutionary biology, especially in evolutionary and functional genomics and phylogeography. KIZ also has an active DNA barcoding center. PIFI applicants interested in these areas can also contact me for quick introductions to other KIZ faculty.

Kunming, in Yunnan province, China, is a very pleasant place to live and visit, with several new microbreweries and great weather (see gokunming.com)

MaxPlanck Germany AvianCulturalEvolutionEcol

We invite applications for a postdoctoral position to join an exciting new research group studying the ecology and evolution of animal culture, based at the Max Planck Institute for Ornithology, in Radolfzell, Germany. The postdoc is available initially for 2 years, but can be extended contingent on progress, and will start in early 2018.

Background:

Traditional views of Darwinian evolution focus on selection acting on genetically underpinned variation as a means of adaptation. However this may neglect the potential contribution of the over-generation transmission of information (cultural inheritance) as a source of locally adaptive behaviour - this might be particularly important in long-lived species and when facing novel or changing environments. For example, the capacity for innovation, social learning and cultural inheritance is thought to be vitally important in the success of humans as a species, facilitating our colonization of almost every terrestrial habitat on Earth. But has the cultural transmission and inheritance of behaviour been similarly important in the success of some other species? We investigate these questions using a combination of laboratory experiments and field studies in birds, utilizing state-of-the-art automated tracking technologies and analytical techniques.

The postdoctoral researcher will be part of a team working in two avian systems: firstly laboratory experiments of cultural evolution will test the link between cognition, social structure and emergent cultural phenomenon in captive birds. Secondly, wild fieldwork will be con-

ducted on urban-living Sulphur-crested cockatoos (*Catua galerita*), using a combination of citizen-science, GPS tracking, field observation and experiments. This will test socio-cognitive mechanisms for urban adaptation, and identify the form and patterning of naturally occurring cultural behaviours. The postdoc will work alongside graduate students and research assistants to develop these systems, but will also have the opportunity to focus on a specific area of interest within the larger project. The position will include opportunities for laboratory and field-based work in Radolfzell, and fieldwork in Australia.

Position Details:

Suitable applicants should have a PhD in a related area. Candidates will ideally have experience either undertaking independent fieldwork or running laboratory experiments, and will have demonstrated analytical skills and evidence of research output. High self-motivation and the ability to work both in a team and independently are also important. Finally, applicants with experience in programming and with proficiency in R are particularly encouraged.

The working language in the group is English, and candidates should have proficiency in both written and spoken English. No German language skills are required. We are an inclusive and diverse group, and encourage applications from women, people with disabilities, and all under-represented minorities.

Location:

The lab is based at the world-leading Max Planck for Ornithology (MPIO), in Radolfzell, Germany: http://www.orn.mpg.de/3190/Location_Radolfzell. The MPIO is an internationally renowned research institution with more than 200 employees working in four departments and across 10 research groups. The postdoc will also have the opportunity to interact with collaborators at the University of Konstanz, the Royal Botanic Gardens Sydney, and the Australian Museum.

Application Process:

Interested applicants should send a short summary of their research interests, a CV, and the name and contact details for at least one referee compiled in a single pdf to Dr. Lucy Aplin at laplin@orn.mpg.de. Applications will be received until 6 October 2017, with interviews conducted from October-November 2017. The position will ideally start in January 2018, however a flexible start date is possible if needed. Lucy Aplin <laplin@orn.mpg.de> Max Planck for Ornithology; Radolfzell, Germany. www.sites.google.com/site/lucymaplin/ “Aplin, Lucy” <laplin@orn.mpg.de>

MaxPlanckInstitute EvolutionaryGenomics

Computational / Experimental Postdoc Position

The Research Group “Computational Biology and Evolutionary Genomics” at the Max Planck Institute in Dresden, Germany has a Postdoc opening.

Project description:

The postdoc will utilize numerous sequenced mammalian genomes to discover the genomic basis of repeatedly evolved phenotypic differences. By focusing on natural phenotypes that resemble human diseases, we aim at connecting basic evolutionary with translational research to identify novel genes associated with genetic disorders.

The postdoc will apply and further develop our genomics methods, and analyze the results by integrating biomedical knowledge and functional genomics data. Promising candidate genes will be tested experimentally, either by the Postdoc or in collaboration. The Postdoc will work closely with other members of the lab and our institute on the computational and experimental aspects. Funding is according to the German TVöD scale.

Our group:

We combine computational biology, comparative genomics and experiment to investigate how nature’s fascinating phenotypic diversity evolved and how it is encoded in the genome. On the computational side, we generate high-quality genome alignments, apply comparative methods to discover key differences in genes and regulatory elements, and use statistical approaches to associate genomic to phenotypic differences. On the experimental side, we use RNA-seq, ATAC-seq, functional assays and CRISPR-Cas9 to reveal the molecular function of genomic regions and to test causality between genomic and phenotypic differences.

Our group is located at the Max Planck Institute of Molecular Cell Biology and Genetics (MPI-CBG) and we are jointly affiliated with the Max Planck Institute for the Physics of Complex Systems (MPI-PKS), both in Dresden. Both institutes are highly interactive and interdisciplinary workplaces, provide an international atmosphere with English as working language and access to cutting-edge computational and experimental infrastructure and facilities. The MPI-CBG was awarded one

of the “Best Places To Work for Postdocs” in 2011.

Requirements:

Applicants with a background in both computational and biological sciences are encouraged to apply. Applicants with a computational background should have a strong interest in integrating experiments in their research and a desire to deeply understand the biology underlying mammalian phenotypes and human disease. Applicants with a biological background should be experienced in using text file processing tools in a Linux shell environment and should have good programming skills, for example in a scripting language. Excellent communication skills and a strong publication record is expected. Previous experience in large-scale genomic data analysis is an advantage.

How to apply:

If interested, please email - your CV including publication list and contact information for at least two references - a summary of previous research experience (max 1 page) to Michael Hiller (hiller@mpi-cbg.de). Further information: <https://www.mpi-cbg.de/hiller> Michael Hiller <hiller@mpi-cbg.de>

MichiganStateU ConsevationBiol PopGenomics

The Meek Lab at Michigan State University is looking for a highly motivated postdoctoral scholar to study population and conservation genomics in fish and other species. The lab uses field studies and next-generation sequencing to address fundamental ecological questions that are directly relevant to the conservation and management of threatened species. We study biodiversity at the level of the genome, transcriptome, and epigenome. Some major questions being addressed in the lab are:

1. What is the genomic basis for thermal tolerance and local adaptation? We aim to understand if there are differences in gene expression patterns among fish from populations with different thermal histories, and if so, what are the regions of the genome associated with differences in phenotypic response to thermal stress. The information gained from this study will be invaluable for understanding the molecular basis for local adaptation and its relation to climate change resiliency planning, and in designing management actions that sustain imperiled species into the future.

2. How do human activities affect genetic diversity and

local adaptation? We are interested in understanding how anthropogenic forces, such as hatchery propagation, fishery stocking, and habitat alteration, are influencing diversity patterns and fitness in the wild. This understanding will allow us to better design propagation techniques and target habitat restoration activities to protect the genetic diversity needed for populations to persist into the future.

3. What controls complex life history patterns? Salmonids are an excellent model for looking at the molecular control of life history, due to their variation in migration timing and propensity to migrate. We are integrating across genetic, transcriptomic, and epigenetic pathways in steelhead and Chinook salmon to understand the molecular basis for this life history diversity.

Please look at our website (meeklab.com) to get a more complete picture of the work we do. The post-doc will have the opportunity to work on one or several of the ongoing projects in the lab, based on interest and fit. There is also potential for developing new projects, based on the candidate’s interests. We are a very interactive lab and are looking for an excellent scientist, who cares about conservation, and is a good collaborator. The Meek lab strives to be a safe space and support diversity in STEM.

The initial hire is for one year with an additional year of funding contingent upon satisfactory progress. The position will be based in the Department of Integrative Biology at Michigan State University. Start date is negotiable and position is open until filled.

Qualifications

Applicants should have a PhD in ecology, evolution, genetics, bioinformatics, or related fields. We are looking for a creative and talented scientist with a good publication record and excellent organizational and communication skills. We are especially interested in candidates with a strong computational background and previous experience with next-generation sequencing data analysis. Experience working in the Unix environment is essential and familiarity with one or several programming languages is highly desirable.

How to apply

Interested candidates should apply through the MSU Applicant Page at <http://careers.msu.edu/cw/en-us/-job/496482/research-associatefixed-term> .Please feel free to email (mhmeek@msu.edu) to ask questions, putting “Postdoctoral opportunity” in the subject line. Required application material:

- 1) Brief cover letter describing research interests and motivation

- 2) CV
 - 3) Names and email addresses for 3 references
 - 4) 2-3 published papers or manuscripts in preparation
- Mariah Meek, PhD Assistant Professor Department of Integrative Biology Michigan State University East Lansing, MI meeklab.com
- Mariah Meek <mhmeek@msu.edu>

MIT Evolutionary Plant Physiology

The Des Marais Lab at MIT seeks a post-doctoral associate in plant biology. The associate will participate in new and ongoing research on plant-environment interactions. The lab is particularly interested in the intersection of growth, resource use, and life history/phenology, studying the multiple evolutionary transitions in niche occupation and life history observed in *Brachypodium*. We use tools in comparative genomics, molecular genetics, quantitative genetics, and ecophysiology and we expect that a post-doctoral associate will bring excellence in one or more of these areas to the project. Opportunities for developing new research projects under the general area of plant-environment interactions are available.

The Des Marais Lab (<http://desmarais-lab.mit.edu>) is located in the Parsons Laboratory of Environmental Science and Engineering, within the Department of Civil and Environmental Engineering at MIT. Parsons is home to a highly interdisciplinary group of ecologists, environmental chemists, hydrologists, modelers, and microbiologists with a strong tradition of research across these scales. More broadly, MIT hosts outstanding expertise in systems biology, high-throughput phenotyping, and development of leading-edge analytical tools. We seek a highly motivated candidate interested in interdisciplinary science who will initiate and lead collaborations within the department and across MIT. The Des Marais Lab maintains close ties with plant biologists at Harvard and The Arnold Arboretum, located nearby in Boston's Jamaica Plain neighborhood.

Applicant Requirements A PhD in plant ecology, evolution, or physiology as well as a strong publication record and communication skills are essential. We seek candidates with experience designing and executing manipulative experiments in the field and/or laboratory settings. A background in statistics, phenomics, bioinformatics, gas-exchange measurements, and/or measure-

ment and modeling of growth rate are also desirable. The position is available 1 January 2018, with the start date negotiable thereafter.

Interested candidates should formally apply for the position online:

https://careers.peopleclick.com/careerscp/client_mit/-external/en-us/gateway.do?functionName=viewFromLink&jobPostId=10788&localeCode=en-us&referralCode=42580-00264-01091 David L. Des Marais, PhD

Senior Fellow of The Arnold Arboretum and Research Associate in Organismic and Evolutionary Biology Harvard University

Starting October 1, 2017 Assistant Professor Civil and Environmental Engineering MIT

Dave Des Marais <dldesmar@mit.edu>

NortheasternU Genomics

A postdoctoral position is available in the laboratory of Dr. Kathleen Lotterhos at Northeastern University. The postdoc will also be mentored by Dr. Sam Yeaman at the University of Calgary. The successful candidate will be part of an NSF-funded project to study the behavior of genome scans across a range of genomic architectures, from monogenic to highly polygenic. The successful candidate will be expected to generate a large set of realistic simulations, evaluate various types of statistical methods for analyzing genomic data, and manage a diverse team of developers and collaborators. **Qualifications** Applicants will be expected to develop and lead projects. Candidates are required to have a Ph.D. in Evolutionary Genetics, Statistics, Computational Biology (bioinformatics), or related disciplines. A computing background is required, especially experience with Unix, and knowledge in one or several programming languages (R/BioConductor, Python, C/C++, etc).

Candidates should demonstrate a strong track record of publication; have strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team. The appointment is for 24 months.

To apply, please prepare a CV, cover letter, references, and one peer-reviewed publication and upload them at this site: <https://neu.peopleadmin.com/postings/49443> Deadline for applications is August 31, 2017. Start date is flexible and we will accept a start date until May

2018.

The Lotterhos Lab is based at the beautiful in Nahant campus north of Boston (NUMSC). The NUMSC has a strong research presence in evolution and ecology research and there are many opportunities for interaction and collaboration both there and in the greater Boston area. More information about our lab's research can be found here: <https://sites.google.com/site/katielotterhos/home>. The successful candidate will also have opportunities to travel to Calgary and work with Yeaman. We welcome applications from candidates with diverse educational backgrounds.

For more information contact Dr. Lotterhos at k.lotterhos@neu.edu

"k.lotterhos@northeastern.edu"

<k.lotterhos@northeastern.edu>

OklahomaStateU EvolutionaryBiology

(Note: the ad below ad does not specify subfield but includes evolutionary biology in multiple potential academic departments)

Diversity Post-Doctoral Fellowships

Fellowship Description

The College of Arts and Sciences of Oklahoma State University seeks scholars who are committed to supporting the learning needs of students from diverse backgrounds and to engaging communities underrepresented in higher education. These fellowships will support the early development of scholars who show promise for successful academic careers in the Fine Arts, Humanities, Mathematics, Sciences, or Social Sciences. The two-year fellowships (one in Fine Arts or Humanities, one in Social Sciences, and two in Mathematics or Sciences) with competitive salaries will begin in August 2018 and may be renewed for a third year. There is the possibility of a tenure-track appointment at the completion of the post-doctoral fellowship.

Post-docs will carry a teaching load of one course per semester and will receive institutional support for their research/creative activities and their professional development in instruction. They will be closely mentored by faculty and housed in one or more of the following departments:

- Art, Graphic Design, and Art History - Chemistry -

Computer Science - English - Foreign Languages and Literatures - Geography - Geology - History - Integrative Biology - Mathematics - Media and Strategic Communications - Microbiology and Molecular Genetics - Music - Philosophy - Physics - Plant Biology, Ecology, and Evolution - Political Science - Psychology - Sociology - Statistics - Theatre

Preferred Qualifications: Candidates who have completed their terminal degree within the discipline (PhD, MFA, or DMA) no more than three years before the August 2018 start date and who have not yet had a tenure-track faculty position are preferred.

To apply, please submit by 1 October 2017 the following in a single PDF file: Letter of application - please indicate department(s) with which you would seek affiliation if selected for a post-doctoral fellowship. - CV Statement outlining commitment to integrating multicultural experiences into instructional methods and engaging students underrepresented in the academy. - Statement outlining two-year plan for research/creative activity. - Names of three professional references.

Applications should be submitted to one of the following email address: Fine Arts or Humanities: DiversityPostDoc-fah@okstate.edu Social Sciences: DiversityPostDoc-ss@okstate.edu Mathematics or Sciences: DiversityPostDoc-ms@okstate.edu

Additional questions should be directed to: Dr. Bruce Crauder, Associate Dean College of Arts and Sciences 201 LSE Stillwater, OK 74078 bruce.crauder@okstate.edu 405-744-5663

Positions are contingent upon available funding. Oklahoma State University is an Affirmative Action/Equal Opportunity/E-verify employer committed to diversity and all qualified applicants will receive consideration for employment and will not be discriminated against based on age, race, color, religion, sex, sexual orientation, genetic information, gender identity, national origin, disability, protected veteran status, or other protected category. OSU is a VEVRAA Federal Contractor and desires priority referrals of protected veterans for its openings. OSU will not discharge or in any other manner discriminate against employees or applicants because they have inquired about, discussed, or disclosed their own pay or the pay of another employee or applicant. However, employees who have access to the compensation information of other employees or applicants as a part of their essential job functions cannot disclose the pay of other employees or applicants to individuals who do not otherwise have access to compensation information, unless the disclosure is (a) in response to a formal complaint or charge, (b) in furtherance of an investigation, proceeding, hearing, or action,

including an investigation conducted by the employer, or (c) consistent with the contractor's legal duty to furnish information. 41 CFR 60-1.35(c)

Daniel Moen <daniel.moen@okstate.edu>

Oregon ForestBioinformaticsGenomics

Position available: Postdoctoral scholar, Developing and applying multispecies metagenomic assessments in Pacific Northwest forests

We are seeking a skilled and enthusiastic post-doctoral research scholar to provide bioinformatics and genomics leadership on a project developing multi-species metabarcoding approaches for assessing diversity and health in forest riparian ecosystems in the Pacific Northwest of North America. The goal of the project is to develop and apply multigene multiplexing approaches that characterize and quantify species-level diversity of aquatic organisms found in streams (e.g., fish, amphibians, molluscs, insects) and adjacent riparian habitats (e.g., plant pathogens). The postdoctoral scholar will be responsible for developing, testing, and evaluating analytical pipelines that convert next-generation sequences into count data that describe presence/absence, abundance, and spatial genetic diversity of target taxa. For many studies, molecular results will be compared with field assessments, providing the opportunity to validate molecular results and estimate true and false positive/negative rates.

This full-time position (Postdoctoral Scholar, 1.0 FTE, salary \$52,000/year with health care benefits) requires a one-year commitment, with the potential of a one-year extension, starting as early as November 1, 2017. The position will be based in Tiffany Garcia's research group (<http://garcia.fw.oregonstate.edu/>) in Nash Hall, Department of Fisheries and Wildlife, at Oregon State University (OSU). Applicants must have been awarded a Ph.D. <5 years ago.

The postdoctoral scholar will work with Dr. Garcia and collaborators at the US Forest Service, Brooke Penaluna (<https://www.fs.fed.us/pnw/lwm/aem/people/penaluna.html>) and Richard Cronn (<https://www.fs.fed.us/research/people/profile.php?alias=-rcronn>). The postdoctoral scholar will develop and test the most appropriate approaches, share in the preparation of required reports for grant-related activity (interim reports; final reports), and share in

the development of manuscripts suitable peer-reviewed journals. A mentorship plan will be developed in collaboration with the postdoctoral scholar, under the direction of Dr. Garcia and co-PIs.

Qualifications: A Ph.D. in a relevant field (computational biology, bioinformatics, phylogenomics, fish/plant/microbial genomics, or evolutionary genomics) is required, as is expertise with unix and one or more programming languages (e.g., perl, Python, C++), excellent quantitative skills, and a demonstrated ability to publish research in peer-reviewed journals. Experience with designing genomics experiments based on high throughput genomic technologies is preferred.

Qualified applicants are invited to electronically submit an application, including (1) a cover letter; (2) a full-length curriculum vitae (CV); and (3) the names and contact information of three referees. Visit the application web site <https://jobs.oregonstate.edu/postings/47422> for further details about position # P01495UF and information on how to apply. OSU is an AA/EOE/Vets/Disabled employer

Richard Cronn Research Geneticist

Forest Service PNW Research Station

p: 541-750-7291 f: 541-750-7329 rcronn@fs.fed.us

3200 SW Jefferson Way Corvallis, OR 97331

rcronn@fs.fed.us

PennStateU PlantEvolutionaryGenomics

The Renner lab at The Pennsylvania State University is hiring a Postdoctoral Scholar in the area of evolutionary genomics. This particular position is focused on resolving taxonomic relationships, elucidating the genomic architecture underlying biochemical diversity, and identifying adaptations for arthropod prey digestion using phyla/comparative genomics among the carnivorous plants within Caryophyllales. Specific projects will be developed in conjunction with the incumbent's skill set and research interests. The candidate must have broad knowledge of systematics, molecular evolution, and molecular biology. Candidates that have experience with phylogenomics and functional/comparative genomics will be highly considered. Experience with the generation, handling, and downstream analyses of next-generation sequencing data is also highly desirable,

as is familiarity with computer programming/scripting in Python, Perl, Java, C++, R or other language.

Preference will be given to candidates with a PhD in Evolutionary Biology, Plant Ecological Genetics, Plant Systematics, Plant Biology, Molecular Evolution or related field. Excellent oral and written communication is essential, as the candidate will be responsible for writing publications, contributing to proposals, and presenting research at local, national, and international scientific conferences. Additionally, the candidate will train and mentor graduate students, undergraduate students, and work with a diverse team of researchers. This is a fixed-term position for one year from date of hire, with an excellent possibility of extension for an additional year.

Interested candidates should formally apply for the position online (<https://psu.jobs/job/73959>). As part of the process, please upload your CV, at least two letters of reference, and a 2-3 page written description of previous research experience or statement of research. Review of applications will begin immediately and continue until the position is filled.

For more information, please contact Tanya Renner, Assistant Professor, Department of Entomology, Penn State University, trenner@psu.edu. Laboratory Webpage: <https://sites.psu.edu/rennerlab/> tanz.renner@gmail.com

PurdueU Conservation

Purdue Post-doctoral Scholars in Natural Resources

Purdue University's Department of Forestry and Natural Resources seeks candidates for 1-2 post-doctoral positions for its annual recurring competition for post-doctoral scholars in natural resources science or management. The department has a broad environmental scope with nationally ranked doctoral programs, emphasizing interdisciplinary approaches across a spectrum of research areas including ecology, genetics, forest biology, forest measurement and assessment/GIS, wood products, wildlife, fisheries and aquatic sciences, and natural resources social science (www.ag.purdue.edu/fnr). Departmental faculty members actively participate in interdisciplinary initiatives including the Center for Advanced Manufacturing, Center for the Environment, Purdue Water Community, Purdue Interdisciplinary Center for Ecological Sustainability, Hardwood Tree Improvement and Regeneration Center, Tropical Hardwood Tree Improvement and Regeneration Center,

Center for Global Soundscapes, Center for Regional Development, Purdue Climate Change Research Center, Illinois-Indiana Sea Grant, and the Natural Resources Development Institute.

Requirements for the position(s) include a Ph.D. in natural resources or related discipline, evidence of initiative, independence, and productivity, and a commitment to conservation of natural resources. The program is open to U.S. and non-U.S. citizens.

Positions will be 2-year appointments at a salary of \$47,500, plus benefits and a discretionary fund of \$5,000/year in addition to any research funds that are provided by mentors.

Application Process: Before applying, interested individuals should contact prospective postdoctoral mentors in the department to discuss project ideas. A list of faculty mentors is available at <https://ag.purdue.edu/fnr/Pages/dirpostdocprgrm.aspx>. Mentoring may be sought from individual faculty or by faculty teams, whichever is more appropriate to successfully conduct the proposed work.

To apply to the Natural Resources Scholars program candidates must submit a) names of one or more faculty who have agreed to serve as mentors for the proposed project, b) a curriculum vitae, c) a proposal describing the work to be undertaken, d) two letters of reference, and e) a 1-page statement of support from the proposed mentor(s). Materials should be submitted as PDF files via email to mmann@purdue.edu with the subject line ³Application: Postdoc Scholars in Natural Resources². Letter writers should submit their recommendations directly using the email address above. The deadline for receiving completed applications is October 16, 2017.

Applicants may propose projects that complement, extend, or synthesize existing efforts and interests of the faculty. The proposal should identify the issue to be addressed, summarize the current level of knowledge as it relates to the issue, describe the objective(s) of the proposed work, provide the study design and methods used to meet the objective(s), explain expected results and deliverables, and highlight their scientific and broader significance. The proposal is limited to a 300-word summary page and three (3) single-spaced pages, not including references, using one-inch margins and a minimum 11-point standard font.

Applications will be judged on overall quality including prior performance, support letters, and the scientific and technical merit and feasibility of the proposal. For additional information, please contact Douglass Jacobs, Fred M. van Eck Professor and Associate Department

Head of Research (djacobs@purdue.edu).

Purdue University is an equal opportunity/equal access/affirmative action employer fully committed to achieving a diverse workforce.

“DeWoody, James Andrew” <dewoody@purdue.edu>

SantaFeInstitute Omidyar EvolutionaryBiol

The Omidyar Fellowship at the Santa Fe Institute is unique among postdoctoral appointments. It offers select early-career scholars the opportunity to join a collaborative research community that nurtures creative, transdisciplinary thought in pursuit of key insights about the complex systems that matter most for science and society.

The Omidyar Fellowship at the Santa Fe Institute offers you:

transdisciplinary collaboration with leading researchers worldwide up to three years in residence in Santa Fe, New Mexico discretionary research and collaboration funds competitive salary and generous benefits a structured leadership training program unparalleled intellectual freedom The Institute has no formal programs or departments. Research is collaborative and spans the physical, natural, and social sciences. Most research is theoretical (SFI does not have lab facilities) and/or computational in nature, although it may include an empirical component. SFI has 18 Omidyar Fellows and postdoctoral researchers, 12 resident faculty, 100 external faculty, and averages 1000 visitors per year. Descriptions of the research themes and interests of the faculty and current Fellows can be found at SFI Research < <http://www.santafe.edu/research/> >. As thought leaders who shape the future of science, Omidyar Fellows participate in a provocative training program structured to develop leadership skills throughout their three-year residencies and beyond. The program focuses on sustained mentoring relationships with SFI resident and external faculty, skill development workshops, off-campus research and teaching experiences, and the variety of scholarly leadership and science management opportunities at SFI.

Requirements:

- a Ph.D. in any scientific discipline (granted within 6 years of the application deadline or completed by September 2018) - strong computational and quantita-

tive skills - an exemplary academic record - a proven ability to work both independently and collaboratively - a demonstrated interest in multidisciplinary research - evidence of the ability to think outside traditional paradigms SFI is an Equal Opportunity Employer. US citizenship is not a requirement, women and members of underrepresented groups are especially encouraged to apply

Application Materials:

Interested candidates must submit the following:

Curriculum vitae (including publications list). Statement of research interests (max. 2 pages) including a short description of the research you would like to pursue and why. Description of interest in SFI (max. 1 page) that describes your potential contribution to the SFI community and also explains the potential impact of SFI on your research. Consider addressing one or more of the following: What kind of input from other fields would most improve your future research? What type of multidisciplinary workshop might you want to organize during your Fellowship? What aspects of your present or future research are difficult to pursue in a traditional academic environment? Three letters of recommendation from scholars who know your work. (The letters should be sent independent of the application. When you complete the online application, please be prepared to provide e-mail addresses of the three individuals who will recommend you. SFI will contact them directly with instructions for submitting letters.) (Optional) A copy of one paper you have written in English, either published or unpublished. To apply: <https://sfiomidyar.fluidreview.com> Applications for the 2018 Omidyar Fellowships will be accepted on line from August 7th until October 29th, 2017.

hilary@santafe.edu

StellenboschU CamouflageEvolutionStonePlants

The evolution of camouflage in stone plants

A postdoc position is available in the Dept. of Botany and Zoology at Stellenbosch University in South Africa studying the evolution of camouflage in stone plants (Lithops). While their name reflects their striking resemblance to stones, the hypothesis of stone-mimicry in Lithops has not been tested, nor has visual camouflage received much attention in plants generally. The project

involves using NGS approaches to build a phylogenetic hypothesis for the genus, a combination of multispectral image analysis and visual modelling to explore the visual components of camouflage and their evolution across gravel types, and field experimentation to mechanistically test the fitness implications of camouflage phenotypes. The candidate would be involved in all these aspects of the project. Previous experience with NGS would be an advantage. The candidate would also work closely with another postdoc working on crypsis in stone-mimicking grasshoppers that share the gravel plain habitats with *Lithops*, with the ultimate goal of exploring convergence of camouflage phenotypes in these groups across the mosaic of lag gravel types that characterise the arid parts of southern Africa. The project is a collaboration between Tommi Nyman (UEF, Finland), Tony Verboom (Univ. Cape Town) and myself, Allan Ellis (Stellenbosch Univ.).

Interested candidates can contact me (Prof Allan Ellis - agellis@sun.ac.za) directly for more information (also see <http://www.biointeractionslab.com/prof.-allan-g.-ellis.html> and <http://www.lithopsproject.org/>).

A tax-free Fellowship (R200 000 per year) is available for one year and can be extended for a second year depending on the candidates progress. The candidate would be expected to start as soon as possible.

Applications including a motivation letter, a CV and details of three contactable references should be sent to me directly at the above email address. Applications will close on 30 September 2017 or once a suitable candidate has been selected.

Dr. Allan Ellis Associate Professor Botany and Zoology Department Stellenbosch University Private Bag X1 Matieland 7602 e-mail: agellis@sun.ac.za tel no: +27 21 8083158 fax no: +27 21 8082405

“Ellis, AG, Prof <agellis@sun.ac.za>”
<agellis@sun.ac.za>

StockholmU YeastExperimentalEvolution

Postdoctoral position in Experimental Evolution with Yeast at Stockholm University, Sweden.

Project: Hybridization and adaption in stressful environments

Host: Rike Stelkens Start date: November 2017 (nego-

tiabile) Application date: September 17 2017

Description: Candidates will use experimental evolution with the budding yeast *Saccharomyces cerevisiae* (and its relatives) to study evolutionary processes. The overall aim of the project is to develop an empirical system for studying adaptation in rapidly changing and stressful environments - a major challenge falling within the nexus of evolutionary genetics and conservation biology. Potential topics include but are not limited to 1) the effects of hybridization on rates and mechanisms of adaptation to environmental stress, 2) the genomic basis of hybrid fitness, and 3) the genomic basis of reproductive isolation.

Qualifications: I am looking for people with a strong interest in evolution, especially in speciation and conservation genetics. Ideally, you have experience in experimental evolution methods, molecular genetics/genomics techniques, bioinformatics, and you have knowledge of the principles of population and quantitative genetics. Prior training in *Saccharomyces* yeast cultivation are highly desirable. Candidates should be well-organized, good communicators, and happy to work in a team as well as independently. You must have a PhD in evolutionary biology, population genetics, or a similar subject. You should also have a strong desire to develop a successful and highly productive research career.

Environment: The campus is located four metro stops from the center of Stockholm, one of the most beautiful and dynamic capitals in Europe. The campus is home to a vibrant scientific community, including the Science for Life Laboratory (a leading genomics core facility that we routinely use) and the Swedish Museum of Natural History. Sweden is a free and open society, and strives to be one of the worlds most innovative and research-intensive nations. People here enjoy a respected system of democracy and individual rights, freedom of speech, a free press, the right to scrutinize those in power, and access to beautiful nature. Most Swedes speak English.

Application: Please send a statement of motivation including relevant expertise, a CV and the contact details of at least two references through this platform: <http://www.su.se/english/about/vacancies/vacancies-new-list> Further details on research in the department and staff: <http://www.zoologi.su.se/en/index.php> To discuss the role please contact Rike Stelkens directly by email: rike.stelkens@zoologi.su.se

Closing date for applications is 17 September 2017. Interviews will take place on Skype. Following that, short-listed candidates may be invited to visit the department to meet with colleagues and present their work.

References: Stelkens, Brockhurst, Hurst, and Greig,

(2014). Hybridization facilitates evolutionary rescue. *Evolutionary Applications* 7, 1209-1217

Stelkens, Brockhurst, Hurst, Miller, and Greig, (2014). The effect of hybrid transgression on environmental tolerance in experimental yeast crosses. *Journal of Evolutionary Biology* 27, 2507-2519

Stelkens and Greig (2016). Fungal evolution: On the origin of yeast species. *Nature Microbiology* 1, 15017

Rike Stelkens Assistant Professor Division of Population Genetics Department of Zoology Stockholm University, Sweden

email: rike.stelkens@zoologi.su.se website: <http://www.zoologi.su.se/en/> rike.stelkens@zoologi.su.se

TUMunich Museomics

We are looking for an ambitious and excellent postdoc to develop a Museomics-based monograph of the melon genus (*Cucumis*) in the framework of the Priority Program "Taxon-Omics: New Approaches for Discovering and Naming Biodiversity" funded by the German Science Foundation for the next 3 years. S/he will be responsible for the generation and analysis of genomic data mainly from old herbarium material using the hyRAD-Seq approach. In addition, the project requires nomenclatural research and some morphological analyses of herbarium specimens. The fellow will be based in the Plant Biodiversity Research group at the TUM campus in Freising, a small town just outside Munich. The nearby Alps offer plenty of opportunities for hiking and skiing, Munich city centre is just 25 min by train, Munich airport is 15 min away.

Applications should include letter of motivation, CV with publication list, details on bioinformatics and lab skills, and any other experience relevant to this position (preferably everything in a single pdf).

Please send applications and contact information for two references to hanno.schaefer@tum.de until September 1st, 2017.

The postdoc should start ideally between October and November 2017.

Hanno Schaefer <hanno.schaefer@tum.de>

UArizona ProteinEvolutionBioinformatics

Postdoc position: long-term trends in protein evolution

A postdoc position is available with PI Joanna Masel (<http://eebweb.arizona.edu/faculty/masel>) at the University of Arizona in Tucson. A popular tourist destination surrounded on all four sides by mountainous national and state parks, Tucson is a vibrant city of nearly a million people with an attractive climate. The EEB department was ranked in the top 10 by US News & World Report.

We recently found that genes of different ages encode proteins with different computationally predictable structural properties, forming an extraordinarily long-term trend. This project will use bioinformatics techniques to discover whether these long-term trends are really a consequence of evolution by descent with modification that continues for long periods of time in a consistent direction. More details of the project, including preprints of preliminary findings, are available upon request.

Techniques used may include phylostratigraphy (assigning ages to gene families), ancestral sequence reconstruction, and porting macroevolutionary techniques for studying speciation and extinction to the study of gene duplication and loss. A high level of statistical sophistication is required throughout.

Excellent computer programming skills are strongly preferred, ideally with bioinformatics / genomics and statistics experience. Exceptionally strong candidates who come from a more experimental background within evolutionary biology, and who now wish to retrain as bioinformaticians, will also be considered. A background in evolutionary biology is also strongly preferred, although again, exceptionally strong computational scientists from highly quantitative backgrounds outside evolutionary biology will also be considered. Statistical knowledge, and knowledge about protein structure and folding, are advantages. Start date is negotiable, and the position is renewable, with funding secured through July 2020.

Contact Joanna Masel at masel@u.arizona.edu for more information and to apply.

masel@email.arizona.edu

UCalifornia Davis AedesAegyptiPopulationGenomics

Job Title: Post-doctoral Scholar in Mosquito Population Genomics

Location: University of California, Davis, California USA

Duration: 2 years, starting immediately, but no later than January 1, 2018

Unit: The Vector Genetics Laboratory, UC Davis

Hours/Benefits: Full time with competitive benefits. Salary contingent on candidate experience.

The Vector Genetics Laboratory (VGL) at the University of California, Davis is seeking applications for a post-doctoral research scholar position in the area of MOSQUITO POPULATION GENOMICS. The VGL is dedicated to research and training in the areas of population & molecular genetics, genomics and bioinformatics of insect vectors of human and animal disease. The VGL research agenda is aimed at expanding knowledge that may be applied to improving control of disease vectors and at the same time addresses problems of interest in the field of evolutionary genetics. The VGL has links to multiple Graduate Groups and Centers on the UC Davis campus, including the Center for Population Biology, Department of Evolution and Ecology and the One Health Institute. Find out more about the VGL at: <http://popi.ucdavis.edu/vgl/> Background:

The goal of the project associated with this position is the development of models aimed at describing the behavior of transgenes with gene drive that might be introduced into natural mosquito populations. The application of gene drives for the control of mosquito-borne diseases, in this case dengue, Yellow Fever and ZIKA, has been at the center of attention since the development of the CRISPR/Cas 9 method. This project will deal with the application of this technology to real mosquito populations. There is a great deal of uncertainty about how these systems will behave in nature. This project aims to provide insights into this problem.

The individual who fills this position will be working with exceptionally well-qualified teams with expertise in mosquito ecology, molecular genetics and bioinformatics as well as in population genetics. The team is located across the University of California system, including UC

Irvine, UCLA, UC Berkeley, UC San Diego, UC Santa Barbara and of course UC Davis. The person filling this position will be located here at UC Davis. A brief description of this position follows:

(position reference number: Aa02)

Project Description. This position is focused on the population genetics of the invasive mosquito species *Aedes aegypti* in California. This species was introduced into the Fresno area of California in 2013 and has since spread across the state (although its distribution is very patchy). This mosquito poses a significant threat to human health worldwide being the primary vector of dengue, Yellow Fever, Chikungunya and ZIKA viruses. The goal of this project focuses on collecting genetic data (WGS data) describing populations of *A. aegypti* in California and that relates to the prediction of how well-characterized transgenes that include gene drive will behave if introduced into these populations.

Job Description. We are seeking a person with a strong background in population genomics, an interest in the genetics of invasive species and experience in the analysis of whole genome sequencing data. The person filling this position will have the opportunity to participate in field work throughout the state in collaboration with state-wide mosquito abatement district personnel. Support is available for two years with the possibility of extension beyond. This position is available starting immediately, but not later than January 1, 2018. The position will remain open until filled. This is a 2 year position with the possibility of extension pending availability of funding.

How to Apply

Please e-mail cover letter explaining your interest and qualifications, resume and the names and contact information for three references to gclanzaro@ucdavis.edu with the subject line "Mosquito Population Genomics".

Montgomery SLATKIN <slatkin@berkeley.edu>

UCalifornia Davis MosquitoEvol

Job Title: Post-doctoral Scholar in Mosquito Ecology

Location: University of California, Davis, California USA

Duration: 2 years, starting no later than January 1, 2018

Unit: The Vector Genetics Laboratory, UC Davis

Hours/Benefits: Full time with competitive benefits. Salary contingent on candidate experience.

The Vector Genetics Laboratory (VGL) at the University of California, Davis is seeking applications for a post-doctoral research scholar position in the area of MOSQUITO ECOLOGY. The VGL is dedicated to research and training in the areas of population & molecular genetics, genomics and bioinformatics of insect vectors of human and animal disease. The VGL research agenda is aimed at expanding knowledge that may be applied to improving control of disease vectors and at the same time addresses problems of interest in the field of evolutionary genetics. The VGL has links to multiple Graduate Groups and Centers on the UC Davis campus, including the Center for Population Biology, Department of Evolution and Ecology and the One Health Institute. Find out more about the VGL at: <http://popi.ucdavis.edu/vgl/> Background:

The goal of the project associated with this position is the collection of data related to the development of models aimed at describing the behavior of transgenes with gene drive that might be introduced into natural mosquito populations. The application of gene drives for the control of mosquito-borne diseases, in this case malaria, has been at the center of attention since the development of the CRISPR/Cas 9 method. These projects will deal with the application of this technology to real mosquito populations. There is a great deal of uncertainty about how these systems will behave in nature. These projects aim to provide insights into this problem.

The individual who fills this position will be working with an exceptionally well-qualified team with expertise in population genetics, molecular genetics and bioinformatics as well as in mosquito ecology. The team is located across the University of California system including UC Irvine, UCLA, UC Berkeley, UC San Diego

and of course UC Davis. The person filling this position will be located here at UC Davis, but will have opportunities to interact with all members of the team. A brief description of this position follows:

Project Description. The Anopheles Mosquito Ecology post-doc will be part of a project that is focused on the ecology and genetics of island populations of the primary malaria vector, *Anopheles gambiae*. The study will include field surveys on four islands located off the coast of sub-Saharan Africa (yet to be determined). The goal of the project is the collection of data related to the development of models aimed at describing the behavior of driving transgenes that might be introduced into these field populations to achieve malaria control and ultimately to select a site(s) that would be suitable for a trial release of genetically engineered *An. gambiae*. An assessment of all potential island sites based on available information will be used to identify four candidate sites. Each of these four sites will be visited for the purpose of collecting data on *An. gambiae* ecology and genetics. The ecologist filling this position will play a leading role in the conduct of this field work.

Job Description. We are seeking a person with a strong background in mosquito ecology, an interest in island ecology and experience in conducting field work. The *Anopheles* mosquito ecologist will be responsible for providing leadership in the conduct of all project related field work. He/she should be capable of dealing with the logistical challenges often faced while conducting field work in the tropics and be capable of managing field collection teams. The effort at each field site will include evaluation of best adult trapping methods, intensive collection of adult and larval *Anopheles* species, careful collection of GPS coordinates for each collection site, an evaluation of the potential for establishing laboratory colonies of collected *An. gambiae*. On return to the lab at Davis the mosquito ecologist will identify all *Anopheles* species collected, extract DNA from the *An. gambiae* s.l. samples and utilize established molecular methods to: (i) identify species within the *An. gambiae* complex, (ii) identify *Plasmodium* infected individuals, (iii) identify insecticide resistance genotypes, and (iv) identify blood meal sources. We have developed multiplex molecular assays for this work. The *Anopheles* mosquito ecologist will work with our population genetics team in the application of novel whole genome sequence-based methods for the estimation of (i) dispersal/gene flow and (ii) population size.

Applicants who utilize techniques such as the application of molecular

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>

UCambridge 2 EvoMicrobialGenomics

Applications are invited for two Research Associates in the evolutionary genomics of bacteria at the Department of Veterinary Medicine at the University of Cambridge, UK.

The main focus of the research will be understanding the evolution and molecular epidemiology of the zoonotic pathogens, *Streptococcus suis* and *Salmonella* spp.. These posts will be based in Cambridge led by Dr Lucy Weinert and Dr Dan Tucker, with opportunities to develop independent projects and to work with collaborators from Europe, USA, Myanmar and Vietnam. These projects will use genome sequencing data and tools from evolutionary genetics and epidemiology in the first instance but could also involve the use of laboratory experiments depending on the applicant's strengths.

Applicants should have a PhD in evolutionary biology, microbiology, computational biology or a related discipline. Desirable skills will be experience with next generation sequencing data, microbiological laboratory practice and programming skills in Unix, Python or Perl, and R. A good understanding of bacterial genomics and evolutionary genetics would be an advantage. The candidate must value teamwork and collaboration, and have good administrative and interpersonal skills.

Where a PhD award is pending (e.g, the thesis has been submitted but has not yet been examined), an appointment will be made as a Research Assistant and amended to Research Associate when the PhD is awarded.

Futher information and application procedure can be found here: <http://www.jobs.cam.ac.uk/job/14587/>
lucy.weinert@googlemail.com

UChicago ComputationalGenomics

I am looking for two highly-motivated postdoctoral fellows to join my lab at the University of Chicago. As the lab will be brand new, you will be working closely with me on developing and using cutting-edge computational methods to study gene regulation and disease. (For more information about potential research topics please visit <http://web.stanford.edu/~yangili/research.html>.) My goal is to provide ample supervision and support for you to be highly successful in academia or industry.

At UChicago, you will have the opportunity to work with leading experts in genomics, gene regulation, statistical genetics, and single-cell experimentalists among many others.

The ideal candidate will have a strong background in computational biology, statistics, and/or genetics, and will also be passionate about biological and cellular mechanisms.

The position is available for 2 years. If you are interested, you should directly contact me at yangili1@uchicago.edu and include a CV, a brief description of your research interests, and the names of two references.

Thanks, Yang

“yangili@stanford.edu” <yangili@stanford.edu>

UChicago PopulationGenetics

Post-doctoral Scholar Positions available in:

STATISTICAL POPULATION GENETICS

Two postdoctoral scholar positions are available in the research group of John Novembre at the University of Chicago. The Novembre group develops statistical methods to understand evolutionary processes in humans and other species. The exact projects for the scholars will be flexible, though based around funded projects to develop visualization methods for geographic structure in population genetic data, to develop novel methods using haplotype models, and to study the impact of recent rapid population growth on human genetic variation. We also have active collaborative projects using

ancient and modern DNA to study population genetics in Sardinia, high-altitude adaptation in Tibetans, and canid genomics.

The scholars will benefit from training at a campus with mutual reinforcing strengths in evolutionary biology, statistics, and human genetics. We maintain especially close interactions with groups focusing on statistical/computational problems in population/human genetics (e.g., Stephens, Steinrucken, He, Abney, Nicolae, McPeck, Wu) and empirical evolutionary genetics (e.g., Di Rienzo, Gilad, Kreitman, Kronforst, Lynch, Thornton).

Suitable candidates may come from a wide variety of quantitative / data science backgrounds. Those with strong expertise in computational statistics, particularly in the context of population genetics and genomics, will be preferred. The expected start date is negotiable, and the salary will be competitive and based on level of experience.

To apply please send a brief cover letter, curriculum vitae, and contact information for three references to novembregrp@gmail.com. Candidates from diverse backgrounds are particularly encouraged to apply. Applications will be considered on a rolling basis, and should be received before September 22, 2017 to guarantee consideration. Please see <http://jnpopgen.org> to learn more about the group and send any questions regarding the position to jnovembre@uchicago.edu.

John Novembre, PhD

Professor

Department of Human Genetics

Department of Ecology and Evolutionary Biology

University of Chicago

<http://jnpopgen.org/> The University of Chicago is an Affirmative Action/Equal Opportunity/Disabled/Veterans Employer and does not discriminate on the basis of race, color, religion, sex, sexual orientation, gender identity, national or ethnic origin, age, status as an individual with a disability, protected veteran status, genetic information, or other protected classes under the law. Job seekers in need of a reasonable accommodation to complete the application process should call 773-702-5671 or email ACOppAdministrator@uchicago.edu with their request.

John Novembre <jnovembre@uchicago.edu>

UColorado Boulder DispersalEvolution

Postdoctoral Position in Dispersal Ecology & Evolution
Department of Ecology & Evolutionary Biology

A postdoctoral position is available in the Emery lab at the University of Colorado Boulder. Our lab studies plant evolutionary ecology with an emphasis on understanding plant adaptation in variable environments and the ecological and evolutionary drivers of species' distribution patterns. Additional information can be found at <http://www.colorado.edu/lab/emery/> This opening is for one full-time postdoctoral researcher who will contribute to an NSF-funded project investigating the evolutionary feedbacks between dispersal and habitat specialization. The specific goals are to (1) quantify patterns intra- and inter-specific variation in functional traits that influence dispersal patterns in several closely related plant species, (2) test for the relationships between dispersal traits and habitat characteristics, and (3) experimentally test hypotheses about the evolution of dispersal by measuring patterns of selection and plasticity in dispersal traits under different environmental conditions.

The primary responsibilities of this position include establishing and monitoring field and greenhouse experiments, managing and analyzing data, and contributing to the dissemination of results through manuscripts and presentations. The position requires travel to California for several weeks each spring and fall to establish and maintain field experiments at the Jepson Prairie Reserve (<http://www.ucnrs.org/reserves/jepson-prairie-reserve.html>). The postdoc will be expected to engage in a highly collaborative lab environment by mentoring undergraduate students and supporting the research and professional development of graduate students, and to be an active member of the vibrant EBIO community. Opportunities for teaching and outreach activities are also available.

Candidates must have PhD in Ecology, Evolutionary Biology, Botany, or a related field, and experience conducting field experiments with plants. Candidates are also expected to have a background in quantitative and statistical methods, a strong work ethic, and excellent interpersonal, communication, and time management skills. A clear track record of publications and independent research experience are also required. The start

date for the position is no later than November 1, 2017. The expected duration of the position is 30 months.

TO APPLY: Please submit a single PDF that includes (1) a cover letter describing past research experience and qualifications for this position, (2) a current CV, and (3) contact information for 3 references, as well as separate PDFs of 3 published manuscripts, to Dr. Nancy C. Emery (nancy.emery@colorado.edu). Review of applications will begin immediately and continue until the position is filled.

Nancy C. Emery Assistant Professor Department of Ecology & Evolutionary Biology Campus Box 334 University of Colorado Boulder Boulder, CO 80309-0334 Phone (office): (303)735-7548 Website: <http://www.colorado.edu/lab/emery> Nancy Emery <Nancy.Emery@Colorado.EDU>

UColorado Boulder MolecularEvolution

Postdoc in Genomics & Molecular Evolution Department of Ecology and Evolutionary Biology, University of Colorado, Boulder

Hiring Department*: Ecology and Evolutionary Biology & Museum of Natural History, Molecular Laboratory of Dr. Erin Tripp* *Applicant to be based in Boulder, Colorado for the duration except for 1 or 2 short visits (ca. 1 week in duration) to Rancho Santa Ana Botanic Garden, to collaborate with CoPIs and students supported by this research project

Nature of Work: The Department of Ecology and Evolutionary Biology and Museum of Natural History at the University of Colorado, Boulder is seeking applicants for one, full time postdoctoral researcher to work on a current NSF-funded project is focused on understanding the potential importance of gene regulation and/or structural mutations of key genes involved in the Anthocyanin Biosynthesis Pathway (ABP) in flowering plants. Possible areas of research include: (1) genome-wide association study through targeted sequencing (e.g., ChIPseq) to assess relationships between genomic variants and flower color traits; (2) cloning core ABP structural genes to study impacts of mutations in coding regions; (3) enzyme assays to assess importance of substrate specificity on flower color transitions; (4) VIGS experimentation using already identified candidate loci. Preliminary data have been generated in the non-model system *Ruellia* (RNAseq data from 12 species, 1 fully annotated nu-

clear reference genome, existing phylogenomic (ddRAD) framework for > 500 taxa).

Possible Areas of Responsibility: - DNA variant identification, genome-wide association study (GWAS) using targeted sequencing, RNAseq analysis - Virus induced gene silencing (VIGS) - Gene cloning - Data management: storage and backup of sequence data, tracking of data from samples (expected) - Manuscript writing and presentation of results at meetings (expected)

Minimum Qualifications: - PhD in molecular biology, genetics, bioinformatics, molecular evolution, or evolutionary biology - Experienced and skilled in both the wet lab and in computational approaches - Ability to work independently and write manuscripts within reasonable time frame (~2 manuscript per year) - Comfortable with using a Linux platform and conducting server-based analyses

Preferred Qualifications: - Previous experience/expertise in one or more of the analytic techniques described above is strongly preferred - CRISPR Cas9 genome editing skills - Additional skills in DNA variant calling (e.g. GATK, samtools) or programming (e.g. R, Python, PERL, C++) is highly desired - Previous analytical experience and first-author publications from a molecular biology or genetics-related dissertation will be considered as primary determinants for choosing the candidate

Salary and Benefits: Commensurate with experience as well as the cost of living in Boulder, Colorado

Duration: 12 months; renewal is possible pending funding (successful candidate will be encouraged to seek additional funding beyond the 12 months through his/her own venues, if he/she chooses)

Special Instructions to Applicants: Review of applications will begin immediately and continue until position is filled

Application Materials Instructions: All applicants should submit a single PDF document containing all required items (see below) to Erin Tripp via email at erin.tripp@colorado.edu

Application Materials Required: - A cover letter that addresses the candidate's research experiences, skills, qualifications, and capacity to fulfill the requirements of this job - A short statement specifically describing which aspect of this project you are most excited to work on, and why - A current CV (If degree is pending, please specify expected graduation) - 3 examples of published manuscripts; first-authored mss preferred - The names, addresses, daytime telephone numbers, and e-mail addresses for three professional references

Erin Tripp <erin.tripp@colorado.edu>

UEastAnglia 2 BeeEvolution

1. Postdoctoral Position on Social Evolution and the Evolution of Ageing in Bumble Bees

PI: Prof Andrew Bourke

University of East Anglia - School of Biological Sciences

Location: Norwich, UK Salary: 32,548 to 38,833 per annum Hours: Full Time Contract Type: Fixed-Term/Contract Placed on: 10th August 2017 Closes: 8th September 2017 Job Ref: RA1432

An experienced postdoctoral researcher is sought to work on a three-year, NERC-funded project in a team supervised by Professors Andrew Bourke and Tracey Chapman. The aim of the project is to investigate costs of reproduction and the fecundity-longevity trade-off in the bumble bee *Bombus terrestris* and the fruitfly *Drosophila melanogaster*. The wider goal is to determine the effects of social evolution on the evolution of ageing. * You will have a minimum of a PhD in a relevant area, research experience of working with bumble bees or similar model systems, and be able to fulfil all essential elements of the person specification.

This full-time post is available from 1 October 2017, for a fixed term up to 36 months or until 30 September 2020.

The University is a Bronze Athena Swan Award holder, currently working towards Silver

To apply: <http://www.jobs.ac.uk/job/BDL506/senior-research-associate/> -----

2. Postdoctoral Bioinformatician Position on Social Evolution and the Evolution of Ageing in Bumble Bees

PI: Prof Andrew Bourke

University of East Anglia - School of Biological Sciences

Location: Norwich, UK Salary: 32,548 to 38,833 per annum, pro rata Hours: Part Time Contract Type: Fixed-Term/Contract Placed on: 10th August 2017 Closes: 8th September 2017 Job Ref: RA1433

Faculty of Science

(0.8 FTE)

We have an opportunity for an experienced postdoctoral bioinformatician to work on a three-year, NERC-funded

project in a team supervised by Professors Andrew Bourke and Tracey Chapman. The aim of the project is to investigate costs of reproduction and the fecundity-longevity trade-off in the bumble bee *Bombus terrestris* and the fruitfly *Drosophila melanogaster*. The wider goal is to determine the effects of social evolution on the evolution of ageing. The postholder will analyse RNA-Seq data generated by experimental manipulations of the bumble bees and flies. * You will have a minimum of a PhD in a relevant area, research experience in bioinformatics including the analysis of RNA-Seq data through writing scripts, programming and deployment of software packages, and be able to fulfil all essential elements of the person specification.

This part-time (80% FTE) post is available for a fixed term period of up to 36 months from 1 October 2017.

The University is a Bronze Athena Swan Award holder, currently working towards Silver

To apply: <http://www.jobs.ac.uk/job/BDL835/senior-research-associate/> "Tracey Chapman (BIO)" <Tracey.Chapman@uea.ac.uk>

UExeter ArcticConservation

1+1 year postdoctoral research position Context Mercury (Hg) still raises high environmental concerns in the Arctic.

This toxicant is indeed found in high concentrations in Arctic marine food webs and these concentrations might keep on increasing in some Arctic regions under the effect of global change.

In that context, understanding impacts of Hg on the Arctic wildlife, and especially on top-predators which are among the most vulnerable organisms to environmental pollution, is a major objective. Toxic effects of Hg have been widely investigated, including on Arctic species. However, in polar seabirds, a very few studies have assessed long-term population effects of Hg and almost nothing is known about effects of the parental mercury contamination on offspring phenotype and survival prospects. This is unfortunate as chick body condition, growth and ultimately survival will play a role in the dynamics of these vulnerable populations and their future distribution around the Arctic.

Telomeres are long repetitive noncoding sequences of DNA located at the end of linear eukaryotic chromosomes. These telomeres inexorably shorten through life

and this rate of shortening can be modulated by environmental conditions and exposure to environmental stressors such as pollutants. A couple of studies recently demonstrated in Arctic seabirds how telomere dynamics is linked to bird contamination by some persistent organic pollutants (OCPs and PFASs). Exposure to stressors is also well known to have transgenerational effects, with stress levels in the parental line having long-term negative consequences on offspring health. Recent studies have shown that these transgenerational effects might be mediated, at least in part, by telomere attrition. For instance, birds experimentally stressed during egg production produced chicks with shorter telomeres than controls. Hg, as a major environmental stressor, could therefore impact stress and telomere length of both parents and their chick, with potential subsequent consequences on chick phenotype and survival.

Position We are seeking for an enthusiastic postdoctoral researcher to work on a project aiming at understanding the long-term effects of Hg accumulated by adult Arctic seabirds on the next generation. More specifically, by focusing on a little auk (*Alle alle*) population from Greenland, the postdoctoral researcher will in a first step study how adult Hg contamination impact their chick's Hg contamination and ecophysiological condition (telomere length, oxidative stress, growth, body condition) and ultimately survival capacity. In a second step, the role played by adult movements and distribution during the non-breeding period on Hg concentrations accumulated by females prior the laying period and subsequently on chicks will be investigated.

The position will involve some lab work as the postdoctoral researcher will be in charge of analyzing telomere length from little auk blood samples at the CEBC institute. Oxidative stress data will be provided as well as ecological data.

Qualifications - PhD in evolutionary biology, ecotoxicology or ecophysiology - Experience with lab work - Knowledge of Arctic marine ecosystems and/or seabird ecophysiology will be an asset

We offer a 1-year contract starting at the latest on 1 October 2017 with potential for 1-year extension. Gross monthly salary is 2500 euros. The postdoctoral researcher will be based at the LIENSs institute (<http://lienss.univ-larochelle.fr/?lang=en>), La Rochelle, France within the research group AMARE (Responses of marine animals to environmental variability).

Main supervisor: Jerome Fort (jerome.fort@univ-lr.fr).

Co-supervisors: Mathieu Giraudeau (University of Exeter, UK giraudeau.mathieu@gmail.com) and Frederic Angelier and Olivier Chastel

(CEBC, France, frederic.angelier@cebc.cnrs.fr and olivier.chastel@cebc.cnrs.fr).

Application Please send your CV, cover letter, contact information for three references and any inquiries to Jerome Fort (jerome.fort@univ-lr.fr) by 27 August 2017

Mathieu Giraudeau <giraudeau.mathieu@gmail.com>

U**Gothenburg** **TreeOfLife** Deadline**EXTENDED**

A 2-year post-doc position is now available at the University of Gothenburg, Sweden, on building the tree of life from molecular sequences using the tree-building platform SUPERSMART (<http://www.supersmart-project.org/>). If you have a strong background in computational biology, molecular phylogenetics, bioinformatics, computer science, or related field, and you are interested in a new challenge, then welcome to apply by August 20th.

For more information on the position and how to apply please visit: http://www.gu.se/english/-about_the_university/job_opportunities/vacancies-details/?id=1015 Best, Allison Perrigo

Allison Perrigo, PhD Coordinator Antonelli Lab < <http://antonelli-lab.net/> > & GGBC < <http://ggbc.gu.se> > allison.perrigo@bioenv.gu.se Carl Skottsbergs gata 22 B 413 19 Göteborg

allison.perrigo@bioenv.gu.se

U**Helsinki** Sex**Conflict**Resolution**In**Salmon

A postdoc position is available for up to 5 years in Professor Craig Primmer's research group (<http://users.utu.fi/-primmer/>) at the University of Helsinki, Finland. The position is available until the August 2020 with a further 2 year extension possible. The position is funded by an ERC Advanced Grant entitled "Age at maturity in Atlantic salmon: molecular and ecological dissection of an adaptive trait".

The postdoc will conduct and co-supervise research that follows up our earlier research reporting the resolution

of a sexual conflict in Atlantic salmon via means of sex-dependent dominance leading to sex-specific patterns of maturation timing and size (see Barson et al. 2015). More specifically, the aim is to better quantify the sexual conflict using evolutionary ecological approaches and to understand the population genetic consequences of its resolution. This work is complemented by quantitative and molecular genetic research being conducted by others in the group.

An appointee to the position shall hold a doctoral degree and have the ability to conduct independent scholarly work. Suitable applicants will have a strong background in evolutionary ecology and/or evolutionary genetics as demonstrated by publications in relevant fields. Previous research experience in the field of sexual conflict resolution is advantageous as is experience studying balancing selection, selection co-efficient estimation and/or mate-choice at the phenotypic or genetic levels. The ability to work as a part of a larger research team addressing related questions is also important.

Informal inquiries can be directed to Professor Craig Primmer ([craig.primmer\(at\)helsinki.fi](mailto:craig.primmer(at)helsinki.fi)).

Formal applications should include as a single pdf file: - a CV (with names and contact details of at least two referees) - a publication list and - a max. 2 page letter of motivation

To apply, please submit your application using the University of Helsinki electronic recruitment system by clicking on the 'Apply link' on the following page: <https://www.helsinki.fi/en/open-positions/-postdoctoral-researcher-in-evolutionary-ecology-and-genetics>. The deadline for applications is Wednesday 6 September 2017, with the preferred starting date being January 2018 at the latest (the position is available immediately).

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 performance with the overall starting salary amounting c. 3155-3500 EUR per month, depending on the previous relevant research experience of the candidate.

Finland is a member of the EU, has high quality free schooling (also in English), generous family benefits and healthcare, and was recently ranked as the best country in the world for expat families and in the world's top 10 most liveable cities. The University of Helsinki is a top 100 ranked university in most ranking lists, and is currently investing heavily in life sciences research (see <https://www.helsinki.fi/en/helsinki-institute-of-life-science>).

science).

Relevant articles:

Barson et al. (2015) Sex-dependent dominance at a single locus maintains variation in age at maturity in salmon. *Nature* 528:405-408.

Aykanat et al. (2016). From population genomics to conservation and management: a workflow for targeted analysis of markers identified using genome-wide approaches in Atlantic salmon. *Journal of Fish Biology*, 89, 2658-2679.

Aykanat et al. 2015. Low but significant genetic differentiation underlies biologically meaningful phenotypic divergence in a large Atlantic salmon population. *Molecular Ecology* 24, 5158-5174

Johnston et al. 2014. Genome-wide SNP analysis reveals a genetic basis for sea-age variation in a wild population of Atlantic salmon (*Salmo salar*). *Molecular Ecology* 23:3452-3468.

New affiliation Craig Primmer, Academy Professor PO Box 56 Dept. of Biosciences | Biotechnology Institute 00014, University of Helsinki, FINLAND Visiting: Room 4006, Biocenter 1 Mobile +358 503116374 craig.primmer@helsinki.fi

Twitter @FishConGen

craig.primmer@helsinki.fi

Ullinois FunctionalGenomicsBum- bleBeePathogens

UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN
DEPARTMENT OF ENTOMOLOGY FUNCTIONAL
GENOMICS OF DISEASE AND PESTICIDE SUS-
CEPTIBILITY IN BUMBLE BEES

POSTDOCTORAL POSITION SALARY \$43,000-
\$47,500 per yr.

Applications are invited to join the Cameron Lab in the Department of Entomology at the University of Illinois. Research will focus on experimental studies of the functional genomics and ecological effects on bumble bee health of the fungal pathogen *Nosema bombi*, and its interactive effects with neonicotinoid pesticides. We are looking for expertise in the laboratory production and bioinformatic analysis of gene expression data (RNAseq, qPCR, etc.).

The collaborative research team includes Dr. Ben Sadd, Illinois State University, (<https://faculty.sharepoint.illinoisstate.edu/bmsadd>) and James Strange, Utah State USDA Bee Biology Lab (<https://www.ars.usda.gov/pacific-west-area/logan-ut/pollinating-insect-biology-management-systematics-research/people/dr-james-strange/>).

The research includes a series of lab experiments on both declining and stable populations of bumble bees, with the broad goal of understanding causal factors of decline in U.S. bumble bee populations. We will examine how bumble bee species vary in susceptibility to pathogens and pesticides, investigating how these stresses can interact to the detriment of bee viability. An integration of colony-level, whole-organism, cellular, and transcriptomic approaches will address how susceptibility is linked to decline status. The postdoc will play a key role in setting up and analyzing RNAseq data, with an ultimate goal to identify expression and genetic diversity associated with infection and pesticide susceptibility. Major responsibilities will be to interact with the research collaborators to participate in experiments and develop the transcriptome datasets.

A strong bioinformatics or statistical genetics/population genetics background with a PhD degree in the relevant areas is required. Communication skills are essential; programming and analytical skills are desirable.

To apply for this position, please submit your CV and a Statement of your interest in the position, including discussion of how your skills are concordant with the project's research needs, along with names and contact information including email addresses for three professional references. We will consider all applications until selection of the appropriate candidate is made.

For informal inquiries please contact Sydney Cameron (scameron@life.illinois.edu).

The University of Illinois is an Equal Opportunity, Affirmative Action employer. Minorities, women, veterans and individuals with disabilities are encouraged to apply. For more information, visit <http://go.illinois.edu/EEO>. To learn more about the University's commitment to diversity, please visit <http://www.inclusiveillinois.illinois.edu>. The University of Illinois conducts criminal background checks on all job candidates upon acceptance of a contingent offer.

– Sydney A. Cameron Professor Department of Entomology and Program in Ecology, Evolution and Conservation (PEEC) University of Illinois 320 Morrill Hall 505 S. Goodwin Ave. Urbana, IL 61801

ofc ph. 217-333-2340 lab ph 217-333-2170 cell ph 217 766-5631 scameron@life.illinois.edu www.life.illinois.edu/scameron “scameron@life.illinois.edu”
<scameron@life.illinois.edu>

UKentucky EvolutionaryEpigeneticsGenomics

Post-Doctoral Position Investigating Epigenetic Mechanisms of Tissue Regeneration

A postdoctoral position is available to work collaboratively between the Voss and Smith labs at University of Kentucky. The successful candidate will investigate epigenetic changes during salamander development and tissue regeneration. The training environment is exceptional for those seeking to learn how to extract biological meaning from large-scale genomics data, and the position provides flexibility to gain empirical experience while pursuing independent projects. Ideal candidates will be highly motivated, have excellent communication skills, and have experience in performing genetics/genomics/bioinformatics research. Please submit a CV and contact information for three references to Randal Voss (srvoss@uky.edu).

jeremiahsmith@gmail.com

UKonstanz CichlidSpeciesDeliniation

Three year Postdoctoral Position in Evolutionary Bioinformatics on

“Species delimitations in East African Cichlid Fish adaptive radiations”

A three year postdoctoral position working with Axel Meyer in the Evolutionary Biology Group at the University of Konstanz in Germany is available immediately. Funding will be provided through a grant of the German Science Foundation (Deutsche Forschungsgemeinschaft, DFG) within the framework of the Priority Program SPP 1991 Taxon-OMICS.

The project focuses on empirical and conceptual issues regarding species delimitation and hybridization in East African Rift Lake cichlid fishes. The research will center around the use of whole genome level data to resolve species boundaries in rapidly diversifying cichlid lineages in Lakes Victoria, Malawi, and Tanganyika. The work will make use of previously sequenced high-quality genomes as well as de novo sequencing of cichlid genomes to generate marker sets and guidelines within modern analytical frameworks for genomically diagnosing species. The funding period would be for three years and salary will be determined based on the German salary scheme TV-L E13 (annual before-tax salary is about 68,000 Euros).

The Evolutionary Biology group in Konstanz is composed of ~25 postdoc and graduate students. The collaborative research environment in the lab is highly integrative, very international, and operates in English. Therefore, the ability to speak German would be a plus, but is not essential. Further information on researchers and research in evolutionary biology in the Meyer lab can be obtained here: <http://www.evolutionsbiologie-uni-konstanz.com/> Konstanz is a very beautiful and pleasant place to live as it borders the third largest lake in Central Europe and lies at the foothills of the Alps. The University of Konstanz is an equal opportunity employer and is rated as one of the best universities in Germany.

Requirements: PhD in biology and/or bioinformatics. Skill we would like you to have: understanding of phylogenetic methodology, knowledge of wet-bench molecular techniques would be a plus, proven familiarity with

high-throughput sequencing analyses, facility with one or more programming languages (such as Python, Perl, or R), and at least three peer-reviewed publications. Applications should be sent to Axel Meyer (axel.meyer@uni-konstanz.de) and include (1) a cover letter explaining your background and motivation, (2) a CV, and (3) email addresses of two references.

The deadline for applications is the 21st of August.

Prof. Dr. Axel Meyer Lehrstuhl für Zoologie und Evolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon + 49 (0)7531 88 4163 fax + 49 (0)7531 88 3018

secretary: Christiane.Weber@uni-konstanz.de tel. + 49 (0)7531 88 3069

<http://www.evolutionsbiologie-uni-konstanz.com/> Axel Meyer <a.meyer@uni-konstanz.de>

UKonstanz GenomicsOfAggression

Two year Postdoctoral Position in Evolutionary Genomics on:

“Genomic basis of aggression”

A two year postdoctoral position working with Axel Meyer in the Evolutionary Biology Group at the University of Konstanz in Germany is available immediately. Funding will be provided through a grant of the Hector Fellow Academy (<https://www.hector-fellow-academy.de/>)

This project focuses on the genomics of aggression. We'll be using a fish model (Siamese fighting fish) to combine empirical behavioral approaches (including behavioral tests, breeding and QTL analyses) and comparative genomic analyses to study the genetics and genomics of aggression. The research will use whole genome data and require knowledge in molecular evolution and bioinformatics. The funding period is two years and salary will be determined based on the German salary scheme TV-L E13 (annual before-tax salary is about 68,000 Euros, depending on experience).

The Evolutionary Biology group in Konstanz is composed of ~25 postdoc and graduate students. The collaborative research environment in the lab is highly integrative, very international, and operates in English. Therefore, the ability to speak German would be a plus, but is not essential. Further information on researchers

and research in evolutionary biology in the Meyer lab can be obtained here: <http://www.evolutionsbiologie-uni-konstanz.com/> . Konstanz is a very beautiful town and a pleasant place to live as it borders the third largest lake in Central Europe and lies at the foothills of the Alps. The University of Konstanz is rated as one of the best universities in Germany.

Requirements: PhD in biology and/or bioinformatics. Skills we would like you to have: understanding of behavioral biology, knowledge of wet-bench molecular techniques would be a plus, proven familiarity with high-throughput sequencing analyses, facility with one or more programming languages (such as Python, Perl, or R), and at least three peer-reviewed publications. Applications should be sent to Axel Meyer (axel.meyer@uni-konstanz.de) and include (1) a cover letter explaining your background and motivation, (2) a CV, and (3) email addresses of two references. Please feel free to contact me if you have questions.

The deadline for applications is the 21st of August.

Prof. Dr. Axel Meyer Lehrstuhl für Zoologie und Evolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany fon + 49 (0)7531 88 4163 fax + 49 (0)7531 88 3018 secretary: Christiane.Weber@uni-konstanz.de tel. + 49 (0)7531 88 3069 <http://www.evolutionsbiologie-uni-konstanz.com/> Axel Meyer <a.meyer@uni-konstanz.de>

UMinnesota EvolutionAdaptationInSymbiosis

Postdoctoral position in symbiosis and climate change
Local adaptation in microbial symbionts and prairie plants

We seek a postdoctoral research scientist to investigate local adaptation in microbial symbionts of the prairie plants and their role in facilitating plants' response to climate change. The postdoctoral researcher will join a team investigating the geographic scale of local adaptation and the evolutionary response of prairie plant species to climate change (Professor Ruth Shaw, UMN; postdoctoral research scientist Dr. Shelby Flint, UMN) and the role of microbial symbionts of in local adaptation of these prairie plants (Professor Georgiana May, UMN). The existing infrastructure of experimental reciprocal transplant plots, and collections of microbial strains

and seeds, provide an excellent opportunity for addressing questions of fungal and/or bacterial symbionts of prairie plants and their roles in local adaptation. In addition, opportunities exist for developing conservation and public-private collaborations in restoration activities. The successful applicant will have knowledge of organismal biology for the microbial system of their interest, of genetic and genomic approaches relevant to their questions, evolutionary or ecological statistical analytical expertise, and a strong publication record. Up to three years of postdoctoral research funding are available through a grant from the State of MN. Applicants should write Dr. Georgiana May (gmay@umn.edu) expressing their interests and background in the research area, and attach a current CV. To apply to the UM job posting, visit <http://www1.umn.edu/ohr/employment/> and search on Job ID# 319039.

The University of Minnesota provides equal access to and opportunity in its programs, facilities, and employment without regard to race, color, creed, religion, national origin, gender, age, marital status, disability, public assistance status, veteran status, sexual orientation, gender identity, or gender expression. To learn more about diversity at the U: <http://diversity.umn.edu> . Georgiana May <gmay@umn.edu>

UMinnesota FungalAdaptiveEvolution

University of Minnesota -Fungal Adaptive Evolution

A postdoctoral research position is available at the University of Minnesota to investigate the invasive ecology and adaptation of *Fusarium virguliforme*, the causal agent of soybean sudden death syndrome (SDS). The project will investigate traits of this fungal pathogen that may enable spread and establishment of the pathogen. The studies will include experimental bioassays to assess variation in selected phenotypic traits across a panel of isolates from a broad geographical distribution of the fungus combined with next-generation sequencing and genome-wide association mapping to identify genetic loci associated with variation for key traits or demonstrating evidence of adaptive evolution. The project also aims to investigate the role of secondary metabolites in the ability of this pathogen to establish and compete in soil microbial communities. This position is part of a larger project funded through the Minnesota Invasive Terrestrial Plants and Pests Center at the University of

Minnesota that will also study the distribution of this pathogen across Minnesota and develop species distribution models to assess risks of further spread under global climate change. The overall goals of the project are to understand the roles of both biotic and abiotic factors contributing to the spread and invasiveness of a fungal pathogen under different climate scenarios.

This will be a joint position between the Malvick Lab (plpa.cfans.umn.edu/people/faculty/dean-malvick) in the Dept. of Plant Pathology) and the Bushley lab (www.cbs.umn.edu/plantbio/faculty/kathrynbushley) in the Dept. of Plant and Microbial Biology. The University of Minnesota is a diverse, interdisciplinary, and stimulating research environment that values ethnic, cultural, and gender diversity. The University of Minnesota is home to a vibrant community of researchers with strong expertise in mycology, genetics, plant pathology, ecology, and host-microbe interactions. Research will also utilize computational resources at the Minnesota Supercomputing Institute (<https://www.msi.umn.edu/>) for high-throughput analysis of genomic data.

Minimum requirements: A Ph.D. in plant pathology, mycology, molecular biology and genetics, ecology, or a related field. Previous laboratory experience working with fungi and generating and analyzing next-generation sequencing data is highly desirable. The initial appointment will be for 1 year, with an opportunity for renewal. Funding is available for at least two years. Salary is competitive and position will include health benefits. The start date is flexible, preferably before October 31, 2017.

To apply: Questions regarding the position should be directed to Dr.

Kathryn Bushley (kbushley@umn.edu) or Dr. Dean Malvick (dmalvick@umn.edu). Informal inquiries are welcome. Review of applicants will begin on August 21st until the position is filled.

Applicants must apply through the University of Minnesota Office of Human Resources <http://www1.umn.edu/ohr/employment/> (JOBID #318449).

Please attach a CV, cover letter, and names and contact information (email and phone) for three professional references. Letters of reference will be solicited once we identify top candidates.

Kathryn Bushley <kbushley@umn.edu>

UMontana Bacterial Evolutionary Genomics

Postdoctoral Research Associate - Bacterial Evolutionary Genomics, University of Montana

The Miller Lab at the University of Montana, Missoula (<http://hs.umt.edu/dbs/labs/miller>) is searching for a postdoctoral research associate to investigate the evolutionary mechanisms responsible for the maintenance and expression divergence of gene duplicates in bacteria with exceptionally high gene duplication rates. Projects will involve analyses of large genomic and transcriptomic data sets. A Ph.D. in biology or a related field is required, and the successful candidate will demonstrate a strong background in molecular evolution and genomics as well as proficiency with programming in Python, Perl and/or R.

The Division of Biological Sciences at the University of Montana (hs.umt.edu/dbs) is home to a diverse and highly interactive faculty, and the Miller lab is housed in newly constructed space dedicated to evolutionary genomics research. Missoula is a great college town located in the heart of the Rocky Mountains with an exceptional quality of life. For further information on this position and our research, please contact Dr. Miller directly at scott.miller@umontana.edu.

To apply, please visit <http://umjobs.silkroad.com> and click the job title for this position (Tracking Code 1811-254) under All Openings. Candidates must apply online and will be asked to upload the following application materials: a cover letter describing your research interests and qualifications, a CV, and the names and contact information for three references. Review of applications will begin on October 1 and the position will remain open until filled. The appointment is a 12-month Letter of Appointment with flexible start date, renewable for up to two years with possible extension to a third year.

University of Montana is an ADA/EOE/AA/Veteran's Preference Employer

"Scott.Miller@mso.umt.edu"
<Scott.Miller@mso.umt.edu>

UNottingham EvolutionaryBiol

Dear All Recruitment to the Nottingham Research Fellowships and Anne McLaren Fellowships 2018 is now open. See <http://www.nottingham.ac.uk/-researchfellows>. The School of Life Sciences is keen to attract applicants in the areas of evolutionary biology and genetics, ecology and animal behaviour.

Best wishes Andrew MacColl (andrew.maccoll@nottingham.ac.uk)

Formal University advert follows:

Background Nottingham Research Fellowships (NRF) and Anne McLaren Fellowships (AMF) target outstanding early career researchers across the University.

The aim our competitive fellowship schemes is to attract and retain exceptional early career researchers to deliver world-leading research. These independent research fellows will be the next generation of outstanding research leaders, and enable a step change in research performance.

Our internally funded fellowships include: three years' salary costs (R&T 4 and 5 - current offers tend to be at R&T bottom level 5 dependent on experience) up to 25,000 per annum research expenses up to 5,000 per annum taxable childcare costs link to permanent academic appointment (subject to performance and the right to work in the UK).

The Anne McLaren Fellowship scheme is targeted at women in STEM subjects, and the Nottingham Research Fellowship is available across all participating schools.

Enhanced recruitment - recruiting 100 fellows over the next 5 years The University recognises the value and contribution of early career researchers in delivering our ambitious research vision. As such, we will recruit 100 Nottingham and Anne McLaren Research Fellows by the end of 2020.

This represents a significant increase on the traditional recruitment model, which appointed on average eight fellows per year, with a slight increase in the 2016/17 recruitment period (12 fellows appointed).

We will do this through expansion of the current recruitment model and through a parallel recruitment model for Beacons of Excellence.

An increase in numbers will not be at the expense of

quality.

Summary of the fellowships offer Our fellowships are funded by the University's Research Strategy and are targeted at exceptional postdoctoral researchers in most academic disciplines represented at the University.

Fellowships are for three years in duration and are linked to an established academic post. Following the three-year fellowship the host school will assume responsibility for the salary of the individual.

All faculties are participating this year, but please note that in Arts and Engineering, applications will be dealt with at the faculty level.

The Faculty of Arts are inviting applications based on research themes, and the final school/department where the applicant is placed at the end of the fellowship will depend on faculty requirements.

Candidates should have no more than eight years of post-doctoral experience following the award of their PhD.

Candidates must have been awarded their PhD in order to apply.

Fellows will be recruited at level 4 or 5 on the Research and Teaching Staff Salary Scales (depending on experience).

We continue to advertise the Anne McLaren Fellowships as targeted at female scholars who are traditionally under-represented in STEM subjects.

Attracting applicants The research fellowships website as now been updated to include: more materials on our existing fellows - case studies and video case studies information on what makes a good candidate updated details on how to apply, eligibility criteria, timeline for recruitment and contact information.

Fellowships are advertised on <http://www.nottingham.ac.uk/jobs/home.aspx>. Alongside this, advertising is scheduled for www.jobs.ac.uk, ResearchResearch, Nature jobs, Research Professional, Times Higher, LinkedIn and Facebook. If you think there are other opportunities (for example specific journals), please let us know.

Promotional postcards for the scheme are under production and will be available in electronic format and hard copy for all staff to use.

A key part of our recruitment is getting the message out to promising academics, both internally and externally. We rely on you to support us in spreading the message of the great package offered, and identifying high quality candidates.

Timeline for recruitment Recruitment to the 2017/18 fellowship programme is now live. The recruitment timeline can be found below, with full details available on the external website.

Announcement of call details July 2017 Candidates discuss and develop application with Host School July–November 2017 Submission of EOI to Host School By 17:00 on 3 November 2017 Candidates invited to submit a full application By 15 December 2017 Submission of full applications By 17:00 on 19 January 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>

UOklahoma ComparativePhylogeography

Postdoctoral Position: Evolutionary ecology of communities

I am seeking a highly motivated postdoctoral researcher to join me in merging comparative phylogeography and geographical ecology to unravel the complex regional history of communities, via the evolution of species pools and historical constraints on community assembly. Research in my lab focuses on integrating comparative phylogeography with community and macroecology to investigate the role of dispersal in shaping large-scale biogeographical patterns and how communities respond to environmental change. Thus, I invite applications from scholars with a strong background in either geographical ecology or comparative phylogeography.

The successful applicant will be a highly motivated, independent, and collaborative scientist with excellent communication and organizational skills. They will have a broad background in either community/macroecology or comparative phylogeography, and a demonstrated record in project design, data analysis and publication. Strong quantitative and analytical skills, including experience handling large geographical or genetic datasets, conducting spatial analyses, and fluency in R or other programming languages, are essential.

The initial appointment will be for one year, with the possibility of extension for an additional year contingent on performance and funding. A PhD is required by the

start date for this position. Screening of candidates will begin 31 August 2017 and continue until the position is filled. Informal inquiries are welcome—please shoot me an email at kamarske@ou.edu! For information on how to apply, click here: <https://kamarske.org/join-us/>
Katharine Marske

Assistant Professor Department of Biology University of Oklahoma kamarske.org

“Marske, Katharine” <kamarske@ou.edu>

UOregon Bioinformatics EvolutionaryGenomics

Phillips Lab, University of Oregon

Postdoc in Bioinformatics/Evolutionary Genomics

The Phillips Lab in the Institute of Ecology and Evolution (IE2) at the University of Oregon seeks applications for a postdoctoral research The successful candidate will provide research leadership for several NIH-funded projects utilizing the analysis large-scale DNA sequence and functional genomic information from natural populations, experimental evolution, and genetic crosses to understand the genetics and evolution of complex traits and/or the systems genetics of aging. The ideal candidate would have strong computer and quantitative skills, as well as some background in genomic analysis and/or evolutionary genetics. Further information on Phillips Lab is available at <http://www.uoregon.edu/~pphil>. Application materials available at <http://careers.uoregon.edu/cw/en-us/-job/521009/postdoctoral-research-scholar> . Patrick C. Phillips, Ph.D. Acting Executive Director | Professor of Biology Phil and Penny Knight Campus for Accelerating Scientific Impact <https://www.uoregon.edu/accelerate> <https://www.uoregon.edu/~pphil> pphil@uoregon.edu | 541-346-0916

“pphil@uoregon.edu” <pphil@uoregon.edu>

UOregon BiologyAging Biodemography

Phillips Lab, University of Oregon

Postdoc in Biology of Aging/Biodemography

The Phillips Lab in the Institute of Ecology and Evolution (IE2) at the University of Oregon seeks applications for a postdoctoral research fellowship in the biology of aging and/or biodemography. The successful candidate will provide research leadership for a set of projects aimed at investigating demographic variation within and between species from the standpoint of understanding the effects of compounds that extend individual lifespan and/or the causes and consequences of genetic, environmental and stochastic variation in reproductive patterns among individuals. This work is supported by multiple NIH grants, including the Caenorhabditis Intervention Testing Program (CITP) and a special program in biodemography. These projects involve the use microfluidic devices and automated lifespan scanners to generate the largest and highest precision demographic database ever assembled for an animal system. The ideal candidate would have strong quantitative skills and a desire to investigate fundamental questions in aging biology and demography using advanced approaches for survival and demographic analysis. Further information on Phillips Lab is available at <http://www.uoregon.edu/~pphil>. Application materials available at <http://careers.uoregon.edu/cw/en-us/-job/521005/postdoctoral-research-scholar>. Patrick C. Phillips, Ph.D. Acting Executive Director | Professor of Biology Phil and Penny Knight Campus for Accelerating Scientific Impact <https://www.uoregon.edu/accelerate> <https://www.uoregon.edu/~pphil> pphil@uoregon.edu | 541-346-0916

“pphil@uoregon.edu” <pphil@uoregon.edu>

UPerpignan France Metabarcoding

***POSITION AVAILABLE * Postdoctoral Research Fellowship Metabarcoding, Trophic ecology**

Duration: 24 Months

The post-doctoral position will be based at the CRIOBE in the core laboratory on the University of Perpignan Campus (France). Some field trips are planned in French Polynesia. The post-doc will work mainly with Valeriano Parravicini (EPHE-CRIOBE) and Serge Planes (CNRS-CRIOBE).

KEY REQUIREMENTS & QUALIFICATIONS The ideal candidate should demonstrate a background in the employment of metabarcoding from next generation

sequencing and experience in the analysis of complex ecological networks. The candidate will be in charge of developing analysis of the trophic niche of reef fish species employing a mixed approach based primarily on DNA metabarcoding of gut and intestinal contents, but also on stable isotopes analysis. The overall goal is to reconstruct the trophic interactions among species based on the identification of exact food consumption. Metabarcoding will mix plants (algae) and animals survey to evaluate the complexity of the diets and introduce the level of admixture on the species diets. The successful candidate will work within the frame of two larger and already funded projects in collaboration with several other international leaders in coral reef ecology.

GLOBAL PROJECT CONTEXT AND OBJECTIVES Trophic interactions among species provide the basis of ecological and evolutionary dynamics as all species have to acquire the resources necessary to survive and reproduce. These constraints tend to organize biodiversity into complex food-webs where species interact directly, via the classic resource-consumer interaction, or indirectly via multiple resource-consumer interactions linked to one another. Therefore, the topology of food-webs determines synergies, competition and antagonism among species, mediates the effects of external disturbances and is a key property of ecosystems. However, the empirical characterization of trophic networks is generally limited to simplified architectures (e.g. bi-trophic predator-prey relationships, plant-pollinator and host-parasite interactions). Detailed information on food-web architecture for coral reefs relies mainly on data from the Caribbean, Cuba and simplified Pacific food-webs. These architectures are based mainly on gut content analysis, literature or expert opinion and their level of detail is limited to broad trophic guilds (e.g. herbivores, detritivores, invertebrate feeders). This low resolution impairs our ability to understand the complexity of coral reefs and to evaluate the disturbance potential to propagate through the interaction network. The main goal of this project is to combine metabarcoding analysis based on the existing global DNA-barcode library (cf. BIOCODE project) and stable isotopes analysis to assess reef fishes dietary preferences in the Insular Pacific.

HOW TO APPLY Interested applicants should send a cover letter, a statement of research goals and a CV to valeriano.parravicini@gmail.com. Applicants will receive an e-mail confirming their application has been received.

CLOSING DATE All applications should be submitted by 30 September 2017. However, until the position is filled, we will continue to accept application materials. The position aims to start early 2018 at the latest.

Valeriano Parravicini <valeriano.parravicini@gmail.com> Description Participate in research on domestication and breeding of cultured marine species. Research activities focus on (i) controlling the reproductive cycle in captivity and enabling the implementation of controlled crossing designs e.g using in vitro fertilization (ii) Studying the larval development and optimizing husbandry protocols for the production of juveniles, and (iii) Estimating genetic parameters for characters of interest to aquaculture production and developing genetic and genomic tools for domestication and selective breeding.

UPittsburgh EvolutionaryEcology

The Turcotte Lab at the University of Pittsburgh is looking for a postdoc to experimentally test the dynamic interplay between rapid evolution and community ecology in the field. The goal is to disentangle and quantify how ecological and evolutionary processes reciprocally impact each other and understand their importance in nature using robust experiments.

The University of Pittsburgh is a leading research university and the Department of Biological Sciences is a dynamic and growing team of enthusiastic researchers and educators. The department also runs the Pymatuning Lab of Ecology, which is equipped with lab space and housing to facilitate field-based research in northwestern Pennsylvania. The City of Pittsburgh is a vibrant and beautiful place to live and is often voted the 'Most Livable city in the U.S.'

If you are interested and you are attending ESA please contact me at turcotte@pitt.edu so can meet in person.

More details about the lab and applying here: www.martinturcotte.net Martin Turcotte, Ph.D. Assistant Professor, Department of Biological Sciences University of Pittsburgh

mart.turcotte@gmail.com

USouthernMississippi FinfishGenetics

Location Gulf Coast Research Laboratory

Title Post-Doctoral Scientist - Marine Finfish Breeding and Genetics Company University of Southern Mississippi

Closing Date 8/31/2017

Salary \$45,000 yearly + benefit

Qualifications A Ph.D in reproductive physiology, animal genetics or related disciplines is required and experience with aquaculture research on these topics is desirable.

Contact Name Eric Saillant Contact Phone 228-818-8007 Contact Email eric.saillant@usm.edu

Eric Saillant <Eric.Saillant@usm.edu>

USouthFlorida EvolutionaryGenomics

Postdoctoral Position in Evolutionary Genomics

University of South Florida

The Cassin Sackett Lab at the University of South Florida is looking for a highly motivated postdoctoral scholar to study population and conservation genomics in prairie dogs. The lab uses ancient DNA, field methods, next-generation sequencing and bioinformatic approaches to answer fundamental questions in evolutionary biology, especially those with practical conservation applications. Some major questions being asked in the lab are:

§How do humans influence the evolution of wildlife? We study the ways in which climate change, habitat alteration, and introduced diseases impact the distribution of genetic variation, the rates of gene flow, and the probability of adaptation.

§What is the genomic basis of rapid adaptation to novel pathogens? We examine the demographic and environmental constraints to adaptation and whether genomic architecture of rapid adaptation differs from that of more gradual adaptation (e.g., to climate).

Please visit the lab website for more details on current projects: www.cassinsackett.com The postdoc will be involved in a project that uses genomic approaches to analyze genetic diversity in prairie dogs and investigate the potential for resistance to plague. Specific duties may include: 1) sampling historical museum specimens, 2) developing and optimizing genomic assays (e.g., SNP capture, highly multiplexed amplicon sequencing), 3)

performing wet lab work to genotype individual prairie dogs (both modern and historical), 4) conducting bioinformatic analyses of population genomics and adaptation, 5) writing and submitting manuscripts related to the project.

The position is funded for one year, and candidates are encouraged to work with lab members and collaborators to pursue additional funding for extension. The position will be based at the University of South Florida in the Department of Integrative Biology, but requires travel to at least one museum (e.g., Smithsonian), including the possibility of a short-term stay in another city. Application review will begin September 15 and will continue until the position is filled. The desired start date is November 1, but is negotiable.

Qualifications:

Applicants should have a PhD in ecology, evolution, genetics, bioinformatics, or a related field. We are looking for a scientist with a record of scholarly publication, excellent organizational and communication skills, experience working in a Unix environment, and the desire/willingness to engage in occasional outreach. Preference will be given to candidates with experience working on ancient DNA and with strong bioinformatics skills. The Cassin Sackett lab is committed to increasing diversity in STEM, and we especially encourage applications from women, minorities, veterans and other underrepresented groups. We also welcome applications from international candidates. The University of South Florida conducts background checks on all job candidates upon acceptance of an offer.

How to apply:

Interested candidates should apply by sending an email to SackettL@usf.edu that includes: (1) cover letter describing research interests and motivation, including discussion of how your skills are aligned with the needs of the project, (2) CV, (3) names and emails of 3 references, and (4) 2-3 published papers or manuscripts in preparation.

Please email SackettL@usf.edu with any questions.

- Loren Cassin Sackett, Ph.D. Assistant Professor, Integrative Biology University of South Florida 4202 E Fowler Ave, SCA 312 Tampa, FL 33620-5200 www.cassinsackett.com Loren Cassin Sackett <sackettl@usf.edu>

USouthFlorida SpartinaEvolutionaryEpigenomics

Epigenomic response to complex environments in foundation coastal plant species

The Richards Lab at the University of South Florida is seeking a highly motivated postdoctoral scholar to study population genomics and epigenomics of coastal plant species. The position will be primarily focused on an NSF-funded project in collaboration with Randall Hughes (Northeastern U) and Kitty Gehring (Northern Arizona U) aimed at understanding the interplay between the salt marsh grass *Spartina alterniflora* and bacterial and fungal endosymbionts across a salinity gradient, with opportunities for involvement in additional projects, based on the candidate's interest.

The duties of the postdoc will include primarily bioinformatics and statistical analyses of reduced representation bisulfite sequencing data (epiGBS). The postdoc will be responsible for statistical modeling of both genomic and phenotypic results as well as writing manuscripts. In addition, the postdoc will be supervising and training graduate students working on this project.

Expertise in statistics, genomics or bioinformatics is desirable. Additionally, previous experience with bisulfite sequencing, reduced representation approaches, and polyploidy will be ideal. Strong candidates will also possess the following attributes:

- Creativity, independence, and the desire to learn new things.
- Excellent communication skills, both written and oral.
- Proficiency in python and R

Applicants should have received a Ph.D. in ecology, evolution, genetics, bioinformatics, or a related field. The position is available for 1 year with opportunities for additional funding. Application review will begin September 1, 2017 and will continue until the position is filled. Start date is flexible, but ideally by January 2018. To apply, please email a brief cover letter, curriculum vitae, and the names and contact information for three references to clr@usf.edu.

Tampa is a growing city close to the beach, with an affordable cost of living, and a growing food and drink scene. The Richards lab is committed to a diverse workplace, and prospective postdocs of all races, genders,

and sexual orientations are encouraged to apply.

For further information about the Richards lab, please visit the lab website at <http://www.ecologicaepigenetics.com> Christina Richards, Ph.D. Associate professor University of South Florida Department of Integrative Biology 4202 East Fowler Avenue SCA 127 Tampa, FL 33620 (813)974-5090 (813)974-3263 FAX <http://www.ecologicaepigenetics.com> Twitter: @EcolEpig Facebook: Ecological Epigenetics clr@usf.edu

“Richards, Christina” <clr@usf.edu>

UTexas-Houston InferringDemographicHistory

Postdoctoral Fellow - Method Development in Inferring Demographic History. A postdoctoral fellow position in computational population genomics is available at Liu Lab (www.liulab.science) at University of Texas School of Public Health (UTSPH), Houston, Texas, USA. The hired postdoctoral fellow will engage in method development and application related to inferring population demographic history using large-scale DNA sequence data (see references below). A graduate level training in population genetics is required. Previous methodology development and/or Java programming experience is preferred. PhDs without population genetics training but with extensive algorithm development and Java programming experience and strong interest in population genetics questions are also encouraged to apply. The hired postdoctoral fellow will also have chance to work with Dr. Yun-Xin Fu at UTSPH and our collaborators at Human Genome Sequencing Center at Baylor College of Medicine on other exciting population genetics studies of human and primate populations. Contact: Xiaoming Liu (Xiaoming.Liu@uth.tmc.edu). Reference: Liu X and Fu YX. (2015) Exploring population size changes using SNP frequency spectra. *Nature Genetics*. 47(5):555-559.

“xiaoming.liu@uth.tmc.edu”

UWisconsin Madison EvolPopGenomics

Postdoctoral Position in Evolutionary/Population Genomics

A postdoctoral position is available to work on an NSF-funded project in the laboratory of Professor Carol Lee, in the Department of Integrative Biology and the Center of Rapid Evolution at the University of Wisconsin, Madison.

This project focuses on Rapid Evolutionary Responses to Global Change using the copepod *Eurytemora affinis* as a model system. With changes in global climate, the coastal oceans and estuaries at high latitudes are experiencing rising temperature along with rapid declines in salinity, due to increases in ice melt and precipitation. We have found evolutionary shifts in ion transport function, gene expression, and population genomic signatures of selection associated with changes in salinity. This postdoc project will entail conducting population genomic analyses along temperature and salinity gradients in the wild, and during selection experiments in the laboratory.

A key advantage of the *E. affinis* system is its short generation time (20d), ease of culturing large numbers (thousands per population), and ability to generate inbred lines. We have a full genome sequence of *E.*

affinis and several reference transcriptome sequences. Additionally, the multiple independently-derived environmental clines enable the observation of parallel evolution.

The ideal candidate should hold a Ph.D. and have publications in peer-reviewed journals. A strong background in evolutionary biology is required, especially in population genetics/genomics. Relevant areas of expertise include computational and programming skills and statistics, with background in comparative physiology preferred.

Review of applications will begin immediately and will continue until the position is filled. The appointment could begin as early as October 2017 and can persist for up to three years. Interested candidates should email the application to Prof. Carol Lee (carollee@wisc.edu), including: (1) a CV, (2) a cover letter describing qualifications and relevant experience, (3) a list of references, and (4) samples of first authored publications. Enquiries

regarding this position are most welcome.

The University of Wisconsin-Madison offers a large and intellectually vibrant community of evolutionary/population biologists, providing ample opportunities for interaction with excellent scientists (see http://www.evolution.wisc.edu/view_facultymembers). Madison is a culturally-rich community, in relatively close proximity to Chicago.

The University of Wisconsin is an Equal Opportunity/Affirmative Action Employer.

Carol Eunmi Lee, Ph.D. Professor Center of Rapid Evolution (CORE) and Department of Integrative Biology 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu <http://carollee.labs.wisc.edu> Carol Eunmi Lee <carollee@wisc.edu>

UZurich LifeHistoryEvolution

Postdoc position in Evolutionary Ecology

**

On: life history evolution

**

at the University of Zurich, Switzerland

**

A postdoctoral position in evolutionary ecology, of 24 months duration, is available at the University of Zurich working with Prof Hanna Kokko and her international team www.kokkonuts.org. We are a team that places a lot of emphasis on creating theoretical work that integrates well with empirical findings. We work on life history theory (and data), interpreted in a very broad sense: examples include life histories of modular organisms, facultative sex, spatial evolution, and sexual dimorphism in a broad sense (including e.g. dispersal polymorphisms). The most up to date version of our current interests can be best described by the list of journal club articles that we discuss each week (www.kokkonuts.org, click on 'journal club'). This implicitly defines our current interests, and applicants will quickly notice that they are broad. In the past, successful applicants have included theoreticians but also empiricists who can bring knowledge of a particular system to our group.

The working language in the group is English (German skills are not essential). The position is available as soon

as the candidate has been found. The evaluation of applications begins on August 31, 2017, and will continue until a suitable candidate has been found.

Applicants should send a cover letter with a

-Statement of their research interests, especially in relation to the journal club articles as mentioned above

-C.V. (including publication list), and

-The names and contact details of at least one referee.

Applications should form a single pdf file and this should be sent to: hanna.kokko@ieu.uzh.ch

Petra Zehetmaier Administrative Assistant Prof. Dr. Hanna Kokko

Department of Evolutionary Biology and Environmental Studies University of Zurich Winterthurerstr. 190 8057 Zurich

Tel.: +41 (0) 44 635 47 61

Email: petra.zehetmaier@ieu.uzh.ch Office: Y13-H-81

Petra Zehetmaier <petra.zehetmaier@ieu.uzh.ch>

Versailles France Plant VirologyBioinformatics

Postdoctoral Position to Explore the Expanding Field of Plant Virology

Scientific context Sequencing and assembling the genomes of eukaryotes can help elucidating the evolution of viruses. Indeed, genomes of plants, animals and protists can contain viral sequences that have been inserted either by active or by passive integration mechanisms and in many cases retained there over extended periods of time, sometimes millions of years. The study of endogenous viral elements (EVEs), coined "paleovirology", does allow the evolution of viruses to be traced, much like a fossil record (Aiewsakun and Katzourakis, 2015). For example, the study of endogenous retroviruses has enabled to uncover their hidden diversity and host range, and has provided evidence that retroviruses have a marine origin, and that they developed in parallel with their vertebrate hosts more than 450 million years ago (Hayward et al., 2013) (Hayward et al., 2015) (Aiewsakun and Katzourakis, 2017). The Caulimoviridae is one of the five families of reverse-transcribing viruses or virus-like retrotransposons that occur in eukaryotes (Pringle, 1998), and is the only family of viruses with a double-stranded DNA genome

that infects plants. Unlike retroviruses, Caulimoviridae do not integrate their DNA in the genome of their host to complete their replication cycle. Nevertheless, caulimovirid DNA can occasionally integrate their host genome passively. Using paleovirology approaches, we have determined that EVEs from several Caulimoviridae genera are found in virtually all vascular plant genomes, including ferns, gymnosperms and angiosperms, often at high copy number (Geering et al., 2014) (Diop et al., 2017). A major conclusion stemming out from previous work is that, instead of representing a single element, endogenous Caulimoviridae often appear to define complex networks of related sequences with structural and genetic variants. For instance, Caulimoviridae EVEs can be re-organized in plant genomes into sequences capable to generate episomal infection (Gayral et al., 2008). In addition, several Caulimoviridae genera have bipartite genomes (Geering et al., 2014) - each viral genome is defined by two “chromosomes” - but it is unclear whether this genomic organization has emerged once or repeatedly. Furthermore, in the oak genome, we found a very high number of short Caulimoviridae segments with movement protein domain relative to the number of full length viral genomes (Plomion et al., submitted), suggesting that they represent satellite sequences and so that their duplication relies on the production of proteins by autonomous entities, either from exogenous Caulimoviridae, or from endogenous elements.

Proposed work Combining information from several endogenous copies enables reconstructing consensus sequences that closely determine native elements. To disentangle the genetic relationships and functional interactions defining these networks, we will perform an accurate reconstruction of Caulimoviridae and related EVE sequences in several plant genomes, starting with species such as oak, vine, and citrus, for which we have collected exemplary data. The acquired methodology will be automatized and transposed to dozens of plant genomes to identify, characterize and compare Caulimoviridae sequence networks. Comparing Caulimoviridae networks across plant families with high EVE content and for which a substantial set of genomes are publicly available (e.g. Solanaceae) or to which we have access in the context of collaborations (e.g. Rutaceae) will allow determining the time of emergence and performing detailed co-evolution analyses to gain further insights into the evolution of this complex plant pathosystem.

Profile §The successful applicant will have a Ph.D in bioinformatics and substantial experience in the fields of evolutionary biology, virology or genomics. §He/She will be familiar with different programming languages.

§He/She will be autonomous, creative and dedicated, and will have good English writing proficiency.

Working environment §The host lab (URGI) is located in the INRA Center of Versailles, approx. 15km from Paris. URGI is a transdisciplinary unit dedicated to genome analysis and data integration. It is composed of over 20 permanent members, including several developers and researchers. The genome analysis team is internationally recognized for his expertise in the annotation and analysis of selfish genetic elements, including transposable elements and endogenous viruses. §URGI will provide a friendly and formative environment. The INRA Versailles Center can rent on-site institutional temporary accommodation under specific conditions. §The position is for 18 months to begin early 2018 in the frame of the ANR-funded project EVENTS (coordinated by Pierre-Yves Teycheney). §Monthly salary is approx. 2,000 euros (net). §Incoming researchers are welcome to apply for mobility allowance

— / —

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>

VirginiaTech Macroevolution

Virginia Tech Postdoctoral Associate in Biological Sciences

A postdoctoral position is available in the newly instituted Uyeda lab at Virginia Tech (www.uyedalab.com). My lab develops and applies phylogenetic comparative methods in a variety of empirical systems with the goal of connecting analysis of macroevolutionary patterns with a process-based understanding of evolution. Candidates will have substantial opportunity to develop their own research projects and interests so long as they have overlap with the goals of the lab. Examples of current research topics include the evolution of physiological and metabolic traits, integrating biomechanical performance landscapes into comparative models, and using phenotypic ontologies in trait evolutionary models. Experience with programming (particularly in R), computational biology, Bayesian statistical modeling, quantitative genetics, and/or phylogenetics are also desirable. Candidates from either math/theory/computational or empirical backgrounds are encouraged to apply. Initial

appointment is for 1 year with the possibility of renewal. I will begin considering applicants on September 15th, 2017; but position will remain open until filled. For questions and informal inquiries, please contact me at juyeda@vt.edu.

Required Qualifications: PhD in relevant field (evolution, organismal biology, statistics, computational biology, etc.)

Preferred Qualifications: Experience in the development of phylogenetic comparative methods Programming experience Experience with Bayesian statistical modeling

How To Apply: Qualified applicants must electronically submit online application, cover letter, resume/curriculum vitae, and list of references to <https://listings.jobs.vt.edu/postings/79124> . About Virginia Tech: Virginia Tech is a public land-grant university, committed to teaching and learning, research, and outreach to the Commonwealth of Virginia, the nation, and the world. Building on its motto of Ut Prosim (that I may serve), Virginia Tech is dedicated to InclusiveVTâ euro “serving in the spirit of community, diversity, and excellence. We seek candidates who adopt and practice the Principles of Community, which are fundamental to our on-going efforts to increase access and inclusion, and to create a community that nurtures learning and growth for all of its members. Virginia Tech actively seeks a broad spectrum of candidates to join our community in preparing leaders for the world.

Virginia Tech does not discriminate against employees, students, or applicants on the basis of age, color, disability, gender, gender identity, gender expression, national origin, political affiliation, race, religion, sexual orientation, genetic information, or veteran status; or otherwise discriminate against employees or applicants who inquire about, discuss, or disclose their compensation or the compensation of other employees, or applicants; or any other basis protected by law. For inquiries regarding non-discrimination policies, contact the executive director for Equity and Accessibility at 540-231-2010 or Virginia Tech, North End Center, Suite 2300 (0318), 300 Turner St. NW, Blacksburg, VA 24061. If you are an individual with a disability and desire accommodation please contact the hiring department.

Josef C Uyeda <juyeda@vt.edu>

WSL Switzerland Environmental Genomics

PostDoc in environmental genomics

The Swiss Federal Institute for Forest, Snow and Landscape Research WSL is a part of the ETH domain. Approximately 500 people work on the sustainable use and protection of the environment and on the handling of natural hazards.

The Research Unit Biodiversity and Conservation Biology studies the diversity of life in its various forms, from genetic diversity to the diversity of species and ecosystems as well as their interactions. In the frame of a SNSF-supported research project on the associations between environment and genotype, we are searching for 9 months, starting October 1, 2017 and with an option for prolongation,

a PostDoc in environmental genomics.

You will analyze transcriptome-based data from an exome capture experiment in natural populations of Swiss stone pine (*Pinus cembra*). On the basis of available next-generation sequencing data, you will study environment genotype associations and comparative transcriptomics, and you will publish the results in international scientific journals and present them at dedicated conferences.

You have acquired a PhD in biology or environmental sciences, with a strong background in ecological genetics and evolutionary biology as well as competence in bioinformatics, the analysis of environmental and genomic data (environmental associations). You are ambitious and highly motivated, are used to a high standard of independent, structured and careful working attitude, demonstrate a high level of team spirit.

Please submit your complete application online to Monika Lips-Sandmeier, Human Resources WSL. Felix Gugerli, phone +41 (0)44 739 25 90 or felix.gugerli@wsl.ch, and Christian Rellstab, phone +41 (0)44 739 25 42 or christian.rellstab@wsl.ch, will be happy to answer any questions or offer further information. The evaluation process will start September 1, 2017, but the position remains open until filled. The WSL strives to increase the proportion of women in its employment, which is why qualified women are particularly called upon to apply for this position.

“christian.rellstab@wsl.ch” <christian.rellstab@wsl.ch>

WorkshopsCourses

Berlin GWASusingR Oct23-27	120	Groningen ESEBFundingPolicies Aug24	129
Berlin PythonForBiologists Oct2-6	121	Heraklion Crete MetagenomicsBarcoding Mar19-23	129
Berlin PythonForBiologists Oct2-6 deadline	122	SICB SanFrancisco PositiveSelectionPolarOrganisms	
Berlin StatisticsForBiologistsUsingR Sep18-22	123	Jan3	130
Berlin StatisticsForBiologistsUsingR Sep18-22 2 ..	125	Tokyo EvolutionLife Jan22-Feb2	131
cE3c Portugal EvolutionaryBiol Oct-Nov	125	UHuddersfield ComputingSkills Sep13-15	131
Crete ComputationalMolEvol May6-17	126	UHuddersfield ComputingSkills Sep13-15 2	132
CzechRepublic PopulationSpeciationGeomics Jan21-		UK DataScienceForPopulationGenetics Oct23-27 .	132
Feb3	126	UK ModellingEvolution Oct23-27 Scholarships ...	133
CzechRepublic WorkshoponGenomics Jan7-20	127	UK PopulationGeneticsUsingR Oct23-27 Scholarships	
Groningen ESEB2017 Aug20-25 DrosophilaPopula-		135	
tionGenomics	128		

Berlin GWASusingR Oct23-27

Practical GWAS Using Linux and R
23-27 October 2017, Berlin (Germany)

<https://www.physalia-courses.org/courses/course15/>
INSTRUCTOR

Dr Jing Hua Zhao (<https://www.physalia-courses.org/-instructors/t20/>)

Trained in medicine, medical statistics and statistical genetics, he had worked on statistical and computational methods for epidemiological and public health studies at several institutions until 2005, when he joined the MRC Epidemiology Unit, University of Cambridge, to work on design and analysis of GWAS such as the EPIC-Norfolk, the Fenland and the InterAct. He has also participated in numerous genetic analysis workshops which involve both simulated and real data such as those from the Framingham heart study. Besides methodological development, data analysis, and other academic activities, he has also had tutorials on genetic dissection of complex traits with focus on GWAS at User! 2008, 2009, and 2010 Conferences and contributed a Henry-Stewart talk on genetic association with R.

Overview

The past decade has witnessed an astonishing development and the universal use of genome wide association studies (GWAS) in identification and characterisation

of genetic variants underlying disorders and other variations in human and other species, which has an immense impact in biomedical research. This is owing to the ability to efficiently generate and process large quantity of genetic polymorphisms as well as to integrate with other sources such as gene expression and methylation. To tackle challenges in GWAS, a lot of methods and techniques have been established but many others are still evolving. The workshop therefore intends to give a grand picture as well as practical aspects of GWAS.

Targeted audience and assumed background

The purpose of this workshop is to render both a broad picture and computational details of GWAS to biomedical researchers and related fields. It sets to explore the biological, statistical, and computational concepts, methodologies and practices involving a variety of software based on Linux and R. Examples of consortium contributions will also be given. These will be particularly beneficial to those who come with their own problems and wish to implement the analysis.

Structure

The workshop contains both lecture and computer sessions, designed to help participants to understand the background, methodology and implementation. The computer session is designed to facilitate data analysis and interpretation.

Session content

Monday 23rd - Classes from 09:30 to 17:30

Module 1 -Overview

The purpose of this module is provide a grand view

of genetic dissection of complex traits as well as the technological development which lead to GWAS. It will also set stage for later parts of the workshop.

* Introduction - background, purpose * The roadmap to GWAS * Background, study designs, implementations * GWAS catalog <http://www.ebi.ac.uk/gwas/> * Workshop outlines

Tuesday 24th - Classes from 09:30 to 17:30

Module 2 - Elements of genetic association

The purpose of this module is to get into the basic considerations of the genetic association studies. At end of the module, you will be able to conduct the relevant analyses.

* Chromosomes, DNA, QC, alleles, genotypes, HWE, mode of inheritance, haplotypes and linkage disequilibrium, GxG and GxE interactions * Phenotype: QC, transformation * Study designs: case-control, case-cohort, family * Association models: linear, logistic, Cox regression models; R^2 , AUC, Cstat * Meta-analysis: fixed and random effects models * Missing data models * Population stratification and genomic controls

Wednesday 25th - Classes from 09:30 to 17:30

Module 3 -GWAS

This module focuses on main analyses for GWAS.

* gene chips, HapMap, 1000 genomes project * QC-HWE, call rates, MAF * Genotype imputation, imputation quality * Multiple testing, FDR, q-value * Discovery, replication studies * Report of results and GSEA * Prediction

Thursday 26th - Classes from 09:30 to 17:30

Module 4-Advanced topics

This module covers several areas of GWAS in more details.

* Rare variants * Longitudinal data * Polygenic modelling * Bayesian methods * Machine learning

Friday 27th - Classes from 09:30 to 17:30

Module 5 - Additional topics

The module will look further into several other areas of research in GWAS.

* Conditional/joint analysis * Mendelian randomization * Microarray, methylation, TWAS

Available packages:

1) Course-only: includes course material and refreshments (430 euros; VAT incl.)

2) All-inclusive: includes course material, refreshments,

meals (breakfast, lunch and dinner), accommodation (695 euros; VAT incl.)

The full list of our courses and Workshops:

— / —

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>

Berlin PythonForBiologists Oct2-6

Introduction to Python for Biologists

<https://www.physalia-courses.org/courses-workshops/-course2/> 2-6 October 2017, Berlin (Germany)

Instructor:

Dr. Martin Jones (founder, Python for biologists)

<https://www.physalia-courses.org/instructors/t1/>
Course overview

Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at complete beginners and assumes no prior programming experience. It gives an overview of the language with an emphasis on practical problem-solving, using examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackling problems in their own research and (2) continue their Python education in a self-directed way. 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. Intended audience

This workshop is aimed at all researchers and technical workers with a background in biology who want to learn programming. The syllabus has been planned with complete beginners in mind; people with previous programming experience are welcome to attend as a refresher but may find the pace a bit slow. If in doubt, take a look at the detailed session content below or drop Martin Jones (martin@pythonforbiologists.com) an email.

Session content

Monday 2nd - Classes from 09:30 to 17:30

Session 1 - Introduction

In this session I introduce the students to Python and explain what we expect them to get out of it and how learning to program can benefit their research. I explain the format of the course and take care of any housekeeping details (like coffee breaks and catering arrangements). I outline the edit-run-fix cycle of software development and talk about how to avoid common text editing errors. In this session, we also check that the computing infrastructure for the rest of the course is in place (e.g. making sure that everybody has an appropriate version of Python installed). Core concepts introduced: source code, text editors, whitespace, syntax and syntax errors, Python versions

Session 2 - Output and text manipulation

In this session students learn to write very simple programs that produce output to the terminal, and in doing so become comfortable with editing and running Python code. This session also introduces many of the technical terms that we'll rely on in future sessions. I run through some examples of tools for working with text and show how they work in the context of biological sequence manipulation. We also cover different types of errors and error messages, and learn how to go about fixing them methodically. Core concepts introduced: terminals, standard output, variables and naming, strings and characters, special characters, output formatting, statements, functions, methods, arguments, comments.

Tuesday 3rd - Classes from 09:30 to 17:30

Session 3 - File IO and user interfaces

I introduce this session by talking about the importance of files in bioinformatics pipelines and workflows, and we then explore the Python interfaces for reading from and writing to files. This involves introducing the idea of types and objects, and a bit of discussion about how Python interacts with the operating system. The practical session is spent combining the techniques from session 2 with the file IO tools to create basic file-processing scripts. Core concepts introduced: objects and classes, paths and folders, relationships between variables and values, text and binary files, newlines.

Session 4 - Flow control 1 : loops

A discussion of the limitations of the techniques learned in session 3 quickly reveals that flow control is required to write more sophisticated file-processing programs, and I introduce the concept of loops. We look at the way in which Python loops work, and how they can be used in a variety of contexts. We explore the use of loops and lists together to tackle some more difficult problems. Core concepts introduced: lists and arrays,

blocks and indentation, variable scoping, iteration and the iteration interface, ranges.

Wednesday 4th - Classes from 09:30 to 17:30

Session 5 -Flow control 2 : conditionals

I use the idea of decision-making as a way to introduce conditional tests, and outline the different building-blocks of conditions before showing how conditions can be combined in an expressive way. We look at the different ways that we can use conditions to control program flow, and how we can structure conditions to keep programs readable. Core concepts introduced: Truth and falsehood, Boolean logic, identity and

— / —

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

Berlin PythonForBiologists Oct2-6 deadline

Dear all,

we have the last 4 spots left for the course “Introduction to Python for biologists”, 2-6 October 2017, Berlin (Germany).

Application deadline is: September 2nd, 2017

Please visit our website to register : <https://www.physalia-courses.org/courses-workshops/course2/>
Instructor:

Dr. Martin Jones (founder, Python for biologists).

<https://www.physalia-courses.org/instructors/t1/>
Course overview

Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at complete beginners and assumes no prior programming experience. It gives an overview of the language with an emphasis on practical problem-solving, using examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackling problems in their own research and (2) continue their Python education in a self-directed way. 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. Intended audience

This workshop is aimed at all researchers and technical workers with a background in biology who want to learn programming. The syllabus has been planned with complete beginners in mind; people with previous programming experience are welcome to attend as a refresher but may find the pace a bit slow. If in doubt, take a look at the detailed session content below or drop Martin Jones (martin@pythonforbiologists.com) an email.

Session content

Monday 2nd - Classes from 09:30 to 17:30

Session 1 - Introduction

In this session I introduce the students to Python and explain what we expect them to get out of it and how learning to program can benefit their research. I explain the format of the course and take care of any housekeeping details (like coffee breaks and catering arrangements). I outline the edit-run-fix cycle of software development and talk about how to avoid common text editing errors. In this session, we also check that the computing infrastructure for the rest of the course is in place (e.g. making sure that everybody has an appropriate version of Python installed). Core concepts introduced: source code, text editors, whitespace, syntax and syntax errors, Python versions

Session 2 - Output and text manipulation

In this session students learn to write very simple programs that produce output to the terminal, and in doing so become comfortable with editing and running Python code. This session also introduces many of the technical terms that we'll rely on in future sessions. I run through some examples of tools for working with text and show how they work in the context of biological sequence manipulation. We also cover different types of errors and error messages, and learn how to go about fixing them methodically. Core concepts introduced: terminals, standard output, variables and naming, strings and characters, special characters, output formatting, statements, functions, methods, arguments, comments.

Tuesday 3rd - Classes from 09:30 to 17:30

Session 3 - File IO and user interfaces

I introduce this session by talking about the importance of files in bioinformatics pipelines and workflows, and we then explore the Python interfaces for reading from and writing to files. This involves introducing the idea of types and objects, and a bit of discussion

about how Python interacts with the operating system. The practical session is spent combining the techniques from session 2 with the file IO tools to create basic file-processing scripts. Core concepts introduced: objects and classes, paths and folders, relationships between variables and values, text and binary files, newlines.

Session 4 - Flow control 1 : loops

A discussion of the limitations of the techniques learned in session 3 quickly reveals that flow control is required to write more sophisticated file-processing programs, and I introduce the concept of loops. We look at the way in which Python loops work, and how they can be used in a variety of contexts. We explore the use of loops and lists together to tackle some more difficult problems. Core concepts introduced: lists and arrays, blocks and indentation, variable scoping, iteration and the iteration interface, ranges.

Wednesday 4th - Classes from 09:30 to 17:30

Session 5 -Flow control 2 : conditionals

I use the idea of decision-making as a way to introduce conditional tests, and outline the different building-blocks of conditions before showing how conditions can be combined in an expressive way. We look at the different ways that we can use conditions to control program flow,

— / —

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>

Berlin StatisticsForBiologistsUsingR Sep18-22

STATISTICS FOR BIOLOGISTS USING R.

<https://www.physalia-courses.org/courses/course13/>
Dates: 18 - 22 September 2017

Instructor: Dr. Ken Aho (Idaho State University) <https://www.physalia-courses.org/instructors/t4/>
Course overview This course will demonstrate the extensive capabilities of the R environment, and seek to develop/broaden the competency of participants in the use of R statistical applications. The course will have two components presented in morning and afternoon sessions over five days. Component one (Monday Sept.

18, Tuesday Sept. 19) will emphasize R programming characteristics including data management, use of existing package functions, graphics, customized function writing, calling routines from compiled languages, and documentation. The second component (Wednesday Sept. 20 - Friday Sept. 22) will address implementation of statistical analyses with R, particularly linear models. I will make frequent use of my library `asbio` (Applied Statistics and Statistical Pedagogy for Biologists), and present the materials using biological examples whenever possible.

Intended audience This course is aimed at scientists, particularly biologists. While no previous experience with R is required, participants should have at least a basic familiarity with statistical terms and concepts.

Curriculum

Monday 18th - Classes from 09:30 to 17:30

Session 1 - R basics In this session we will briefly consider the history of R, including trends in usage and package development, the relationship of R to other languages and platforms, and the reliability of R base and user-contributed packages. We will then learn and conduct basic command line operations, including defining R programming options, saving work, mathematical functions, simple descriptive statistics functions, utilization of expressions and assignments, R-objects and classes, auxiliary R-packages, accessing and exploring internal R datasets, and getting help.

Session 2 - R graphics In this session we consider the properties, capabilities, and extensions of R graphics. Session topics will include discussion of the R graphical devices, learning how to alter parameters to make simple plots and multilayer complex plots (e.g., those containing multiple distinct graphs, multiple y and x-axes, unusual fonts, 3d graphics, etc.), lattice graphics, graphical packages (particularly `ggplot`) and the creation of publication-ready high resolution figures.

Tuesday 19th - Classes from 09:30 to 17:30

Session 3 - Handling data in R The session will address handling data in R. Topics will include properties of R data structures (i.e., vectors, matrices, dataframes, and arrays), command line data entry, importing/exporting delimited spreadsheets and other data, subsetting and querying data, testing and coercing objects, pattern matching, and functions for matrix/dataframe/array management and manipulation.

Session 4 - Writing functions The session will consider user-defined functions using several extended examples. Topics will include looping, graphical animation, the uti-

lization and development of GUIs, and calling routines from compiled languages.

Wednesday 20th - Classes from 09:30 to 17:30

Session 5 - Documentation of work in R and basic applications in statistics

This session will conclude topics in function writing by considering approaches for documenting workflow and function characteristics in R. The session will then turn to the topic of statistical analysis in earnest. Topics will include probability density functions, point estimation (including least squares, maximum likelihood and MOM approaches), and intervallic estimators, including conventional confidence intervals on a priori sampling distribution assumptions, along with bootstrapping approaches and Bayesian credible intervals.

Session 6 - General linear models I We will begin this session by considering simple methods for making inferences concerning the difference in measures of population location parameters, e.g., t-tests and their non-parametric analogues. We will then introduce general linear models with simple and multiple regression. Emphasis will be given to model selection approaches.

Thursday 21st - Classes from 09:30 to 17:30

Session 7 - General linear models II

This session will continue exploration of general linear models by considering ANOVA approaches including one way ANOVAs with fixed and random effects, two way designs including factorial designs and blocked designs as fixed and mixed effect models. We will also consider methods for simultaneous inference for factor level comparisons.

Session 8 - Generalized linear models, locally fitted models, and associated topics

This session will briefly consider R applications for specialized response variables and locally fitted models. Topics will include logistic

— / —

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

Berlin StatisticsForBiologistsUsingR Sep18-22 2

Dear all,

we have the last few spots available for the course “STATISTICS FOR BIOLOGISTS USING R” in Berlin (Germany): <https://www.physalia-courses.org/courses-workshops/course13/> Dates: 18-22 September 2017

Instructor: Dr. Ken Aho. Dr. Aho is an associate professor at Idaho State University (USA) and author of the book “Foundational and Applied Statistics for Biologists Using R.”

Registration deadline: August 18th , 2017. Attendees are seated on a first-come, first-served basis.

Course overview: This course will demonstrate the extensive capabilities of the R environment, and seek to develop/broaden the competency of participants in the use of R statistical applications. The course will have two components presented in morning and afternoon sessions over five days. Component one (Monday Sept. 18, Tuesday Sept. 19) will emphasize R programming characteristics including data management, use of existing package functions, graphics, customized function writing, calling routines from compiled languages, and documentation. The second component (Wednesday Sept. 20 - Friday Sept. 22) will address implementation of statistical analyses with R, particularly linear models. The materials will be presented using biological examples, making frequent use of the library *asbio* (Applied Statistics and Statistical Pedagogy for Biologists).

Intended audience: This course is aimed at scientists, particularly biologists. While no previous experience with R is required, participants should have at least a basic familiarity with statistical terms and concepts.

Course programme: <https://www.physalia-courses.org/courses-workshops/course13/curriculum-13/> Registration: <https://www.physalia-courses.org/courses-workshops/course13/curriculum-13/> Full list of our courses and Workshops: <https://www.physalia-courses.org/courses-workshops/> Best regards,

Carlo

–

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator info@physalia-courses.org <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 15771084054 <https://groups.google.com/forum/#!forum/physalia-courses>
Carlo Pecoraro <info@physalia-courses.org>

cE3c Portugal EvolutionaryBiol Oct-Nov

Subject: Portugal-cE3c-Course: four advanced courses with deadlines October-November 2017

cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the four courses with closer deadlines.

Additional informations at:

<http://ce3c.ciencias.ulisboa.pt/training/?cat> Course Bioinformatics analysis of biological sequences by Teresa Nogueira and Rita Ponce - October 23rd to October 27th 2017 @ Lisbon, Portugal

Objectives This five-days intensive course has as main objective to provide the participants with knowledge about the biological sequences from reliable databases, as well as with autonomy and critical attitude in the use of bioinformatics software freely available in the Internet.

Course INSTRUCTORS Teresa Nogueira (cE3c collaborator) <http://ce3c.ciencias.ulisboa.pt/member/teresanogueira> And Rita Ponce (cE3c collaborator) <https://www.linkedin.com/in/rita-ponce-7189283b> Intended audience: The course will be open to a maximum of 20 students, being directed to PhD or MSc students, post-docs, clinical analysts and other professionals working in Biology, Biochemistry and related topics. Minimum formation: bachelor degree in Biology, Biochemistry or related areas.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below).

Deadline for applications: October 2, 2017

For additional details about the programme of the course, fees and to know how to register, click here, and access the specific course <http://ce3c.ciencias.ulisboa.pt/training/?cat> For more infor-

mation about the course, please contact: teresainogueira@gmail.com

Course Natural History Collections and Biodiversity Organized by Maria Judite Alves, Raquel Barata, Cristiane Bastos-Silveira et al. | November 6th to November 10th 2017 @ Lisbon, Portugal

Objectives This course aims to: - evidence the importance of natural history collections for the study of biodiversity. - show new tools and approaches to extract and disseminate biodiversity data from natural history collections - increase awareness of young researchers for the scientific and culture value of Natural History Museums.

Course coordinator Maria Judite Alves (Researcher at the Centre for Ecology, Evolution and Environmental Changes (cE3c), and MUHNAC- Museu Nacional de História Natural e da Ciência)

<http://ce3c.ciencias.ulisboa.pt/member/maria-judite-silva-cardoso-alves> Intended audience This five days intensive course will be open to a maximum number of 16 participants, being directed to PhD or MSc students in Biology, Evolution, Ecology or related areas, and postdocs and other professionals working in related topics. Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below).

Deadline for applications: October 13, 2017

Candidates should send a short CV and motivation letter to Maria Judite Alves (mjalves@fc.ul.pt)

For additional details about the programme of the course, fees and to know how to register, click here, and access the specific course <http://ce3c.ciencias.ulisboa.pt/training/?cat> For more information about the course, please contact by email: Maria Judite Alves (mjalves@fc.ul.pt) Course Production of Science Communication Activities Organized by Cristina Luís, Filipa Vala & Patricia Garcia Pereira | November 13th to November 17th 2017 @ Lisbon, Portugal

Objectives To introduce participants to the details of communicating science to non-specialized audiences, including, but not exclusive to, public and private stakeholders, students and teachers, and media professionals. The course will particularly address the design, organisation, implementation and impact assessment of public engagement activities such as exhibitions, science festi-

vals or games. At the end of the course, students should be able to develop and produce small-budget events or products to communicate scientific results and ideas.

Course INSTRUCTORS

Cristina Luís (Post-doc at MUHNAC- Museu Nacional de História Natural e da Ciência)

— / —

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>

Crete ComputationalMolEvol May6-17

Dear Community,

The 10th summer school on Computational Molecular Evolution organized by Alexis Stamatakis, Ziheng Yang, Nick Goldman, Cilia Antoniou, and Laura Emery will take place from May 6 - 17 2018 in Crete, Greece again.

Please visit the course web-site for further details, applications are now open. Please feel free to circulate this message.

<http://meetings.embo.org/event/18-computational-evolution> Nick Goldman

Nick Goldman <http://www.ebi.ac.uk/research/goldman>
European Molecular Biology Laboratory tel: +44-(0)1223-492530 European Bioinformatics Institute tel: +44-(0)1223-494522 Wellcome Genome Campus, Hinxton, Cambridge CB10 1SD, UK

CzechRepublic PopulationSpeciationGeomics Jan21-Feb3

We are pleased to announce that we are accepting applications for the 2nd Workshop on Population and Speciation Genomics which is being held once again in beautiful $\tilde{\text{A}}\text{esk}\tilde{\text{A}}\frac{1}{2}$ Krumlov, Czech Republic (https://en.wikipedia.org/wiki/\tilde{\text{A}}\text{esk}\tilde{\text{A}}\frac{1}{2}_Krumlov) from

21 January through 3 February, 2018. More information is below and can be found on our website at <http://evomics.org>. An on-line application form can be found at: <http://evomics.org/registration-form/apply-2018-workshop-on-population-and-speciation-genomics-cesky-krumlov/> 2018 Workshop on Population and Speciation Genomics, \check{A} esk \check{A} $\frac{1}{2}$ Krumlov, Czech Republic

Dates: 21 January - 3 February, 2018

Application Deadline: 15 September, 2017 is the preferred application deadline, after which time people will be admitted to the course following application review by the admissions committee. However, later applications will certainly be considered for admittance or for placement on a waiting list.

Registration Fee: \$1800 USD. Fee includes opening reception and access to all course material, but does not include other meals or housing. Special discounted pricing has been arranged for hotels, pensions and hostels. Information regarding housing and travel will be made to applicants following acceptance.

APPLY HERE: <http://evomics.org/registration-form/apply-2018-workshop-on-population-and-speciation-genomics-cesky-krumlov/> Useful Links: Direct Link to the Full Workshop Schedule: <http://evomics.org/workshops/workshop-on-population-and-speciation-genomics/2018-workshop-on-population-and-speciation-genomics-cesky-krumlov/> General Workshop information: <http://evomics.org> Frequently Asked Questions (FAQ) about the Workshop and \check{A} esk \check{A} $\frac{1}{2}$ Krumlov can be found here: <http://evomics.org/workshops/faq/> Workshop Overview: The Workshop on Population and Speciation Genomics brings together an international collection of faculty members and Workshop participants to study and discuss current ideas and techniques for the analysis of genomic data on the level of populations and closely related species. The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of genomics focusing primarily on the analysis of modern sequencing data. Faculty are chosen exclusively for their effectiveness in teaching theory and practice. The course is designed for established investigators, postdoctoral scholars, and advanced graduate students. Scientists with strong interests in the uses of modern sequence data, analytical methods, and the use of modern sequence data to study populations of closely related species are encouraged to apply for admission. Lectures and computer laboratories total ~90 hours of scheduled instruction. No programming experience is required.

Topics to be covered include: - Introductions to UNIX, R, and Python - Analyzing genomic data in the "cloud"

- Genomics data handling and file formats - RAD (Restriction site Associated DNA) data analysis - Analysis of low-coverage resequencing data - Variant detection - Likelihood and Bayesian inference - Coalescent analyses of population structure and demography - Analysis of adaptation and natural selection - Selective sweep analyses - Detection of introgression and admixture - More!

For more information and online application see the Workshop web site - <http://evomics.org> Scott Handley <handley.scott@gmail.com>

CzechRepublic WorkshoponGenomics Jan7-20

We are pleased to announce that we are accepting applications for the 8th Annual Workshop on Genomics which is being held once again in beautiful \check{A} esk \check{A} $\frac{1}{2}$ Krumlov, Czech Republic (https://en.wikipedia.org/wiki/\check{A}esk\check{A}\frac{1}{2}_Krumlov < https://en.wikipedia.org/wiki/%C4%8Cesk%C3%BD_Krumlov >) from 7-20 January, 2018. More information is below and can be found on our website at <http://evomics.org>. An on-line application form can be found at: <http://evomics.org/registration-form/apply-2018-workshop-on-genomics-cesky-krumlov/> 2018 Workshop on Genomics, \check{A} esk \check{A} $\frac{1}{2}$ Krumlov, Czech Republic

Dates: 7-20 January, 2018

Application Deadline: 15 September, 2017 is the preferred application deadline, after which time people will be admitted to the course following application review by the admissions committee. However, later applications will certainly be considered for admittance or for placement on a waiting list.

Registration Fee: \$1800 USD. Fee includes opening reception and access to all course material, but does not include other meals or housing. Special discounted pricing has been arranged for hotels, pensions and hostels. Information regarding housing and travel will be made to applicants following acceptance.

APPLY HERE: <http://evomics.org/registration-form/apply-2018-workshop-on-genomics-cesky-krumlov/>

Useful Links: Direct Link to the Full Workshop Schedule: <http://evomics.org/workshops/workshop-on-genomics/2018-workshop-on-genomics-cesky-krumlov/> General Workshop information: <http://evomics.org> Frequently Asked Questions (FAQ) about the Workshop

and $\frac{1}{2}$ Krumlov can be found here: <http://evomics.org/workshops/faq/> Workshop Overview: The Workshop on Genomics consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of genomics focusing primarily on the analysis of modern sequencing data. Faculty are chosen exclusively for their effectiveness in teaching theory and practice. The course is designed for established investigators, postdoctoral scholars, and advanced graduate students. Scientists with strong interests in the uses of modern sequence data, analytical methods, and the use of modern sequence data to study non-model organisms, variant detection and analysis, genome visualization tools and related areas are encouraged to apply for admission. Lectures and computer laboratories total ~90 hours of scheduled instruction. No programming experience is required.

Topics to be covered include: - Sequencing technologies - Genomics study design - Manipulation of sequence data using the command-line - Sequence data quality assessment and control - Analyzing genomic data in the "cloud" - Assembly and alignment: basic analyses used for de novo and re-sequencing studies - The use of modern sequence data to study non-model organisms - RNA-seq (using model and non-model organisms) - RAD (Restriction site Associated DNA) sequence analysis - Microbiome sequencing analysis - Evolutionary genomics - More!

For more information and online application see the Workshop web site - <http://evomics.org> Scott Handley <handley.scott@gmail.com>

Groningen ESEB2017 Aug20-25 Drosophila Population Genomics

ESEB 2017 SATELLITE WORKSHOP ON TUESDAY,
22 AUGUST

THE EUROPEAN DROSOPHILA POPULATION GE-
NOMICS CONSORTIUM (DROSEU)

We would like to kindly invite you to participate in a satellite discussion workshop on Drosophila population genomics and evolution, held during the ESEB 2017 meeting in Groningen (16th Congress of the European Society for Evolutionary Biology, 20-25 August 2017; Groningen; <http://www.eseb2017.nl>).

The workshop will be held (contrary to our previous announcement) on Tuesday 22 August between 15:00

and 17:00 in room J.

The workshop is open to all interested ESEB participants/evolutionary biologists.

The main aim of the workshop is to present the work and the objectives of the European Drosophila Population Genomics Consortium (DrosEU), funded by an ESEB Special Topics Network (STN) grant, to the ESEB/evolutionary biology community and to discuss future developments in the field of Drosophila adaptation genomics.

The DrosEU consortium, founded in 2013, consists of approx. 70 scientists from Europe and beyond: over the past few years, we have been sampling and sequencing a large number of European Drosophila melanogaster populations through space and time. The overarching goal of DrosEU is to foster the integration and exchange of population genomic information and data in the Drosophila system and to cooperate closely in collecting, generating and analyzing genomic and environmental data for numerous Drosophila populations across Europe and beyond in order to gain a better understanding of adaptation. DrosEU is also closely collaborating with the US-based Drosophila Real Time Evolution Consortium (Dros-RTEC) (<http://web.sas.upenn.edu/~paul-schmidt-lab/dros-rtec>).

More information on DrosEU can be here: <http://eseb.org/prizes-funding/special-topic-networks/european-drosophila-population-genomics-network-droseu/> or at <https://sites.google.com/site/droseuweb/> We are looking forward to seeing you in Groningen.

Best wishes, Josefa González (Barcelona), Martin Kapun (Lausanne), and Thomas Flatt (Fribourg) on behalf of DrosEU

Contact: josefa.gonzalez@ibe.upf-csic.es martin.kapun@unil.ch thomas.flatt@unifr.ch

— Prof. Thomas Flatt Department of Biology University of Fribourg Chemin du Musée 10 CH-1700 Fribourg Switzerland

E-mail: thomas.flatt@unifr.ch

Tel. Office: +41 26 300 88 33 Tel. Secretary: +41 26 300 88 50 Fax: +41 26 300 97 41

Web1: <https://www.unifr.ch/biology/research/flatt/>

Web2: http://www.unil.ch/dee/page94630_en.html

Mechanisms of Life History Evolution: <http://ukcatalogue.oup.com/product/9780199568765.do>

FLATT Thomas <thomas.flatt@unifr.ch>

Groningen ESEBFundingPolicies Aug24

ESEB 2017 WORKSHOP: SCIENCE POLICIES: HOW SHOULD EVOLUTIONARY BIOLOGY BE FUNDED?

We would like to invite you to participate in a discussion workshop on funding and scientific quality to be held during the upcoming ESEB conference in Groningen (20-25 August 2017).

Open: To all researchers attending the ESEB conference (no additional costs) Time: Thursday, 24 August, 13:30-15:30 Place: Room X Organizers: Stephanie Meirmans and Maurine Neiman

The main goal of our workshop is to trigger a translatable discussion of how funding affects scientific quality, what scientific quality is, and whether and how the current funding system could improve. We invite you as active researchers to participate and make contributions to this discussion. Our workshop focus is particularly topical because of recent changes in how science is funded worldwide: increasingly, funding is both assessed by internal scientific quality and by external criteria such as societal relevance and technological-economic impact. These changes have created across-country differences in funding policies, inviting a critical systematic reflection that could have real impact in a time when funding policies are in a phase of transition in many countries.

The workshop will consist of a short comment on this topic by ESEB founder Stephen Stearns, two panel discussions, and one talk by an internationally recognized invited speaker with direct involvement in research funding, Leslie Rissler (US National Science Foundation). The two panels will consist of Roger Butlin, George Gilchrist, Hanna Kokko, and Stephen Stearns (Panel 1), and Anne Charmantier, Jan Engelstädter, Astrid Groot, Kayla King, Pleuni Pennings and Jane Reid (Panel 2). The audience will be invited to actively participate in the discussion, so please come prepared with questions and insights.

This event is funded by the American Genetic Association (AGA).

We are looking forward to seeing you at our workshop!

Best wishes, Stephanie and Maurine

For organizational purposes, please let the organizers

know as soon as possible that you plan to attend the workshop:

Stephanie Meirmans, Leiden University, Netherlands (s.meirmans@hum.leidenuniv.nl) Maurine Neiman, University of Iowa, USA (maurine-neiman@uiowa.edu)

maurine-neiman@uiowa.edu

Heraklion Crete MetagenomicsBarcoding Mar19-23

Dear colleagues,

Registration is open for the course AN INTRODUCTION TO METAGENOMICS AND METABARCODING.

Dates: March 19-23, 2018.

Place: Heraklion (Crete, Greece).

Instructor: Dr. M. Lisandra Zepeda-Mendoza (Chr. Hansen - Bacterial Physiology & Improvement, Denmark).

Metagenomics is the study of the collection of genomes in an environment. Environments as diverse as Antarctic lakes, hot springs, or the human gut can be biologically characterized by extracting and sequencing DNA from samples taken from them. A characteristic of many of these samples is their complexity, posing difficulties to their analysis and characterization. However, metagenomics allows the taxonomic and functional characterization of samples. These two kinds of characterizations also enable the comparison of different habitats for biodiversity assessment.

In this course students will be introduced to the command line environment used to analyze high-throughput sequencing data (HTS). The initial cleaning steps that must be performed on every HTS dataset will be described and we will use the processed data for proper functional and taxonomical characterization of a metagenomic dataset. We will use methods such as mapping to whole genome databases, de novo assembly, gene annotation, building of non-redundant gene catalogue, and metagenomic species concept identification. Due to the wide usage of metabarcoding for the taxonomic characterization of an environment, we will also discuss amplicon sequencing strategies and data analysis. The course will be based on both theory and hands-on exercises.

More information: <http://www.transmittingscience.org/courses/genetics-and-genomics/introduction-metagenomics-metabarcoding/> or writing to courses.crete@transmittingscience.org

This course is organized by Transmitting Science.

Best regards

Sole

Soledad De Esteban-Trivigno, PhD. Scientific Director Transmitting Science www.transmittingscience.org Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.org>

SICB San Francisco Positive Selection Polar Organisms Jan 3

SICB San Francisco Workshop Positive Selection Polar Organisms Jan 3rd

Workshop Announcement: Best practices for using NGS-based datasets to determine statistically robust evidence of positive selection and convergent evolution of polar organisms.

We will conduct a NSF-funded workshop using cross-disciplinary approaches for determining genetic adaptations in polar organisms using Next Generation Sequencing-based datasets. In particular, this workshop will focus on the following:

- 1) Establish collaborative research groups to test for genes under positive selection from diverse polar organisms using genomic and transcriptomic datasets.
- 2) Evaluate current analytical methods for determining positively selected genes and their statistical significance.
- 3) Explore current and novel methodologies for detecting genetic modifications acquired through convergent evolution in response to similar environmental conditions.
- 4) Review lab-based protocols for demonstrating the potential functions of candidate genes. Specifically, we will focus on techniques amenable to frozen or otherwise preserved samples that can be accomplished at the home institutional laboratory.

We will conduct a full-day meeting (9am-5pm) before the start of the next two conference meetings of the

Society for Integrative and Comparative Biology (San Francisco, CA and Tampa, FL, January 3rd, 2018 and 2019, respectively) with collaborative work among the research groups during the interim period. The requested funds will be used to reimburse the costs of travel to each meeting (up to \$300/meeting), SICB meeting registration, and one night of lodging (up to \$200/meeting), for all workshop participants per meeting. Workshop participants will contribute to a final report summarizing our findings that will be available through the iDigBio website. We will also publish a multi-authored paper based on the relative contributions of participants towards data acquisition, NGS-based analyses, and the review of lab-based protocols.

Prospective participants should have documented research backgrounds in ONE or more of the following categories: 1) NGS-based studies of polar organisms, 2) Methodologies for determining genes under positive selection or showing evidence of convergent evolution (PAML, HyPhy, Phytools, etc.), 3) Phylogenomics of polar organisms, and 4) Physiological adaptations of polar organisms.

To apply please email scott.santagata@liu.edu (due date: 09/06/17) with one attached PDF document containing: A) Current CV and B) One-page description detailing your experience in the research backgrounds listed above, and how this workshop fits into your overall career goals. Graduate students, post-doctoral researchers, and early career investigators from under-represented groups are encouraged to apply. Applications may be accepted after the due date depending on the number of applicants and amount of available funds. The preliminary list of agreed participants currently includes investigators, post-doctoral researchers, and graduate students from Auburn University, California State University-Long Beach, Central Michigan University, Long Island University-Post, University of Alabama-Tuscaloosa, University of California-Santa Barbara, University of Florida, and the University of Hawaii.

Scott Santagata, Associate Professor Department of Biology Life Sciences Building, Room 261 Long Island University-Post Campus 720 Northern Blvd. Greenvale, NY 11548-1300 Phone: 516-299-3029 Email: scott.santagata@liu.edu LIU Website: <http://www.liu.edu/CWPost/Academics/Faculty/Faculty/S/Scott-Santagata> Labpage: <http://sites.google.com/site/scottsantagata/> Researchgate: https://www.researchgate.net/profile/Scott_Santagata Scott Santagata <scott.santagata@liu.edu>

Tokyo EvolutionLife Jan22-Feb2

Application open for the EON/ELSI Winter School 2018

We are excited to announce the 2018 EON/ELSI Winter School on Earth-Life Science, taking place in Tokyo, Japan, on January 22 to February 2nd. This interdisciplinary training course for graduate students and post-docs will include lectures from experts and hands-on training in field techniques and computational approaches, with applications for everything related to Earth-Life Science, from planets to microbes and beyond. If you are interested in the evolution of planets, chemicals or life, this is the school for you.

Applications, available at <http://elsischool.com>, are due on September 15, 2017.

For all selected attendees, all onsite costs in Japan will be covered. Travel funding is available for a limited number of attendees, upon request in the application form. For more information: <http://elsischool.com>
Katie Petrie <ktpetrie@gmail.com>

UHuddersfield ComputingSkills Sep13-15

Next Generation Biologists: Essential Computing Skills for Molecular Biology is a BBSRC-STARs programme-funded project to introduce and train researchers in the essential skills and best practices in scientific computing and bioinformatics. The format of the materials and the nature of the delivery is based on the successful “Software Carpentry” (<http://software-carpentry.org/>) blended-learning model where students learn by developing skills through hands-on live coding and peer programming sessions led by experienced Software Carpentry instructors and supported by a small team of helpers. This is the second workshop in the series.

AUDIENCE The workshop is aimed at researchers with little or no experience in programming and data analysis who nevertheless need these approaches in their research in the life sciences.

ORGANISERS AND INSTRUCTORS The main or-

ganisers of the workshops are Dr Mary J. O’Connell (@Evol_Molly), Dr Martin Callaghan (both at the University of Leeds) and Dr Jarek Bryk (@jarekbryk at the University of Huddersfield). Drs Callaghan and Bryk are Software Carpentry Instructors. The project is a joint initiative of the University of Leeds and the University of Huddersfield.

PRELIMINARY PROGRAMME Monday Introduction to the fundamentals of UNIX, command-line interface and shell.

Tuesday Introduction to fundamentals of R with R Studio, including data and analysis reproducibility, concluded with example analysis of high-throughput data.

Wednesday A “hackathon” day, during which participants will use skills learned in earlier days to solve a real-life data analysis problem of their choosing or a walk-through of an analysis of a real-life dataset using learned skills in shell and R.

DATE The workshop will be run on the 13-15th September 2017 (Wednesday to Friday inclusive).

VENUE The workshop will take place at the University of Huddersfield, UK.

COSTS The workshop is free of charge for all BBSRC-funded researchers, as well as staff and students from the Universities of Leeds and Huddersfield. For all other participants a course fee of 170 will apply that will need to be paid before the workshop begins. Travel and accommodation costs are *not* covered by the organisers.

HOW TO APPLY To apply for a place on the workshop, prepare a maximum one-page long curriculum vitae and a 200 word statement detailing why this course is of particular importance to your current research. Please combine the two *into a single pdf file* and send it to Dr Mary J. O’Connell at [m.oconnell\[at\]leeds.ac.uk](mailto:m.oconnell@leeds.ac.uk) *by midnight 31st August 2017*. The selection committee will notify successful applicants by the end of 1st September. The workshop will be limited to 25 participants, who are expected to bring their own computers on the workshop.

More details about the project and the workshop are available on our website at <http://nextgenbiologists.org>. We are also on Twitter at @nextgenbiol (the “l” is important :-).

– Jarek Bryk School of Applied Sciences University of Huddersfield Queensgate, Huddersfield HD1 3DH Office JP3/17 | Tel. +44 (0) 1484 47 2708 j.bryk@hud.ac.uk | @jarekbryk | bryklab.net | nextgenbiologists.org orcid.org/0000-0002-2791-9709

University of Huddersfield inspiring tomorrow’s professionals.

Jarek Bryk <J.Bryk@hud.ac.uk>

UHuddersfield ComputingSkills Sep13-15 2

Dear colleagues,

this is a reminder that the deadline to apply to our workshop on UNIX Shell and R with RStudio in Huddersfield in September is in less than 2 weeks. More information below and on nextgenbiologists.org <<http://nextgenbiologists.org/>>.

Please apply and spread the news! Regards, Jarek

Next Generation Biologists: Essential Computing Skills for Molecular Biology is a BBSRC-STARs programme-funded project to introduce and train researchers in the essential skills and best practices in scientific computing and bioinformatics. The format of the materials and the nature of the delivery is based on the successful “Software Carpentry” (<http://software-carpentry.org/>) blended-learning model where students learn by developing skills through hands-on live coding and peer programming sessions led by experienced Software Carpentry instructors and supported by a small team of helpers. This is the second workshop in the series.

AUDIENCE The workshop is aimed at researchers with little or no experience in programming and data analysis who nevertheless need these approaches in their research in the life sciences.

ORGANISERS AND INSTRUCTORS The main organisers of the workshops are Dr Mary J. O’Connell (@Evol_Molly), Dr Martin Callaghan (both at the University of Leeds) and Dr Jarek Bryk (@jarekbryk at the University of Huddersfield). Drs Callaghan and Bryk are Software Carpentry Instructors. The project is a joint initiative of the University of Leeds and the University of Huddersfield.

PRELIMINARY PROGRAMME Monday Introduction to the fundamentals of UNIX, command-line interface and shell.

Tuesday Introduction to fundamentals of R with R Studio, including data and analysis reproducibility, concluded with example analysis of high-throughput data.

Wednesday A “hackathon” day, during which participants will use skills learned in earlier days to solve a

real-life data analysis problem of their choosing or a walk-through of an analysis of a real-life dataset using learned skills in shell and R.

DATE The workshop will be run on the 13-15th September 2017 (Wednesday to Friday inclusive).

VENUE The workshop will take place at the University of Huddersfield, UK.

COSTS The workshop is free of charge for all BBSRC-funded researchers, as well as staff and students from the Universities of Leeds and Huddersfield. For all other participants a course fee of 170 will apply that will need to be paid before the workshop begins. Travel and accommodation costs are *not* covered by the organisers.

HOW TO APPLY To apply for a place on the workshop, prepare a maximum one-page long curriculum vitae and a 200 word statement detailing why this course is of particular importance to your current research. Please combine the two *into a single pdf file* and send it to Dr Mary J. O’Connell at [m.oconnell\[at\]leeds.ac.uk](mailto:m.oconnell@leeds.ac.uk) *by midnight 31st August 2017*. The selection committee will notify successful applicants by the end of 1st September. The workshop will be limited to 25 participants, who are expected to bring their own computers on the workshop.

More details about the project and the workshop are available on our website at <http://nextgenbiologists.org>. We are also on Twitter at @nextgenbiol (the “l” is important :-).

– Jarek Bryk School of Applied Sciences University of Huddersfield Queensgate, Huddersfield HD1 3DH Office JP3/17 | Tel. +44 (0) 1484 47 2708 j.bryk@hud.ac.uk | @jarekbryk | bryklab.net | nextgenbiologists.org orcid.org/0000-0002-2791-9709

Jarek Bryk <bryk@evolbio.mpg.de>

UK DataScienceForPopulationGenetics Oct23-27

Course on “Reproducible data science for population genetics” (RDPG01)

This course will be delivered by Dr. Thibaut Jombart who authors the `adegenet` package and Dr. Zhian Kamvar.

www.prstatistics.com/course/reproducible-data-science-for-population-genetics-rdpg01/ This course will run

from the 23rd - 27th October at Margam discovery centre in Wales, United Kingdom.

Course Overview: With the increasing availability of various types of genetic and genomic data, population genetics and molecular ecology are becoming largely data driven sciences. Understanding the evolutionary, demographic, and ecological underpinning the genetic makeup of natural populations now relies on a combination of exploratory approaches and models. This course will provide an in-depth introduction to these techniques, with a strong emphasis on reproducibility through the use of modern analytic practices and tools. After an introduction to phylogenetic reconstruction, the course will cover a number of multivariate approaches for the analysis of genetic patterns, including supervised and unsupervised factorial methods, clustering approaches, and advanced methods for describing population diversity and revealing spatial genetic patterns. The approaches introduced will be applicable to most genetic data, including markers such as microsatellites, SNPs, or AFLP, as well as nucleotide and amino-acid sequence data. Every day will start with a lecture dedicated to a type of problem and methods, followed by an introduction to a specific technique for reproducible data analysis; afternoon will be devoted to hands on practicals. The last day will be devoted to open problems, where participants will be able to analyse their own data.

Monday 23rd - Classes from 09:00 to 17:00 Intro to phylogenetic reconstruction Module 1a: reconstructing phylogenies from genetic sequence data. Three main approaches covered: distance-based phylogenies; maximum parsimony; and likelihood-based approaches. Module 1b: reproducible data science using R: an introduction Practical 1: phylogenetic reconstruction using R. Three main approaches plus rooting a tree; assessing/testing for a molecular clock; and bootstrapping. Main packages: knitr, ape, phangorn.

Tuesday 24th - Classes from 09:00 to 17:00 Introduction to multivariate analysis of genetic data Module 2a: key concepts in multivariate analysis. Focus on using factorial methods for genetic data analysis. Module 2b: using R to generate high-quality pdf or word documents. Practical 2: multivariate analysis of genetic data in R. Topics include: data handling, Hardy-Weinberg tests, measures of diversity, tests of population structure, principal component analysis (PCA), multidimensional scaling (MDS). Main packages: knitr, rmarkdown, adegenet, ade4, pegasa, hierfstat, ape.

Wednesday 25th - Classes from 09:00 to 17:00 Exploring group diversity Module 3a: approaches for identifying and describing genetic clusters. Topics include:

hierarchical clustering, K-means, genetic distances between populations, supervised factorial methods including between-group PCA and the Discriminant Analysis of Principal Components (DAPC). Module 3b: using R to generate beamer and html5 slides. Practical 3: applying the approaches covered in morning lecture and emphasising their strengths and weaknesses. Main packages: rmarkdown, adegenet, ade4, hierfstat.

Thursday 26th - Classes from 09:00 to 17:00 Spatial genetic structures Module 4a: on the origins of spatial genetic patterns, how to test for them, and how to reveal and visualise them. Module 4b: asking questions the right way with reproducible code. Practical 4: visualising and analysing spatial genetic data. Topics: spatial density estimates, univariate and multivariate tests of spatial structure (Moran and Mantel tests), mapping principal components from unsupervised methods (PCA), spatial PCA. Main packages: repress, adegenet, sdep, ade4.

Friday 27th - Classes from 09:00 to 16:00 Reproducible data science for population genetics in practice Open problem day - analyse your own data using R Main packages: knitr, rmarkdown, adegenet, ade4, ape, pegas, phangorn, hierfstat, poppr, ggplot2, etc.

If you have any questions please email oliver-hooker@prstatistics.com or visit www.prstatistics.com/course/reproducible-data-science-for-population-genetics-rdpg01/ Other up-coming courses are as follows

1. SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R #SPA 7th - 12th August 2017, Scotland, Prof. Jason Matthiopoulos, Dr. James Grecian

— / —

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>

UK Modelling Evolution Oct23-27 Scholarships

PARTFUNDED SCHOLARSHIPS for the course “Structural Equation Modelling for Ecologists and Evolutionary Biologists”

PR STATISTICS ARE PLEASED TO ANNOUNCE THAT THROUGH THEIR FUNDING SCHEME

THEY CAN OFFER 5 PART-FUNDED SCHOLARSHIPS FOR OUR UP-COMING COURSE "Structural Equation Modelling for Ecologists and Evolutionary Biologists (SEMR01)"

SCHOLARSHIPS CONTRIBUTE TOWARDS COURSE FEES WITH 5 PLACES AVAILABLE AT £405.00 (Fees have been subsidised by 40% from £670.00).

Applications should be sent to oliver-hooker@prstatistics.com and contain the following. 1. Full name 2. Institute name 3. PhD subject title or Post doc research questions 4. Do you hold a funded position 5. 150 words why this course would be relevant to your research or how it would help.

Application deadline is Tuesday 12th September 2017 and decisions will be made by Thursday 14th September 2017

We still have a few places available for anyone else interested.

Full course details are given below

"Structural Equation Modelling for Ecologists and Evolutionary Biologists"

Delivered by Dr. Jarret Byrnes and Dr. Jon Lefcheck

www.prstatistics.com/course/structural-equation-modelling-for-ecologists-and-evolutionary-biologists-semr01/ This course will run from 23rd - 27th October 2017 at Margam Park Discovery Centre, Wales, UK

Course only and all inclusive packages are available.

The course is a primer on structural equation modelling (SEM) and confirmatory path analysis, with an emphasis on practical skills and applications to real-world data.

Structural Equation Modelling (SEM) is a rapidly growing technique in ecology and evolution that unites multiple hypotheses in a single causal network. It provides an intuitive graphical representation of relationships among variables, underpinned by well-described mathematical estimation procedures. Several advances in SEM over the past few years have expanded its utility for typical ecological datasets, which include count data, missing observations, and nested or hierarchical designs. We will cover the basic philosophy behind SEM, provide approachable mathematical explanations of the techniques, and cover recent extensions to mixed effects models and non-normal distributions. Along the way, we will work through many examples from the primary literature using the open-source statistical software R (www.r-project.org). We will draw on two popular R packages for conducting SEM, including lavaan and

piecewiseSEM. Participants are encouraged to bring their own data, as there will be opportunities throughout the course to plan, analyse, and receive feedback on structural equation models.

Course content is as follows

Day 1 Introduction to SEM Module 1: What is Structural Equation Modeling? Why would I use it? Module 2: Creating multivariate causal models Module 3: Fitting piecewise models Readings: Grace 2010 (overview), Whalen et al. 2013 (example)

Day 2 SEM Using Likelihood Module 4: Fitting Observed Variable models with covariance structures Module 5: What does it mean to evaluate a multivariate hypothesis? Module 6: Latent Variable models Module 7: ANCOVA revisited & Nonlinearities Readings: Grace & Bollen 2005, Shipley 2004 Optional Reading: Pearl 2012, Pearl 2009 (causality)

Day 3 Piecewise SEM Module 8: Introduction to piecewise approach Module 9: Incorporation of random effects models Model 10: Autocorrelation Reading: Shipley 2009; Lefcheck 2016

Day 4 Advanced Topics with Likelihood and Piecewise SEM Module 11: Multigroup models and nonlinearities Module 12: Composite Variables Module 13: Phylogenetically-correlated data Module 14: Prediction using SEM Module 15: How To Reject A Paper That Uses SEM Readings: Grace & Julia 1999, von Hardenberg & Gonzalez 2013

Day 5 Open Lab and Final Presentations

Please email any inquiries to oliver-hooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

Other up-coming courses are as follows

1. ECOLOGICAL NICHE MODELLING USING R #ENMR 16th - 20th October 2017, Scotland, Dr. Neftali Sillero <http://www.prstatistics.com/course/ecological-niche-modelling-using-r-enmr01/>
2. REPRODUCIBLE DATA SCIENCE FOR POPULATION GENETICS 23rd - 27th October, Wales, Dr. Thibaut Jombart, Zhian Kavar <http://www.prstatistics.com/course/genetic-data-analysis-exploration-using-r-gdar03/>
3. STRUCTURAL EQUATION MODELLING FOR ECOLOGISTS AND EVOLUTIONARY BIOLOGISTS USING R #SEMR

— / —

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 Population Genetics Using R Oct23-27 Scholarships

PARTFUNDED SCHOLARSHIPS for the course “Reproducible data science for population genetics”

PR STATISTICS ARE PLEASED TO ANNOUNCE THAT THROUGH THEIR FUNDING SCHEME THEY CAN OFFER 5 PART-FUNDED SCHOLARSHIPS FOR OUR UP-COMING COURSE “Reproducible data science for population genetics” (RDPG01)

SCHOLARSHIPS CONTRIBUTE TOWARDS COURSE FEES WITH 5 PLACES AVAILABLE AT 50.00 (Fees have been subsidised by 40% from 580.00).

Applications should be sent to oliver-hooker@prstatistics.com and contain the following. 1. Full name 2. Institute name 3. PhD subject title or Post doc research questions 4. Do you hold a funded position 5. 150 words why this course would be relevant to your research or how it would help.

Application deadline is Sunday 3rd September 2017 and decisions will be made by Tuesday 5th September 2017

We still have ‘normal’ places available for anyone else interested.

Full course details are given below

Course on “Reproducible data science for population genetics” (RDPG01)

This course will be delivered by Dr. Thibaut Jombart who authors the *ade4* package and Dr. Zhian Kamvar.

www.prstatistics.com/course/reproducible-data-science-for-population-genetics-rdpg01/ This course will run from the 23rd - 27th October at Margam discovery centre in Wales, United Kingdom.

Course Overview: With the increasing availability of various types of genetic and genomic data, population genetics and molecular ecology are becoming largely data driven sciences. Understanding the evolutionary, demographic, and ecological underpinning the genetic makeup of natural populations now relies on a combination of exploratory approaches and models. This course will provide an in-depth introduction to these techniques, with a strong emphasis on reproducibility though the use of modern analytic practices and tools.

After an introduction to phylogenetic reconstruction, the course will cover a number of multivariate approaches for the analysis of genetic patterns, including supervised and unsupervised factorial methods, clustering approaches, and advanced methods for describing population diversity and revealing spatial genetic patterns. The approaches introduced will be applicable to most genetic data, including markers such as microsatellites, SNPs, or AFLP, as well as nucleotide and amino-acid sequence data. Every day will start with a lecture dedicated to a type of problem and methods, followed by an introduction to a specific technique for reproducible data analysis; afternoon will be devoted to hands on practicals. The last day will be devoted to open problems, where participants will be able to analyse their own data.

Monday 23rd - Classes from 09:00 to 17:00 Intro to phylogenetic reconstruction Module 1a: reconstructing phylogenies from genetic sequence data. Three main approaches covered: distance-based phylogenies; maximum parsimony; and likelihood-based approaches. Module 1b: reproducible data science using R: an introduction Practical 1: phylogenetic reconstruction using R. Three main approaches plus rooting a tree; assessing/testing for a molecular clock; and bootstrapping. Main packages: *knitr*, *ape*, *phangorn*.

Tuesday 24th - Classes from 09:00 to 17:00 Introduction to multivariate analysis of genetic data Module 2a: key concepts in multivariate analysis. Focus on using factorial methods for genetic data analysis. Module 2b: using R to generate high-quality pdf or word documents. Practical 2: multivariate analysis of genetic data in R. Topics include: data handling, Hardy-Weinberg tests, measures of diversity, tests of population structure, principal component analysis (PCA), multidimensional scaling (MDS). Main packages: *knitr*, *rmarkdown*, *ade4*, *ade4*, *pegasa*, *hierfstat*, *ape*.

Wednesday 25th - Classes from 09:00 to 17:00 Exploring group diversity Module 3a: approaches for identifying and describing genetic clusters. Topics include: hierarchical clustering, K-means, genetic distances between populations, supervised factorial methods including between-group PCA and the Discriminant Analysis of Principal Components (DAPC). Module 3b: using R to generate beamer and html5 slides. Practical 3: applying the approaches covered in morning lecture and emphasising their strengths and weaknesses. Main packages: *rmarkdown*, *ade4*, *ade4*, *hierfstat*.

Thursday 26th - Classes from 09:00 to 17:00 Spatial genetic structures Module 4a: on the origins of spatial genetic patterns, how to test for them, and how to reveal and visualise them. Module 4b: asking questions

the right way with reproducible code. Practical 4: visualising and analysing spatial genetic data. Topics: spatial density estimates, univariate and multivariate tests of spatial structure (Moran and Mantel tests), mapping principal components from unsupervised methods (PCA), spatial PCA.

— / —

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>

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.